```
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A,Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
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                                                                                                                                                                                                                                               A;Cross-references: GB:J04353; NID:g333048; PIDN:AAA46950.1; PID:g4
C;Comment: This protein may be involved in the oncogenic potential
C;Cuperfamily: papillomavirus Eorite
C;Keywords: DNA binding; early protein; zinc finger
F;30-66/Region: zinc finger CCCC motif
F;103-139/Region: zinc finger CCCC motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Title: Nucleotide sequence of human papillomavirus type 31: a cervical neoplasia-assoc
A; Reference number: A94398; MULD:89299478; PMID:2545036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Accession: A32444
R; Goldsborough, M.D
Virology 171, 306-3
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Nature 408, 816-820, 2000
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R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-War-2001 #sequence_revision 02-Mar-2001 #text_change 27-Nov-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           B
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                                                                                                                                                                                                                                                                                                                                                                                                          A; Residues: 1-149 <GOL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Accession: A32444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:AE005172; NID:g5103820; PIDN:AAD39650.1; GSPUB:GN00141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Residues: 1-1451 <STO>
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                                                  15 LSSALEIPYDE 25
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                                                                                                                                                                             Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            yrough, M.D.; Disilvestre, D.; Temple, G.F.; Lorincz, A.T.
171, 306-311, 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                       translation not shown
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54.5%;
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                                                                                                                                                                          74.5%;
63.6%;
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    Mismatches

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Pred. No.
                                                                                                                                                                          Score 35; DB 1; Length 149; Pred. No. 5.1;
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                                                                                                                                                                                                                                                                                                                                                                               PIDN: AAA46950.1; PID: 9459916
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A; Molecule type: DNA
A; Residues: 1-381 < KUZ>
                                                                     A; Reference number: 220836; MUID:99124785; PMID:9887315
A; Accession: T30452
                                                                                                                  A: Title: Sequence and analysis of the genome of a baculovirus pathogenic for Lymantz)
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                                          preliminary; translated from GB/EMBL/DDBJ
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RESULT 10

A:Cross-references: EMBL:AF081810; NID:g3822234; PIDN:AAC70288.1; PID:g3822337

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Biosci. Biotechnol. Blochem. 64, 1416-1421, 2000
A;Title: Pyrithiamin resistance gene (ptrA) of Aspergillus oryzae: Cloning, character
A;Reference number: JC7337; MUID:20399355; PMID:10945258
A;Accession: JC7337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        thiazole biosynthetic enzyme - Aspergillus oryzae N;Alternate names: pyrithiamin resistance protein C;Species: Aspergillus oryzae
                                                                    hypothetical protein ORF102 - Lymantria dispar nuclear polyhedrosis virus C;Species: Lymantria dispar nuclear polyhedrosis virus, LdMMPV C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 21-Jul-2000 C;Accession: T30452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.;
; Bowman, C.; Garland, S.; Fujii, C.; Colton, M.D.; Horst, K.; Roberts, K.; Hatch,
Nature 390, 580-586, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          conserved hypothetical protein BB0267 - Lyme disease spirochete
C:Species: Borrelia burgdorferi (Lyme disease spirochete)
C:Date: 13-Fbb-1998 #scquence_revision 13-Feb-1998 #text_change 08-Oct-1999
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C:Superfamily: thiamin biosynthesis protein thil
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A; Residues: 1-327 < KUB>
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C;Accession: JC7337
R;Kuzlo, J.; Pearson, M.N.; Harwood, S.H.; Funk, C.J.; Evans, J.T.; Slavicek, J.M.; Horrology 253, 17-34, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Experimental source: strain 831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:AE001137; GB:AE000783; NID:g2688160; PIDN:AAC66681.1; PID:g26
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A; Residues: 1-634 <KLH>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Authors: Smith, H.O.; Venter, J.C.
A; Title: Genomic sequence of a lyme disease spirochaete, Borrelia burgdorferi
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Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Yn
C.; Garland, S.; Fujii, C.; Colton, M.D.; Horst, K.; Roberts, K.; Hatch, B
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6; Conserv
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75.0%;
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C;Superfamily: DNA-directed DNA polymerase I
C;Keywords: nucleotidyltransferase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; MaS.; Smith, H.O.; Venter, J.C.; Fraser, C.M. Science 286, 1571-1577, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Reference number: A40597; MUID:93273728; PMID:8501062
A;Accession: A40597
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A; Introns: 201/3; 221/3; 287/1; 410/3; 551/1; 672/3; 723/3
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A;Molecule type: DNA
A;Residues: 1-738 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 04-Mar-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               B
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                                                                                             A; Map position:
                                                                                                                                                 A; Gene: DR1707
                                                                                                                                                                                                C; Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUID:20036896; PMID:10567266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: EMBL:L14581; NID:g290067; PIDN:AAC36974.1; PID:g290068
A;Experimental source: strain R1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-921 <GUT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Superfamily: Caenorhabditis elegans hypothetical protein Y66A7A.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Map position:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: T27289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           submitted to the EMBL Data Library, October 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R; Matthews,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Accession:
                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Accession: E75363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R; Gutman, P.D.; Fuchs, P.; Ouyang, I..; Minton, K.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Experimental source: clone Y66A7A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: EMBL:AL032622; PIDN:CAA21499.1; GSPDB:GNC0021; CESP:Y66A7A.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Reference number: Z20338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein Y66A7A.5 - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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Matches 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
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75.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 50;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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Search completed: January 15, 2003, 12:37:13
Job time : 19.1429 secs
                                                                                                 Db
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                                                                                                                                                                                                                                                                                                                                                                                               A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                    A; Accession: AB1440
                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maltournam, A.; ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehla A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Accession: AB1440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        b
                                                                                                                                                                                                                                                                                                            A; Experimental source: strain Clip11262
                                                                                                                                                                                                                                                                                                                              A;Cross-references: GB:AL592022; PIDN:CAC95290.1; PID:g16412478; GSPDB:GN00178
                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Science 294, 849-852,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Species: Listeria innocua
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein lin0057 [imported] - Listeria innocua (strain Clip11262)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AB1440
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                                                                                                                                                                                Matches
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                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dominguez~Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Jones,
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                                                                                                 221 LFDELEFPYEE 231
                                                                                                                                                                                Local Similarity les 7; Conserv
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Pred. No. 65;
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                                                                                                                                                                                                                           Length 233;
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Result
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Maximum Match 100%
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Database
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  Pred. No. is the number of results predicted by chance to have a score greater than or Equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score
 Query
Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BLOSUM62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   112892 seqs, 41476328 residues
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Y103_METUA
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P19821;
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MEDLINE-96016150; PubMed=7568114;
KOrolev S., Nayal M. Barnes W.M., di Cera E., Waksman G.;
"Crystal structure of the large fragment of Thermus aquaticus polymerase I at 2.5-A resolution: structural basis for thermostability.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-89197950; PubMed-2649500;
MEDLINE-89197950; PubMed-2649500;
Stoffel S., Saiki R.K., Myambo K.,
"Crystal structures of open and closed forms of binary and ternary complexes of the large fragment of Thermus aquaticus DNA polymerase
                                                                                                                                                   EOM S.H., Wang J., Steitz T.A.; "Structure of Tag polymerase with DNA Nature 382:278-281(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kim Y., Eom S.H., Wang J., Lee D.-S., Suh S.W., Steitz T.A., "Crystal structure of Thermus aquaticus DNA polymerase.";
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                                                                       X-RAY CRYSTALLOGRAPHY (2.3 ANGSTR MEDLINE-99077817; PubMed-9857206;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=95204371; PubMed=7896728; Ishino Y., Ueno T., Miyagi M., Ue
                                                                                                                                                                                                                             MEDLINE=96353982; PubMed=8717047;
                                                                                                                                                                                                                                                        X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS)
                                                                                                                                                                                                                                                                                                       Proc. Natl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 376:612-616(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=95364959; PubMed=7637814;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Isolation, characterization, and expression in Escherichia coli of the DNA polymerase gene from Thermus aquaticus.";
J. Biol. Chem. 264:6427-6437(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=271;
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01-FEB-1991 (Rel. 17, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
DNA polymerase I, thermostable (EC 2.7.7.7) (Tag polymerase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TIGREAMS; TIGRO0593; pola; 1.
PROSITE; PS00447; DNA_POLYMERASE_A; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Overproduction of Thermus aquaticus DNA polymerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS).
                                                    Y., Korolev S., Waksman G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LSXELX1PYEE
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vs; TIGR00593; pola;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            analysis by ion-spray . 116:1019-1024(1994).
                                                                                                                                                                                                                                                                                                       Acad. Sci. U.S.A. 92:9264-9268(1995).
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SMART; SM00278; HhH1; 1.
SMART; SM00279; HhH2; 1.
SMART; SM00482; POLAC; 1
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           PROSITE: PS00447; DNA_POLYMERASE_A; 1.
Transferase; DNA-directed DNA polymerase; DNA replication;
DNA-binding; 3D-structure.
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InterPro;
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SMART; SM00475; 53EXOC; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                properties of dideoxynucleotide incorporation.";
Proc. Natl. Acad. Sci. U.S.A. 96:9491-9496(1999).
-!- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=99380545; PubMed=10449720; Li Y., Mitaxov V., Waksman G.;
                                                 FIGREAMS; TIGRO0593; pola; 1
                                                                                                               PRINTS;
                                                                                                                                        Pfam;
                                                                                                                                                                InterPro;
                                                                                                                                                                            InterPro;
                                                                                                                                                                                                               InterPro;
                                                                                                                                                                                                                              InterPro;
                                                                                                                                                                                                                                                                                                                                        , gdd
                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the European Biointormatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -1- BIOTECHNOLOGY: Used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Li Y., Mitaxov V., Waksman G.; "Structure-based design of Tag DNA polymerases with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            X-RAY CRYSTALLOGRAPHY (2.30 ANGSTROMS) OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  dynamics of the enzyme."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fab: the Fab is directed against an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Crystal structure of "lag DNA polymerase in complex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Murali R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS). MEDILINE=98445410; Pubmed=9770525;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Crystal structures of the Klenow fragment of Thermus aquaticus DNA polymerase I complexed with deoxyribonucleoside triphosphates."; Protein Sci. 7:1116-1123(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS)
MEDLINE-98266352; PubMed-9605316;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            I: structural basis for nucleotide EMBO J. 17:7514-7525(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Proc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     thermostability. Has a relatively high error rate became exonuclease proofreading functionality.

SIMILARITY: BELONGS TO THE DNA POLYMERASE TYPE-A FAMILY
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                                                                                                                                                                                                                                                                                                   4KTQ;
                                                                                                                                                                                                                                                                                                                            1KTQ;
2KTQ;
~KTQ;
                                                                                                                                                                                                                                                                                                                                                                  1'FAQ;
                                                                                                                                                                                                                                                                                                                                                                                         A33530; A33530.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                         1BGX;
                                                                                                                                                                                                                                                                                                                                                                                                    J04639;
D32013;
                                                                                                           PF01367; 5_3_exonuclease;
PF02739; 5_3_exonuc_N; 1.
S; PR00868; DNAPOLI.
                                                                                                                                                 PF00476; DNA_pol_A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Natl. Acad. Sci. U.S.A. 95:12562-12567(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kong Y., Korolev S., Waksman G.;
                                                                                                                                                              IPR003584; HHH_2
                                                                                                                                                                            IPR003583;
                                                                                                                                                                                                          IPR001098; DNA_pol.
                                                                                                                                                                                                                             JPR002421;
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22-DEF 99.
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22-DEF 99.
30-SEF 98.
14-OCF 98.
12-MAR-97.
16-AUG-99.
                                                                                                                                                                                                     IPR002298;
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16-AUG-99.
                                                                                                                                                                                                                                                                                                                                                               07-DEC-96.
11-APR-97.
                                                                                                                                                                                                                                                                                                                                                                                                    AAA27507.1;
BAA06775.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                            HHH_1
                                                                                                                                                                                     Exo_N_I.
                                                                                                                                                                                                 DNA_poli.
                                                                                                                                                                                                                       _3_exonuclease.
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POLYMERASE (BY SIMILARITY)
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                       DNA repair;
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DPOL_THECA DI
                                                                                                                      SMART; SM00475; 53EXOC; 1.
SMART; SM00278; HhH1; 1.
SMART; SM00279; HhH2; 1.
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SEQUENCE
                                                                                               SMART; SM00279;
SMART; SM00482;
                                                                                                                                                                                                                                                                                                  InterPro; IPR001098; DNA_pol.
InterPro; IPR002298; DNA_polI.
InterPro; IPR005213; Exc.N.I.
InterPro; IPR003583; HHH_1.
InterPro; IPR003584; HHH_2.
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                                                                                                                                                                                                 Pfam; PF00476; DNA_pol_A; 1.
Pfam; PF01367; 5_3_exonuclease;
Pfam; PF02739; 5_3_exonuclease;
Pfam; PF02739; 5_3_exonucle.N; 1.
PRINTS; PR00868; DNAPOLI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation between the Swiss Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eur. J. Bic. em. 214:135-140(1993).

-i- FUNCTION: THERMOSTABLE ENZYME THAT HAS 5'-TO-3' EXONUCLEASE
-ACTIVITY AND NO 3'-TO-5' EXONUCLEASE ACTIVITY.

-i- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate - N diphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSSP; P19821; 1TAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U62584; AAB81398.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            + {DNA}(N).
-!- SIMILARITY: BELONGS TO THE DNA POLYMERASE TYPE-A FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=93285135; PubMed=8508785; Park J.H., Kim J.S., Kwon S.-T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kwon S.-T., Kim J.S.,
Submitted (AUG-1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Thermus caldophilus.
Bacteria; Thermus/Deinococcus
                     Transferase; DNA-directed DNA polymerase; DNA replication; DNA repair;
                                                    PROSITE; PS00447; DNA_POLYMERASE_A; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Purification and characterization of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 1-21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=GK24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=272;
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                                                                          TIGR00593;
                                                                                                                                                                                                                                                                                                                                                                                                                                 IPR002421; 5_3_exonuclease.
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to the EMBL/GenBank/DDBJ databases.
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Pred. No. 0.19;
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F1731055B5246F03 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Thermus caldophilus
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Matches
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                                                                                                                                                                                                                         PRINTS; PRO0868; DNAPOLI.
SMART; SM00475; 53EXOC; 1.
SMART; SM00278; HhH1; 1.
SMART; SM00279; HhH2; 1.
SMART; SM00482; POLAC; 1.
                                                                                                                                                                                                                                                                                                                                    Pfam; PF00476; DNA_pol_A; 1. Pfam; PF01367; 5_3_exonuclease; Pfam; PF02739; 5_3_exonuc_N; 1.
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SEQUENCE
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01-OCT-1996 (Rel.
15-JUN-2002 (Rel.
                                                                                                                                    DNA-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entities requires a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Cloning, nucleotide sequence, and expression in Escherichia coli of DNA polymerase gene (polA) from Therms thermophilus HBB.";

J. Ferment. Biceen. 76:265-269(1997)

-i- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate — N diphosphate
                                                                                            SEQUENCE
                                                                                                                 DOMAIN
                                                                                                                                                       Transferase; DNA-directed DNA polymerase; DNA replication;
                                                                                                                                                                                 TIGRFAMS; TIGR00593; pola; 1.
PROSITE; PS00447; DNA_POLYMERASE_A; 1.
                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR003584; HHH_2
                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSSP; P19821;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the European Bioinformatics Institute. use by non-profit institutions as 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -1- SIMILARITY: BELONGS TO THE DNA POLYMERASE TYPE-A FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Urabe I.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Asakura K., Komatsubara H., Soga S., Yomo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-HB8 /
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN-HB8 / ATCC 27634;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=274;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Thermus/Deinococcus group; Deinococci; Thermales,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Thermus thermophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA polymerase 1,
                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       D28878; BAA06033.1; -.
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9; Conserv
    Similarity
9; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                        IPR002298;
IPR000513;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1PR001098; DNA_FOI
                                                                                                                                                                                                                                                                                                                                                                                                                                     IPR003583; HHH_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IPR002421; 5_3_exonuclease.
                                                                                          834 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              834 AA;
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    Conservative
                                                                                                                 412
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34, Created)
34, Last sequence update)
41, Last annotation update)
thermostable (EC 2.7.7.7) (Tth polymerase 1).
                                                                                                                 834
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93798 MW;
                                                                                          94049 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   license agreement (See http://www.isb-sib.ch/announce/
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institutions as long as its content
                       93.6%;
81.8%;
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                                          Score 44;
                                                                                                            POLYMERASE (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 44; DB 1;
Pred. No. 0.19;
                     Pred. No. 0.19;
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                                                                                       1A98145DC11A54A9
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Mismatches
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                                          DB 1;
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5
                                          Length 834;
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                                                                                       CRC64;
  Indels
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                                                                                                                                                         DNA repair;
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1 LSXELXIPYEE 11

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680 LSQELAIPYEE

690

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RESULT 5
CG18_YEAST
ID CG18_YEAST
AC P38794;
RESULT 6

WE6_HPV31

ID VE6_J

AC P1731

AC P1731

AC P1731

DT 01-AL

DT 15-UI

DE E6 E1

GN E6.

OS HUMBLE

OC VIRUS

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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                        VE6_HPV31
P17386;
01-AUG-1990
01-AUG-1990
15-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Dover J., Du Z., Favello A., Fulton L., Gattung S., Geisel C., Kirsten J., Kucaba T., Hillier L., Jier M., Johnston L., Langston Y., Latreille P., Louis E.J., Macri C., Mardis E., Menezes S., Mouser L., Nhan M., Rifkin L., Riles L., St Peter H., Trevaskis E., Vaughan K., Vignati D., Wilcox L., Wohldman P., Waterston R., Wilson R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-FEB-1395 (Rel. 31, Created)
01-FEB-1395 (Rel. 31, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
G1/S-specific cyclin PCL5.
PCL5 OR YHF '71W.
Papillomavirus
                      Viruses; dsDNA viruses,
                                                  Human papillomavirus
                                                                                                              E6 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cyclin; Cell cycle; Cell division SEQUENCE 229 AA; 26467 MW; B6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00134; cyclin; 1.
SMART; SM00385; CYCLIN; 1.
PROSITE; PS00292; CYCLINS; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Complete nucleotide sequence of Saccharomyces cerevisiae chromosome \mathtt{VIII."}\,;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Saccharomycetales; Saccharomycetaceae; Saccharomyces NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR; S46696; S46696.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; U00061; AAB68375.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SIMILARITY: BELONGS TO THE CYCLIN FAMILY. MOST SIMILAR TO G1/S-SPECIFIC CYCLINS. PCE1 AND PCL2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Science 265:2077-2082(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE~94378003; PubMed=8091229;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Saccharomyces cerevisiae (Baker's yeast)
                                                                                                                                                                                                                                                                                                                                                                                                                     174 LNYELAIPYDE 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SGD; S0001113; PCL5.
InterPro; IPR004366; Cyclin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 LSXELXIPYEE 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       l Similarity
7; Conserve
                                                                                                                                        (Rel. 15, Created)
(Rel. 15, Last seq
(Rel. 41, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                   STANDARD;
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                                               type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       80.9%;
                                                                                                                                           Last sequence update)
Last annotation update)
                         no RNA stage; Papillomaviridae;
                                                     31
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                                                                                                                                                                                                                                                                   PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            B6839ABB9DB5DD49 CRC64;
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                                                                                                                                                                                                                                                                   149 AA
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Best Local :
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Virology 17:306-311(1989).
-i- FUNCTION: THIS PROTEIN MAX BE INVOLVED IN THE ONCOGENIC POTENTIAL OF THIS VIRUS (CERVICAL NEOPLASIA-ASSOCIATED VIRUS).
-i- FUNCTION: EXHIBIT A STRONG, BUT NON SPECIFIC AFFINITY FOR DOUBLE STRANDED DNA (IN VITRO).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oncogene.
ZN_FING
ZN_FING
SEQUENCE
       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the BMHL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                               Biosci. Biotechnol. Biochem. 64:1416-1421(2000).
-i- FUNCTION: INVOLVED IN BIOSYNTHESIS OF "AB THIAMINE PRECURSOR
                                                                                                                                                                 Characterization and application as a dominant selectable marker transformation.";
                                                                                                                                                                                                                                                                                                                                                                     Q9UUZ9;
16-0CT-2001 (Rel. 40, Crested)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last ampolation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ASPOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commer
                                                                                 Kubodera T., Yamashita N., Nishimura A.; "Pyrithiamine resistance gene (ptrA) of Aspergillus oryzae: cloning,
                                                                                                                                                                                                                                                                                                                                                           16-0CT-2001 (Rel. 40, Last annotation update)
Thiazole biosynthetic enzyme, mitochondrial precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; J04353; AAA46950.1; -. PIR; A32444; W6WL31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                         MEDLINE=20399355; PubMed=10945258;
                                                                                                                                                                                                                                            STRAIN-HL1134
                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes; Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
                                                                                                                                                                                                                                                                                                                                                  THIA OR PTRA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Early protein; DNA-binding; Nuclear protein;
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                                                                                                                                                                                                                                                                                     NCBI_TaxID=5062;
                                                                                                                                                                                                                                                                                                                                   Aspergillus oryzae
                                                                                                                                                                                                                                                                                                                                                                                                                                           THI4_ASPOR
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103
149 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
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63.6%;
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l; Mismatches
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Best Local
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DPO1_DEIRA
P52027;
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                  "Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.";
Science 286:1571-1577(1999).
-i- FUNCTION: IN ADDITION TO POLYMERASE ACTIVITY, THIS DNA POLYMERASE ACTIVITY (BY EXHIBITS 3' TO 5' AND 5' TO 3' EXONUCLEASE ACTIVITY (BY
                                                                                                                                                                                                                                                                                                                                          MEDLINE-20036896; PubMed-10567266;
White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Feterson J.D., Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L., Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Shen M., Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M., Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M., Wamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C., Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.I. Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.I. Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C., Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-OCT-1996 (Rel. 34, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
DNA polymerase I (BC 2.7.7.7) (POL I).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NP_BIND
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF01946; Thi4; 1.
TIGRFAMS; TIGR00292; Thi4; 1.
                                                                                                                                                                                                                                                                                                                              Fraser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-R1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Identification, sequencing, and targeted mutagenesis of polymerase gene required for the extreme radioresistance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Deinococcus radiodurans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Deinococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gutman P.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-R1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Deinococcaceae; Deinococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Thermus/Deimococcus group; Deinococci; Deinococcales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POLA OR DR1707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Thiamine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF217503; AAF25444.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE~93273728; PubMed=8501062;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRANSIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                138 ELGVPYEE 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteriol. 175:3581-3590(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 ELXIPYEE 11
                                                                                                                                            SIMILARITY: BELONGS TO THE DNA POLYMERASE TYPE-A FAMILY.
                                                                                                                                                                                           SIMILARITY).
CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
                                                                                                                                                                                [DNA](N).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                l Similarity
6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       s requires a license agreement (See http://www.isb-sib.ch/announce/
an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   biosynthesis; Mitochondrion; Transit peptide; FAI

MITOCHONDRION (POTENVIAL).

P 327

THIAZOLE BIOSYNTHETIC ENZYME.

P 107

FAD OR NAD (POTENVIAL).

327 AA; 35099 MW; 7C561EE06742B2AE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IPR002922; Thi4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              radiodurans.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fuchs P., Ouyang L., Minton K.W.;
                                                                                                                                                                 SINGLE-CHAIN MONOMER WITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  74.5%;
75.0%;
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1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
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                                                                                                                                                                 MULTIPLE FUNCTIONS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 327
                                                                                                                                                                                                                                                       THIS DNA POLYMERASE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA
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                                                                                                                                                                                                                                                                                                                                                                R.D.
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RESULT 9
THI4_YEAST
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00476; DNA_PO1_A; 1.
Pfam; PF0737; 5_3_exonuclesse; 1.
Pfam; PF02739; 5_3_exonuc_N; 1.
PRINTS; PR00868; DNAPOLI.
SMART; SM00475; 53EXOC; 1.
SMART; SM00278; HhH1; 1.
SMART; SM00279; HhH2; 1.
SMART; SM00279; HhH2; 1.
SMART; SM00482; POLAC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CONFLICT
CONFLICT
CONFLICT
CONFLICT
"The sequence of a 27 kb segment on the right arm of chromosome from Saccharomyces cerevisiae reveals MOL1, NAT2, RPL30B, RSR1, PEM1/CHO2, NSR1 genes and ten new open reading for the pemily of the sequence 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-007-1993 (Rel. 27, Created)
01-007-1993 (Rel. 27, Last sequence update)
16-007-2091 (Rel. 40, Last annotation update)
Thiazole biosynthetic enzyme, mitorhondrial precursor.
TH14 OR MOLI OK MS935 OR YOK1444W OR G6620.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  THI4_YEAST
P32318;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hydrolase;
CONFLICT
                                                                  MEDLINE=96158062; PubMed=8585325;
Skala J., Nawrocki A., Goffeau A.
                                                                                                                                                                                                                                                                                                       Praekelt U.M., Meacock "MOL1, a Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                        Saccharomycetales;
NCBI_TaxID-4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Saccharomyces cerevisiae (Haker's yeast).
Eukaryola; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSSP;
                                                                                                             STRAIN-S288C
                                                                                                                                                               Nawrocki A., del Bino S., Goffeau A.;
Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                         early
                                                                                                                                                                                                                                                                                                                          MEDLINE=93070608; PubMed=1441749;
Praekelt U.M., Meacock P.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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InterPro; IPR003583; HHH_1.
InterPro; IPR003584; HHH_2.
                                                                                                                            SEQUENCE OF 205-326
                                                                                                                                                                                                          van Dyck
                                                                                                                                                                                                                                                                  Yeast
                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               L14581; AAC36974.1;
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                                                                                                                                                                                 Skala J.,
del Bino
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                                                                                                                                                                                                                                                                                                                                                                                                                           Saccharomycetaceae; Saccharomyces
                                                                                                                            FROM
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                                                                                                                                                                                   de Wergifosse
S., Goffeau A.;
                                                                                                                            N.A.
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T -> A (IN KEF. 1)
H -> D (IN KEF. 1)
F -> L (IN REF. 1)
P -> R (IN REF. 1)
P -> R (IN REF. 1)
P -> R (IN REF. 1)
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l; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6ABBF117D75AB84A
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                                                                                                                                                                                                    Purnelle B., Talla
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA repair;
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                        CYS4,
                                                                                                                                                                                                                                                                                                     in
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RESULT 10
MOEA_SYNY3
ID MOEA_SYNY3
ID MOEA_SYNY3
AC Q55368
AC Q55368
OT 01-NOV
DT 01-NOV
DT 16-OCT
DE MO1ybd
GN MOEA O
OS Synech
OC Bacter
OC Bacter
RN [1]
RP SEQUEN
RX MEDLIN
                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                             2
                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
Matches 6; Conser
                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                              01-NOV-1997 (Rel.
01-NOV-1997 (Rel.
16-OCT-2001 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                       Synechocystis sp. (strain Bacteria; Cyanobacteria; C
                                                                                    Molybdopterin biosynthesis protein moeA. MOEA or SIR0900.
MEDLINE=96127529;
                                         NCBI_TaxID=1148;
                                                                                                                                                            Q55368;
                                                                                                                                                                            MOEA_SYNY3
                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                     NP_BIND
                                                                                                                                                                                                                                                                                                                                                                                                  CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                             TIGRFAMS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- MISCELLANEOUS: EXPRESSED AT HIGH LEVELS IN THE I
PHASE OF BATCH CULTURES GROWING ON MOLASSES, AN
-!- SIMILARITY: BELONGS TO THE THI4 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SUBCELLULAR LOCATION: Mitochondrial (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            J. Mol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       damage tolerance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Machado C.R., Praekelt U.M., de Oliveira R.C.,
Byrne K.L., Meacock P.A., Menck C.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=98035046; PubMed=9367751;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Praekelt U.M., Byrne K.L., Meacock P.A.;
"Regulation of THI4 (MOL1), a thiamine-biosynthetic gene
Saccharomyces cerevisiae.";
               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                TRANSIT
                                                                                                                                                                                                                                                                                                                                                                                                                               Thiamine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION IN DNA DAMAGE TOLERANCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Dual role for the yeast THI4 gene in thiamine biosynthesis and DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yeast 10:481-490(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=95028146; PubMed=7941734;
                                                                                                                                                                                                                                                   128 ELEIPYED 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      THIAMINE REGULATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Yeast 11:1421-1427(1995)
[4]
                                                                                                                                                                                                                                                                             4 ELXIPYEE 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3L; X51669; CAA43843.1; -.
3L; X5807; CAA59802.1; -.
3L; Z72929; CAA597157.1; -.
3L; Z72930; CAA97159.1; -.
3L; S27321; S25321.
325321; S25321.
325321; S25321.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FUNCTION: INVOLVED IN BIOSYNTHESIS OF THE THIAMINE PATHIAZOLE. ALSO SEEMS TO HAVE A ROLE IN MITOCHONDRIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOLERANCE
                                                                                                                                                                                                                                                                                                                                                                                                                                          PF01946; Thi4; 1.
AMS; TIGR00292; Thi4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                          biosynthesis; Mitochondrion; Transit peptide; FAD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IPR002922; Thi4.
                                                                                                                                                                                                                                                                                                                                                                   67
326 AA;
                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            273:114-121(1997)
                                                                                                                                                                            STANDARD;
                                                                                                                35,
40,
PubMed=8590279
                                                                                                                                                                                                                                                                                                                                                                   326 T
97 F
; 34991 MW;
                                                                                                                                                                                                                                                                                                                        70.2%;
75.0%;
                                                                                                                Last sequence u
                                                       Chroococcales; Synechocystis
                                                                      PCC 6803)
                                                                                                                              sequence update)
                                                                                                                                                                                                                                                                                                            <u>سر</u>
                                                                                                                                                                                                                                                                                                                        Score 33; DB
Pred. No. 14;
                                                                                                                                                                                                                                                                                                                                                                               THIAZOLE BIOSYNTHETIC ENZYME FAD OR NAD (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                              MITOCHONDRION (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                   843790F2CE00BF02 CRC64;
                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                         390 AA
                                                                                                                 update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OF THE THIAMINE PRECURSOR
                                                                                                                                                                                                                                                                                                                                       DB 1;
                                                                                                                                                                                                                                                                                                                                      Length 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Barbosa
                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EARLY STATIONARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INDUSTRIAL MEDIUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA DAMAGE
                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                          Caps
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ALD DESCRIPTION OF THE PROPERTY OF THE PROPERT
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Y103_M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local S
Matches 6
                                                                                                                                                                                              MEDININE-9637999; pubMed-8688089; Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D., Sutton G.G., Blake J.A., FilzGerald L.M., Clayton R.A., Gocayne J.D., Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I., Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A., Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D., Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.M., Hanna M.C., Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M., Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C., Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C., Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Y103_METJA
Q57567;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  METJA
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TIGRRAMS; TICR00177; molyb_syn; 1.
PROSITE; PS01079; MOCF_BIOSYNTHESIS_2; 1.
Molybdenum cofactor biosynthesis; Complete proteome SEQUENCE 390 AA; 43394 MW; 848183B5610CA314 CRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-JAL-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR005111; MoeA_C InterPro; IPR005110; MoeA_N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA Res. 2:153-166(1995).
-I- FUNCTION: INVOLVED IN THE BIOSYNTHESIS OF A DEMOLYBDO-COFACTOR (MOLYBDOPTERIN), NECESSARY FOR MOLYBDO-ENZYMES (BY SIMILARITY).
-I- PATHMAY: MOLYBDENUM COPACTOR BIOSYNTHESIS (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. 1. Sequence features in the 1 Mb region from map positions 64% to 92% of the genome.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID~2190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Methanocaldococcaceae; Methanocaldococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Archaea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the European
                                                                                                             -!- SIMILARITY: BELONGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kaneko T., Tanaka A., Sato
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   103
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                                                                                    273:1058-1073(1996).
ILARITY: BELONGS TO THE UPF0063 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IPR001453;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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Bioinformatics Institute. There a
-profit institutions as long as i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    / DSM 2661 / ATCC 43067;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         35, Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Mismatches
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Pred. No. 17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sazuka T., Miyajima
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Best Local
                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the RMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
Potassium Channel subfamily K member 5 (Acid-sensitive potassium channel protein TASK-2) (TWIK-related acid-sensitive K+ channel 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CIW5_HUMAN 095279;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                       Genew;
                                                                                                                                                    EMBL; AF084830; AAC79458.1; -.
                                                        InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   channel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Reyes R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=99030343; PubMed=9812978;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KCNK5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein; Complete proteome.
SEQUENCE 433 AA; 49866 MW; F82576531DF12142 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TIGR; MJ0103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; U67467; AAB98083.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Cloning and expression of a novel pH-sensitive two pore domain channel from human kidney.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lazdunski
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Kidney;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF01444; MoaA_NifB_PqqE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000385; MoaA_NifB_PqqE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               33 EVEIPYEE 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 ELXIPYEE 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: Integral membrane protein (Potential).
TISSUE SPECIFICITY: ABUNDANT EXPRESSION IN KIDNEY, ALSO DETENTIAL TUVER, PLACEMA AND SMALL INTESTINE. IN THE KIDNEY, EXPRESTIS RESTRICTED TO THE DISTAL TUBULES AND COLLECTING DUCTS. NO EXPRESSED IN PROXIMAL TUBULES OR GLOMERULI.

MISCELLANEOUS: INHIBITED BY QUININE, QUININDINE AND EXTERNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACIDIFICATION. SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHANNELS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBUNIT: HOMODIMER (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        K+ CONCENTRATIONS
                                                                                              603493;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OR TASK2
                                                                                                                       HGNC: 6280;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , Duprat F., Lesage F., Fink M., Salinas M., Farman N.,
IPR003280;
IPR001622;
IPR000636;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Human).-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
K+channel_pore.
M+channel_nlg.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          70.2%;
75.0%;
                                                           K+channel_2pore
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 33; DB
Pred. No. 19;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DВ
19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KIDNEY, ALSO DETECTED THE KIDNEY, EXPRESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DUCTS. NOT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               <u>~</u>
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InterPro;

,InterPro; MEROPS; C04.005;

IPRO01730; Peptidase_C4

PIR; EMBL; D00615;

JQ0494; JQ0494.

BAA00490.1;

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RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                             01-FMB-1991 (Rel. 17, Created)
01-FBB-1991 (Rel. 17, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
Genome polyprotein [Contains: Nuclear inclusion protein A (NI-A) (NIA)
(EC 3.4.22.44) (49 kDa proteinase) (49 kDa-Pro); Nuclear inclusion protein B (NI-B) (NIB) (RNA-directed RNA polymerase) (EC 2.7.7.48);
                                                    modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                               use
                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                            Coat protein (CP)] (Fragme Ornithogalum mosaic virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00520; ion_trans; 1. PRINTS; PR01333; 2POREKCHANEL.
                                                                                                                                                                                                                        .;
                                                                                                                                                                                                                                         also cleaved.
-i- CATALYTIC ACTIVITY: N sucleoside triphosphate = N diphosphate
                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                   Potyvirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID~12204;
                                                                                                                                                                                                                                                                                                                                                                                                                               Viruses; ssRNA positive-strand viruses, no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P20234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POLG_OMV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ionic channel; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 ELXIPYEE 11
                                                                                                                                                                                                         PIM: THE VIRAL RNA OF POTYVIRUSES IS EXPRESSED AS A SINGLE POLYPROTEIN WHICH UNDERGOES POSTTRANSLATIONAL PROTECLYFIC
                                                                                                                                                        PROCESSING RESULTING IN THE PRODUCTION OF AT LEAST EIGHT INDIVIDUAL PROTEINS.
SIMILARITY: NI-A PROTEINASE BELONGS TO PEDTIDASE FAMILY C4
SIMILARITY: BELONGS TO THE POTYVIRUSES POLYPROTEIN FAMILY.
                                                                                                                                                                                                                                                                     oligopeptides containing the appropriate consensus sequence are
                                                                                                                                                                                                                                    (RNA)(N)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ELSVPYEQ 485
                                                                                              non-prolit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    499 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1
85
113
134
158
190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                77
112
1133
1157
1180
2150
2150
3257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   55130
                                                                                              institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                70.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ¥.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. . .) (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PORE-FORMING 1 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CYTOPLASMIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PORE-FORMING 2 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ion transport; Potassium transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E871A7A4823DDA00 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (POTENTIAL)
                                                                                            as its content
                                                                                                                                                                                                                                                                                                                                                                                                                              DNA stage; Potyviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ₩.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ٠.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 499
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                              ПО
                                                                                              way
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RESULT 14
Y928_METJA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
"head 6; Conserve
밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DR DR DR DR FT FT SQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Y928_METJA STANDARE
Q58338;
15-JUL-1998 (Rel. 36, C
15-JUL-1998 (Rel. 36, I
16-CCT-2001 (Rel. 40, I
                                                                                                                                                                                                                                                                                                                                                  STRAIN=JAL-1 / DSM 2661 / ATCC 43067;

MEDLINE=96337999; PubMed=8683087;

Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,

Button G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,

Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,

Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,

Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nquyen D.,

Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Blauna M.C.,

Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,

Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;

"Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam;
                       Pfam; PF02475; Met_10; 1.
TIGRFAMS; TIGR00537; hemK_rel_arch; 1.
PROSITE: PS00092; N6_MTASE; UNKNOWN_1.
                                                                                                                                                                                       use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical protein MJ0928 MJ0928.
                                                                                                                                                            EMBL; U67536;
                                                                                                                                                                                                                                     the European Bioinformatics Institute. Thuse by non-profit institutions as long
                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Archaea; Euryarchaeota; Methanococci; Meth Methanocaldococcaceae; Methanocaldococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Coat protein; Polyprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam;
           Hypothetical protein; Transferase; Methyltransferase;
                                                                                   InterPro;
                                                                                                  InterPro;
                                                                                                                 REBASE; 4480;
                                                                                                                                                                                                                                                                                                                               Science 273:1058-1073(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=2190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Methanococcus jannaschii
                                                                                                                                                                                                                                                                                                               -!- SIMILARITY: BELONGS TO THE HEMK FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    698 KLSIPYEE 705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 ELXIPYEE 11
                                                                                                                              , Q58292;
, MJ0928;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pr00680; RNA_dep_RNA_po1; 1.
Pr00767; Poty_coat; 1.
Pr00863; Peptidase_C4; 1.
Pr00863; Pransferase; Thiol protease; RNA-directed RNA polymerase;
                                         PF02475; Met_10; AMS; TIGR00537; h
                                                                       IPR003402; Unk_Met10.
                                                                                  IPR004557; HemK_rel_arch IPR000051; SAM_bind.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IPR001592; Poty_coat.
IPR001205; RNA_pol_P3D.
IPR001254; Ser_protease_Try.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         366
884
1136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                 M.MjaHemKP
                                                                                                                                                            AAB98930.1;
                                                                                                                                                lbus.
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75.0%;
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Last annotation updat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               annotation update)
(M.MjaHemkP).
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Pred. No.
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ong as its content is in no
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Best Local
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30-MAY-2000
15-JUN-2002
                                  sterol biosynthesis; Peroxisome; Megnesium.

ACT_SITE 86 86 pv cruzz---
                                                                                                                                                                             entities requires a license agreement (See http://www.isb-sib.ch/aunounce/or send an email to license@isb-sib.ch).
                                                                                                                                MIM;
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  SEQUENCE
                                                                                                                                                        EMBL; X17025;
                                                                                                                                                                                                        modified and this statement is not removed.
                                                                                                                                                                                                                                   the European Bioinformatics Institute.
                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-96400329; PubMed-8806705;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "A human promyelocyte mRNA transiently induced by TPA is homologous to yeast IPP isomerase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q13907
                                                                                        Pfam; PF00293; NUDIX;
                                                                                                     InterPro; IPR002667; IPP_isomerase.
InterPro; IPR000086; NUDIX_hydrolas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHARACTERIZATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Xuan J.W., Kowalski
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. MEDLINE-94292171; PubMed-8020941;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-MAY-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
1sopentenyl-diphosphate delta-isomerase 1 (BC 5.3.3.2) (IPP isomerase
1) (Isopentenyl pyrophosphate isomerase 1) (IPPI1).
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                                                                                                                                             Genew;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         178 ISARLKVPFEE 188
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                                                                                                                                                                                                                                                                                                   PATHWAY: ISOPHENOID BY SYNTHETIC PATHWAY WHOSE END PRODUCTS INCLUDE DAILCHOLS, VITAMINS A. F. E. AND K. STEROID HORMONES. CAROTEMOLDS HILE ACTUS AND CHOLSTERROL.
SUBCELLULAR DACATION: PETOXISORAL.
                                                                                                                                                                                                                                                                                                                                                                               HOMOALLYLIC SUBSTRATE ISOPENTENYL (IPP) TO ITS HIGHLY ELECTROPHILIC ALLYLIC ISOMER, DIMETHYLALLYL DIPHOSPHATE (DMAPP). CATALYTIC ACTIVITY: Isopentenyl diphosphate = dimethylallyl
                                                                                                                                                                                                                                                                                      SIMILARITY: BELONGS TO THE IPP ISOMERASE TYPE I FAMILY.
                                                                                                                                                                                                                                                                                                                                                       COFACTOR: REQUIRES MAGNESIUM FOR ACTIVITY
                                                                                                                                                                                                                                                                                                                                                                       diphosphate.
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225
227 AA;
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                                                                                                                                                       CAA34890.1; ALT_INIT.
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39, Last sec
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227
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 26319 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                    rmatics Institute. There are no restrictions on institutions as long as its content is in no
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45.5%;
                                                                                                  NUDIX_hydrolase.
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Pred. No.
           BY SIMILARITY.
BY SIMILARITY.
MICROBODY TARGETING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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Query Match
68.1%; Score 32; DB 1; Length 227;
Best Local Similarity 63.6%; Pred. No. 16;
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 1 LSXELXIPVEE 11
| | | | | | | |
Db 112 LKAELGIPLEE 122

Search completed: January 15, 2003, 11:21:19
Job time: 11.2857 secs
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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence:
                                                                                                                                                                                                                               Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                Score
  length: 0
length: 2000000000
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1: sp_archea:*
2: sp_bacteria
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11:
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16:
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 80.9
78.7
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                                                                                                                                                                                                                                                                                                                                                 sp_phage:*
sp_plant:*
                                                                                                                                                                                                                                                                                                                                                                      sp_mhc:*
sp_organelle:*
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                                                                                                                                                                                                                                                                                                                                                                                             sp_mamma1:*
                                                                                                                                                                                                                                                                                                                                                                                                        sp_invertebrate:*
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                                                                                                                                                                                                                                                                                                                                                                                                                         sp_fungi:**
                                                                                                                                                                                                                                                                                   sp_unclassified:*
sp_rvirus:*
sp_bacteriap:*
                                                                                                                                                                                                                                                                                                                            sp_rodent:*
sp_virus:*
                                                                                                                                                                                                                                                                            sp_archeap: *
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                                                                                                                                                                                Length
 850
474
1451
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274
291
381
7381
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233
461
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  16
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2 Q9YMM5
Q9XWY5
Q9ZFP6
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Q8YAQ3
Q989F3
Q9Q4W5
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1 P97528
1 Q94849
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Q9UQ52
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Q8U6Z1
Q9XI48
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                                                                         Q8RB89
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(without alignments)
88.635 Million cell updates/sec
                  Q8rb89 thermoanaer
Q9ymm5 lymantria d
Q9xwy5 caenorhabdi
Q9zfp6 listeria in
Q8yaq3 listeria mo
Q8yaq3 rhizobium l
                                                                                                              Q8u6z1 agrobacteri
Q9xi48 arabidopsis
Q44755 borrelia bu
Q9uq52 homo sapien
                                                                                Q9jmb8 mus musculu
P97528 rattus norv
Q94849 drosophila
Q9q4w5
Q9jk62
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Q8u6z1 agrobacteri
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153	151	144	144	1890	1493	1234	1085	634	627	469	417	412	402	359	346	228	228	228	199	186	153	153	132	4717	1056	697	692	597
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Q9РFJ3	Q9PUC3	Q8Y4X6	Q92FK3	049528	067512	Q24690	Q24363	Q8S9X6	Q8SVP8	030094	Q9V1T1	Q8TZZ4	Q9YA31	015268	Q93NQ2	Q9BQ74	Q8WUX8	Q961Z4	9MMN6	Q8U8F0	Q8Y3I4	092607	Q9ZQG2	094248	Q8REF7	Q8TJQ4	Q97YM6	059717
Q9pfj3 xylella fas		Q8y4x6 listeria mo	Q92fk3 listeria in		K Y		drosophila		O		Q9v1t1 pyrococcus	pyrococcus	1 aero		esche	homo	homo	homo	homo sapien		listeria		N		Q8ref7 fusobacteri		7 ym6	059717 schizosacch

ALIGNMENTS

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RESULT 1
066691
                                                                                                                                                              A CONTRACTOR OF THE CONTRACTOR
       Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                      InterPro; IPR001993; Mitoch_carrier.
Pfam; PF00563; EAL; 1.
Pfam; PF00990; GGDEF; 1.
SMART; SM00267; DUF1; 1.
SMART; SM00052; DUF2; 1.
TIGRFAMS; TIGR00254; GGDEF; 1.
PROSITE; PS00215; MITOCH_CARRIER; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L., Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay M., Huber Feldman R.A., Short J.M., Olson G.J., Swanson R.V.; "The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-AUG-1998 (TrEMBLrel. 07, 01-AUG-1998 (TrEMBLrel. 07, 01-JUN-2002 (TrEMBLrel. 21, Hypothetical protein AQ_367.
                                                                                                                                                      Hypothetical protein; Complete proteome. SEQUENCE 850 AA; 97669 MW; C02DCEF91DBCDEB0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001633; EAL.
InterPro; IPR000160; GGDEF.
InterPro; IPR001993; Mitoch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Aquificae; Aquificales; Aquificaceae; Aquifex.NCBI_TaxID=63363;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 392:353-358(1998).
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       Conservative
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                                           80.9%;
54.5%;
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Last annotation update)
3; Mismatches
                                           Score 38; DB 16; Length 850; Pred. No. 15;
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   Indels
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   Gaps
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RESULT
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AC Q9
AC Q9
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DT 01
DT 01
DT 02
CG FG
CG AL
CC SI
OC EL
CC GC EL
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ID Q8
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                                                                                                                                               Q9XI48;
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Q8U6Z1;
Q8U6Z1;
Q8U6Z1;
Q8U6Z1;
Q1-JUN-2002 (TrEMBLrel. 21, Created)
Q1-JUN-2002 (TrEMBLrel. 21, Last sequence update)
Q1-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae: Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons: core eu
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                  F9L1.15 protein. F9L1.15.
                                                                                             01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                         "Genome sequence of the plant pathogen and Agrobacterium tumefaciens C58."; Science 294:2323-2328(2001). EMBL; AE009395; AAL45459.1; ALT_INIT. EMBL; AE008220; AAK88782.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M., Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L., Houniel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F., Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B., Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G., Ciolo C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F., Chen Y., Paulsen I.T., Elsen J.A., Karp P.D., Bovee D.
                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Agrobacterium tumefaciens
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                        Complete proteome.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "The genome of the natural genetic engineer Agrobacterium tumefaciens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=176299;
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LAHDLDIPYEE 210
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7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                              53483 MW;
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63.6%;
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                                                                                                                                                                                                                                                                                                               Mismatches
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Rhizobiaceae group;
                  core eudicots;
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                                  Tracheophyta;
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Best Local
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01-NOV-1996
01-DEC-2001
                                                                                                                                                                                                                                              Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A., Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwinn M. Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D., Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., Hanson M., van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman J., Utterback T., Watthey L., McDonald L., Artiach P., Bowman C., Garland S., Fujii C., Cotton M.D., Horst K., Roberts K., Hatch B., Smith H.O., Venter J.C.; "Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Vysotskaia V.S., Schwartz J.R., Yu G., Toriumi M., Lenz C., I Lee J., Liu A., Li J., Kremenetskaia I., Luros J., Gonzalez A Altafi H., Araujo R., Brooks S., Buehler B., Chao Q., Conn L. Conway A.B., Dunn P., Hansen N., Huizar L., Khan S., Kim C., Rowley D., Shinn P., Walker M., Davis R.W., Ecker J.R., Todaronial N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-ATCC 35210 / B31;
Dunn J.J., Butler-Loffredo L., Kieleczawa J., Medalle J.,
Submitted (DEC-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                              Complete proteome. SEQUENCE 634 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN-ATCC 35210 / B31;
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STRAIN-ATCC 35210 / B31;
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1451 AA;
                                                                                                                                                                                             Nature 390:580-586(1997).
EMBL; U43739; AAA85591.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=98065943; PubMed=9403685;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Borrelia burgdorferi
Bacteria; Spirochaeta
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00005; ABC_tran; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases EMBL, AC007591; AAD39650.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=139;
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InterPro; IPR003439; ABC_transportr.
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                                                                                                                                               AE001137; AAC66681.1;
BB0267; -.
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SM00382; AAA; 1.
  Similarity 6; Conser
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                                                                                                 70752 MW;
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54.5%;
                       74.5%;
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Last annotation update)
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                         Score 35;
Pred. No.
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                                                                                              E8AFB112B121F3B8 CRC64;
ed. No. 48;
Mismatches
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                                              16;
                                           Length 634;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Luft B.J.;
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                                                                                                                                                                                                                                                                                                           Q9_MB8;
Q1-OCT-2000 (TrEMBLrel. 15, Created)
O1-OCT-2000 (TrEMBLrel. 15, Last sequence update)
O1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
O1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                        "Expression and regulation of a gene encoding neural recognition molecule NB-3 of the contactin/F3 subgroup in mouse brain."; Gene 245:253-266(2000).
                                                                                              SEQUENCE FROM N.A.
STRAIN=129SVJ; TISSUE-BRAIN;
MEDLINE=20183687; PubMed=10717476;
Lee S., Takeda Y., Kawano H., Hosoya H.,
Takahashi N., Watanabe K.;
                           EMBL; AB032602; BAA92367.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00041; fn3; 4. —
Pfam; PF00047; ig; 6. —
SMART; SM00060; FN3; 3.
SMART; SM00408; IGC2; 5.
SMART; SM00410; IG_like; 1.
PROSITE; PS00211; ABC_TRANSPORTER; UNKNOWN_1.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
    HSSP; P20241; 1CFB.
                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                              NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                            Mus musculus (Mouse).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE-98146168; PubMed=9486763;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HNB-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Neural adhesion molecule NB-3.
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les 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 SXE.XIPYEE 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P20241;
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AB003592; BAA82612.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IPR003439; ABC_transportr
IPR003961; FN_III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IPR003006; Ig_MHC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IPR003598; Ig_c2.
IPR003600; Ig_like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1028 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            74.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       113956 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Taketani Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 35;
Pred. No. 8
2; Mismatch
                                                                                                                                                                                                                                               Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                       1028 AA
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                                                                                                                         Nomoto M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2;
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                                                                                                                         Fujimoto D.,
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RESULT 8
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ID Q948
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RESULT 7
P97528
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Best Local &
Matches
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Best Local
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01-MAY-1997
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                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN=WISTAR; TISSUE=BRAIN;
STRAIN=WISTAR; TISSUE=BRAIN;
MEDLINE=97101230; PubMed=8945756;
MODAWA J., Kaneko H., Masuda T., Nagata S., Hosoya H., Watanabe K.;
"Novel neural adhesion molecules in the Contactin/F3 subgroup of the immunoglobulin superfamily: Isolation and characterization of cDNAs from rat brain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR003598; Ig_c2.
InterPro; IPR003600; Ig_like.
InterPro; IPR0036016; Ig_MHC.
Pfam; PF00041; In3; 4.
Pfam; PF00047; ig; 6.
                                                                                                                    SEQUENCE
                                                                                                                                                                             SMART; SM00060; FN3; 4.
SMART; SM00408; IGC2; 5
                                                                                                                                                                                                         Pfam; PF00041; fn3; 4. Pfam; PF00047; iq; 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa;
Mammalia; Eutheria;
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PROSITE; PS00290; IG_MHC; UNKNOWN_1.
Immunoglobulin domain.
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SMART; SM00408; IGC2; 5.
SMART; SM00410; IG_like; 1
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                                                                                                                                                  PROSITE;
                                                                                                                                                             SMART; SM00410; IG_like; 1
                                                                                                                                                                                                                                     InterPro; IPR003598; Iq_c2.
InterPro; IPR003600; Ig_like.
InterPro; IPR003006; Ig_MHC.
                                                                                                                                                                                                                                                                                                                  Neurosci. Lett. 218:173-1
EMBL; D87248; HAA13320.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus norvegicus (Rat)
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InterPro; IPR003961; FN_III.
                                                                                                                               PROSITE; PS00211; ABC
                                                                                                                                                                                                                                                                      InterPro; IPR003598;
                                                                                                                                                                                                                                                                                   InterPro; IPR003439; ABC_transport..
InterPro; IPR003961; FN_III.
 959
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tes 6; Conserv
                            2 SXELXIPYEE 11
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SAELLVPFEE 968
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                                                          Similarity 6; Conserv
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7 (TrEMBLrel.
1 (TrEMBLrel.
                                                                                                                    1028 AA;
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                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                218:173-176(1996).
                                                                                                                                             ABC_TRANSPORTER; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chordata; Craniata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae; Rat
                                                                     74.5%;
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                                                                                                                  114065 MW;
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19,
                                                       Score 35; DB
Pred. No. 80;
2; Mismatches
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Last annotation update)
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                                                                                                                 47EFD8A370CF4923 CRC64;
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                                                                                   DB 11; Length 1028;
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PRELIMINARY;

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RESULT
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Best Local
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Best Local
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01-JUN-2001
                                                                                                                                                                                                                                             EMBL;
                                                                                                                                                                                                                                                                                            MEDLINE=21992816; PubMed=11997336;
Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Don Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X.,
Tan H., Chen R., Wang J., Yu J., Yang H.;
"A complete sequence of T. tengcongensis genome.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Thermoanaerobacter tengcongensis.
Bacteria; Firmicutes; Bacillus/Clostridium group; (
Thermoanaerobacteriales; Thermoanaerobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Branched-chain amino acid aminotransferase/4-amino-4-deoxychorismate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Pattern of ecological shifts in the diversification of Hawaiian Drosophi.a inferred from a molecular phylogeny."; Cur. Biol. 5:1129-1139(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila buzzatii (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN-MB4T / JCM11007;
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                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                      Transferase;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FlyBase; FBgn0016167; Dbuz\Yp1.
InterPro; IPR000734; Lipase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases. EMBL; U52126; AAC47249.1; -
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01-FEB-1997
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                              1 LSXELXIPYEE 11
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AE013059; AAM24189.1; -
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                                                                                                         Similarity
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                                                                                                                                                                                             291 AA;
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                                                                                      Conservative
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                                                                                                                                                                                          Aminotransferase; Complete proteome.
91 AA; 32346 MW; 105072D27AB06FFE CRC64;
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                                                                                   Score 34;
Pred. No.
3; Mismato
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                                                                                      Mismatches
                                                                                                                                   34;
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33;
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                                                                                                                                        16;
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                                                                                                                                     Length 291;
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; Thermoanaerobacter.
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                                                                                   Caps
                                                                                   0;
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RESULT 10
Q9YMM5
ID Q9YMM
AC Q9YMM
DT 01-MA
DT 01-DE
DE LJOORF
OS LYMBAD
OC LYMBAD
OC NUCLE
OX NCCL
RN [1]
RN [1]
RA KUZIO
RT LYMBAD
RT LYMBAD
RT LYMBAD
RT LYBRAD
RT 
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                            Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.
Craxton M., Dear S., Du Z., Duzbin R., Favello A., Fulton L.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen I
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OL-NOV-1999 (TrEMBLIE]. 12, 01-NOV-1999 (TrEMBLIE]. 12, 01-JUN-2001 (TrEMBLIE]. 17, V66874 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LdOrf-102 peptide.
Lymantria dispar multicapsid nuclear polyhedrosis virus (LdMNPV).
Viruses: dsDNA viruses, no RNA stage; Baculoviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Nemato
Rhabditidae; Peloderinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9XWY5;
01-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9XWY5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kuzio J., Pearson M.N.,
Slavicek J.M., Rohrmann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-1999 (TrEMBLrel. 10,
01-MAY-1999 (TrEMBLrel. 10,
01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SWWA60
Nature 368:32-38(1994).
[3]
                                                          elegans
                                                                watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
elegans.";
                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE=94150718; Pubmed=7906398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Y66A7A.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Y66A7A.5 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCB1_TaxID=10449;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9YMM5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matthews
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (MAR-1999) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Sequence and analysis of the genome of a baculovirus pathogenic for 
Lymantria dispar.";
Virology 253:17-34(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE-99124785; PubMed-9887315;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41 ELDLPYEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 ELXIPYEE 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IARELNIPFEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AF081810; AAC70288.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    381 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conscrvative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       43418 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nematoda;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      72.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Harwood S.H., G.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Caenorhabditis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    iast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hast sequence update)
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    Mismatches

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Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 34;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chromadorea; Rhabditida; Rhabditoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EA63951C43C3ACA6 CRC64;
                                                                                                                                                                                                                                                                                      ., Baynes C., Berks M.,
Copsey T., Cooper J., Coulson A.,
R., Favello A., Fulton L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     738 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              381
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DВ

12;

Length 381

Indels

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Evans J.T.,

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RESULT 12
Q92FPD
AC Q92FPD
DT 01-DED
      Q8YAQ3
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                                                                RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              RA Baquero F., Berche P., Bloecker H., Brandt P., Chakraborty T.,
RA Charbit A., Chetouani F., Couve E., de Daruvar A., Deboux P.,
RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Pussurget O.,
RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Pussurget O.,
RA Gautier L., Goebel W., Garcia-del Portillo F., Garrido P.,
RA Gautier L., Goebel W., Genez-Lopez N., Hain T., Haut J., Jackson D.,
RA Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kutapkat G.,
RA Madueno E., Maitournam A., Mata Vicente J., Mg E., Nodjari H.,
RA Madueno E., Maitournam A., Mata Vicente J., Mg E., Nodjari H.,
RA Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
RA Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
RA Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
RA Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
RA Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
RA Vazquez-Doland J.-A., Voss H., Webland J., Cossart P.;
RA Vazquez-Boland J.-A., Voss H., Webland J., Cossart P.;
Science 294:849-852(2001).
DR EMBL, AL59613; CAC952901; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local
                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                          Best
                                                                                                                                                                                                                                                                                                                                                Query Match
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         Q8YAQ3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN-CLIP 11262 / SEROVAR 6A;
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01-DEC-2001 (TrEMBLrel 19, Last sequence update)
01-MAR-2002 (TrEMBLrel 20, Last annotation update)
Hypothetical protein lin0057.
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PROSITE; PS50071; HOMEOBOX_2;
SEQUENCE 738 AA; 87325 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AL032622; CAA21499.1; --
EMBL; AL590342; CAC35859.1; --
InterPro; IPR001356; Homeobox.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A Sulston J.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Glaser P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PubMed=11679669;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=1642;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Listeriaceae; Listeria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Listeria innocua
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LIN0057
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             none;
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                                                                                                                                                              221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       673 LALELDVPYE 682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'Genome sequence of the nematode C.elegans: A platform
                                                                                                                                                                                                                                                                                      Local Similarity hes 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
nes 6; Conserv
                                                                                                                                                                                                                            1 LSXELXIPYEE 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 LSXELXIPYE 10
                                                                                                                                                              LFDELEFPYEE 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ., Frangeul L.,
                                                                                                                                                                                                                                                                                                                                                                                                              233 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
         PRELIMINARY;
                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                    protein; Complete proteome.
33 AA; 27625 MW; E1E405DC3C6048EB CRC64;
                                                                                                                                                                                                                                                                                                                   70.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            72.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Buchrieser C., Rusniok C., Amend A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 34; DB 5; Length 738; Pred. No. 93; 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                      Pred. No. 45;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                   Score 33; DB 16; Length 233;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2.
FAA0174853A0E2A7 CRC64;
         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
         233 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     233
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                                                                                                                                                                                                                                                                                         indeis
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                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
RESULT 14
Q989F3
ID Q989F
AC Q989F
DPY 01-Q0
DPY 01-Q0
DPY 01-Q1
DPY 02-Q1
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   Complete proteome
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Query Match
Best Local
InterPro: IPR001088; GH_4.

Pfam; PF02055; Glyco_hydro_4; 1.

PR1NTS; PR00712; GLYDRLASE4.

ProDom; PD006892; GH_4; 1.

PROSITE; PS01324; GLYCOSYL_HYDROL_F4; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Domann E., Dominquez-Bernal G., Duchaud E., Durant L., Dussurget O., Entian K.-D., Fsihi H., Garcia del Portillo F., Garrido P., Gautier L., Goebed M., Gonez-Lopez N., Hain T., Hauf J., Jackson D., Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G., Madueno E., Maitournam A., Mata Vicence J., Ng E., Nedjari H., Nordsiek G., Novella S., de Pablos H., Perez-Diaz J.-C., Purcell R., Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A., Varquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
                                                                                                                                                                                                                                                                                   Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Koshida Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.
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Baquero F., Berche P., Bloecker H., Brandt P., Chakraborty T.,
Bonder A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
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01-MAR-2002 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                              MEDITINE=21082930; PubMed=11214968;
                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=MAFF303099;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rhizobium loti (Masorhizobium loti).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group:
Phyllobacteriaceae; Mesorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-00 2001 (Tremmeret 18, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Comparative genomics of Listeria species.";
Science 294:849-852(2001).
EMBL: AL591973; CAC98279.1; -.
                                                                                                                                                                                                          "Complete genome structure of the nitrogen-fixing symbiotic bacterium Mesorhizobium loti.";
                                                                                                                                                                                                                                                                 Takeuchi C., Yamada M., Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical protein; Complete proteome. SEQUENCE 233 AA; 27647 MW; ZEDZB06E4FB2C481 CRC64;
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7; Conserv
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64.68;
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20, Last annotation updat
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Pred. No. 45;
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RESULT 15
Q9Q4W5
ID Q9Q4W
AC Q9Q4W
DT 01-MA
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Search completed: January 15, 2003, 12:35:38 Job time: 35.5714 secs
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Best Local Simi urity
Matches 6; Conserv
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Q9Q4W5;
Q1-MAY-2000 (TrEMBLrel. 13, Created)
Q1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
Q1-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Polyprotein (Fragment).
Qrnithogalum mosaic virus.
Qriuses; ssrNA positive-strand viruses, no DNA stage; Polyviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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NCBI_TaxID=12204;
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27 KLSIPYEE 34
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Minimum DB seq length: 0
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47
1 LSXELXIPYEE 11
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Ygapop 10.0 , 1
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January 16, 2003, 08:03:43; Search time 1525.14 Seconds (without alignments)
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Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result

Query

No.

O Score Match Length 116000 11600 116000 116 DB AR063636 AR086117 AR089547 AR112315 AR112316 AX093143 AX093145 AX317584 AX317576 AX317576 AX317576 AX317578 AR206169 AX317151 AR093632 AR193571 AR023961 AR054698 AX404966 AX404972 AR093638 AR193577 AR063642 AR086123 AR061700 AR061941 138585 176140 AR061935 AR061694 AX317586 AK023936 AR206175 AR089553 AR023967 AF315118 I24097 AR112315 Sequence AR112316 Sequence AX093143 Sequence AX093145 Sequence AX317584 Sequence AX317568 Sequence AX317576 Sequence AX317576 Sequence AX317578 Sequence AX404968 Sequence AX404968 Sequence AR023967 Sequence AR054704 Sequence AR061900 Sequence AR061941 Sequence AR063642 Sequence AR086123 Sequence AR08953 Sequence AR089573 Sequence AR093638 Sequence AR093638 Sequence AR0936375 Sequence AK023936 Sequence AX317586 Sequence I15437 Sequence 5 AR063636 AR086117 AR093632 AR193571 AR2061 AX3171 AR054698 Sequence AR061694 Sequence AR023961 124097 Sequence 12 138585 Sequence 12 176140 Sequence 12 AF315118 Description 124091 Sequence Sequence Sequence Sequence Sequence Sequence Sequence Populus Sequence Sequence Sequence Sequence Sequence

RESULT 1

ALIGNMENTS

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Percent Similarit: Best Local Similarity: Query Match: DB:
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AUTHORS
TITLE
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AUTHORS
TITLE
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ACCESSION
VERSION
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                                                                                                                       Dahlberg, J.E., Lyamichev, V.I. and Brow, M.Ann.D. Synthesis-deficient thermostable DNA polymerase Patent: US 5795763-A 12 18-AUG-1998; Location/Qualifiers
                                                                                                                                                                                                                                                                    Sequence 12 from patent AR023967
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Huiming, Z. and Xin, S.
Direct Submission
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/dev_stage="two years old"
/note="isolated using suppression subtractive
hybridization of uninduced vs. salt-induced root tips;
cloned using RACE"
1. 1079
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/db_xref="taxon:75702"
/clone="PSR1"
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AR054704
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AR061700
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Sequence 12
AR054704
AR054704.1
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Sequence
AR061700
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Heisler, L.K., Fors, L. and Brow, M. Ann. D.
Rapid detection of mutations in the p53 gene
Patent: US 5843654-A 12 01-DEC-1998;
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Dahlberg, J.E., Lyamichev, V.I. and Brow, M.Ann.D.
Detection of target nucleic acid molecules using thermostable
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US-09-823-649A-2 (1-11) x AR061700 (1-1600)

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Raiser, M.W., Lyamichev, N.I. and Lyamichev, N.
Cleavage of nucleic acid acid using thermostable methoanococcus jannaschii FEN-I endonucleases
Patent: US 5843669-A 12 01-DEC-1998;
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Brow,M.Ann.D., Hall,J.Steven.Grotelueschen., Lyamichev,V.,
Olive,D.Michael. and Prudent,J.Robert.
Detection of nucleic acid sequences by invader-directed cleavage
Patent: US 5846717-A 12 08-DEC-1998;
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AR089553
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Hall,J.G., tyamichev,V.I., Mast,A.L. and Brow,M.Ann.D
Detection of nucleic acids by multiple sequential inva

                                                                                                                                                                                                                                                                                                Unknown
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Prudent, J.R., Hall, J.G., Lyamichev, V.I.,
Dahlberg, J.E.
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Sequence 12 from patent US 6348314.
AR193577
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  AR206175
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I38585
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124097
124097.1
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Dahlberg,J.E., Lyamichev,V.I. and Brow,M.Ann.D.
Nucleic acid encoding synthesis-deficient thermostable DNA
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AR206175
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Patent: US 5541311-A 12 30-JUL-1996;
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No.:
                                                             Sequence 1 from patent US 6130045.
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Dahlberg,J.E., Lyamichev,V.I. and Brow,M.Ann.D.
Detection of target nucleic acid molecules using
synthesis-deficient thermostable DNA polymerase
Patent: US 5691142-A 12 25-NOV-1997;
Location/Qualifiers
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Dahlberg, J.E., Lyamichev, V.I. and Brow, M.Ann.D.
5' nucleases derived from thermostable DNA polymerase Patent: US 5614402-A 12 25-MAR-1997;
1 (bases 1 to 1682)
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Unclassified.
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JOURNAL FEATURES
Search completed: January 16, 2003, 11:02:19 Job time: 1534.14 secs
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                                                                                                   US-09-823-649A-2 (1-11) x AR112315 (1-1682)
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Best Local Similarity:
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                                                                                                                                           Query Match:
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TITLE
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                                                   1202 CTCTCCCAGGAGCTAGCCATCCCTTACGAGGAG 1234
                                                                 1 LeuSer***GluLeu***1leProTyrGluGlu 11
                                                                                                                                                                                                                                                                                                  Wurst,H. and Qiu,Z.-H.
Thermostable polymerase
Patent: US 6130045-A 1 10-OCT-2000;
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Conservative:
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Result

SUMMARIES

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Title:
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Listing first 45 summaries
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1: /SID$2/gcgdatta/geneseq/geneseqn-emb1/NA1980.DAT:*

2: /SID$2/gcgdatta/geneseq/geneseqn-emb1/NA1981.DAT:*

3: /SID$2/gcgdatta/geneseq/geneseqn-emb1/NA1983.DAT:*

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190.345 Million cell updates/sec
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ALIGNMENTS

XX Dd	PN	SO X	W.	YY DE	XX	XX AC	RESU AAQS ID XX
22-DEC-1994.	WO9429482-A.	Thermus aquaticus YT-1.	DNA-polymerase; DNAP; Taq; DNA cleavage; RNA cleavage; 5' nuclease;	5' Nuclease from Taq DNAP.	19-JUL-1995 (first entry)	AAQ80745;	RESULT 1 AAQ80745 ID AAQ80745 standard; DNA; 1600 BP. XX

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AAT27686

AAT27686

AAT27687

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AAT2

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AAT2

AAT2
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The Taq DNA-polymerase (DNAP) gene was amplified by PCR. Amplified fragments were ligated into pTTQ18 vector, which contains the hybrid trp-lac (tac) promoter. An amplification/selection protocol was used to isolate clone 4B containing a mutated Taq DNAP gene (mutTag) (sequence given in AAQ80746) having normal 5 nuclease activity but less than 1% of the wt Taq DNAP activity. mutTaq was cut from pTTQ18 by EcoRI-SalI digestion and cloned into pET-3c. Thus clone was digested with BstXI and BamHI. The DNA was treated with DNAPECI Xienow fragment and dNTPs, blunt-ended and religated, resulting in an in-frame deletion of 903 nucleotides. The DNA sequence of the resulting 5' nuclease is given in AAQ80745.
                                                                                                                                                                                                                                                                                                                                                                                  p53; mutant; mutation; cleavage; nuclease; cleavase; Thermus; Escherichia; Saccharomyces; Campylobacter; Mycobacterium; Shi Staphylococcus; identification; detection; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1133
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No.:
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30-AUG-1995;
09-NOV-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mutant
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                                                                      09-NOV-1995;
                                                                                                                     23-MAY-1996
                                                                                                                                                                  W09615267-A1
                                                                                                                                                                                                                                                                                                                                     Thermus aquaticus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAT27686;
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  94US-0337164
                         95US-0520946
                                                                      95WO-US14673
                                                                                                                                                                                                                                                               Location/Qualifiers 14..1600
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   553 G; 242 T;
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Matches:
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Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                              Mycobacterium; Shigella,
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                      Thermus aquaticus
                                                                                       DNA polymerase; tag polymerase gene; DNAP; 5' nuclease activity;
                                                                                                                                                           Synthesis deficient Taq DNA polymerase gene clone 4F.
                                                                                                                                                                                                               03-APR-1998
                                                                                                                                                                                                                                                                                                               AAT70347 standard; DNA; 1600
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                                                  Synthetic
                                                                                                                                                                                                                                                               AAT70347;
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                                                                                                                                                                                                                                                                                                                                                                                                         CTCTCCCAGGAGCTAGCCATCCCTTACGAGGAG 1165
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(first entry)

44.00 81.82% 81.82% 93.62% 1.89

Mismatches: Indels: Gaps:

Conservative:

Length: Matches:

B δÃ

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Escherichia, Mycobacterium, Salmonella, Shigella and Staphylococcus. The method may also be used for the identification of viruses, especially hepatitis C virus and simian immunodeficiency virus. Thermus, aquaticus (Taq) DNA polymerase was amplified using two primers (AAT27679, AAT27680). The Taq polymerase DNA was inserted into the BamHI restriction site of the expression vector pET-3c and mutant genes were created from that construct. This mutant was created after the vector was digested with BstXI and BamHI. The DNA was then treated with the Klenow fragment of DNAPECI to trim both 3' overhangs to blunt ends which were then ligated together, resulting in an in frame deletion of 903 nucleotides. The resulting mutant Taq polymerase is also referred to as the Cleavase BB enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alternatively, microbial gene sequences. Cleavage products are compared to the cleavage products of reference gene sequences. The method is used for detecting mutation in the human p53 gene; for identifying strains of microorganisms, especially bacteria selected from the the group of members of the genera Campylobacter.
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07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 polymerase, Escherichia coli ExoIII and the Saccharomyces cerevisiae Radl/RadlO complex. The nucleic acid substrate is preferably an oligonucleotide containing a human p53 gene sequence or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cleavage of nucleic acids using an enzyme, especially a nuclease selected from the group consisting of Cleavase (RTM) BN enzyme, Thermus aquaticus DNA polymerase, Thermus thermophilus DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cleavage of nucleic acids to detect esp. in human p53 gene, to identify
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 2A; Page 257-258; 433pp; English
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95US-0484956.
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strains of microorganisms
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RESULT 4
AAT76647
ID AAT7
XX AAT7
AC AAT7
XX Taq
DT 14-A
XX Taq
DX Taq
XX Nucl
KW Taq;
XX Ther
OS Ther
OS Synt
XX W097
XX W097
XX 22-J
PR 22-I
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PR 22-I
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DB:
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Best Local Similarity:
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                   02-DEC-1996;
24-JAN-1996;
12-JUL-1996;
29-NOV-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence, clone 4F, encodes a Taq DNA polymerase enzyme that has normal 5' nuclease activity, but reduced synthetic ability. This sequence was derived from the mutTaq construct described in AAT70343. The entire mutTaq gene was cut from the plasmid, and cloned into pET-3c. This clone was digested with BetX1 and BamHJ, at unique sites. The 3' overhang of BetX1 was trimmed to a blunt end, while the 5' overhang of BamHJ was filled in. The blunt ends were ligated together. This resulted in an in-frame deletion of 93 nucleotides. The enzyme
                                                                                                                                                                                                     Thermus aquaticus YT-1. Synthetic.
                                                                                                                                                                                                                                                   Nucleic acid cleavage; DNA cleavage; RNA cleavage; Taq; DNA polymerase; Cleavase BB; ds.
                                                                                                                                                                                                                                                                                                      Taq gene 5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1600 BP; 286 A; 519 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 2A; Columns 79-82; 93pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Thermostable 5' nuclease derived from thermostable polymerase - has reduced synthetic activity useful in nucleic acid detection assays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1997-201481/18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Brow MAD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              04-JUN-1993;
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   02-DEC-1996
                                                                                                      22-JAN-1997;
                                                                                                                                      31-JUL-1997
                                                                                                                                                                                                                                                                                                                                          14-APR-1998
                                                                                                                                                                                                                                                                                                                                                                           AAT76647;
                                                                                                                                                                                                                                                                                                                                                                                                             AAT76647 standard; DNA; 1600 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  encoded by the present protein is also referred to as Cleavase BB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (THIR-) THIRD WAVE TECHNOLOGIES INC
                                                                                                                                                                       WO9727214-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 LeuSer***GluLeu***IleProTyrGluGlu 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTCTCCCAGGAGCTAGCCATCCCTTACGAGGAG 1165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dahlberg JE,
                                                                                                                                                                                                                                                                                                        nuclease clone 3F (Cleavase BB).
                                                                                                                                                                                                                                                                                                                                          (first entry)
                   96US-0759038.
96US-0599491.
96US-0682853.
96US-0756386.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92US-0986330.
93US-0073384.
                                                                                                      97WO-US01072
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94US-0254359
   96US-0758314
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     553 G; 242 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels:
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   AAV65786
                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 5
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Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                           1133 CTCTCCCAGGAGCTAGCCATCCCTTACGAGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   material for the construct. Cleavase BB is a thermostable structure-specific nuclease preferred for use in nucleic acid cleavage methods of the invention. Mutant genes (AAT76644-47) were constructed in order to determine which portions of the Tag polymerase domain can be altered without eliminating 5' nuclease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NA. It relates to methods for forming a NA cleavage structure on a target sequence and cleaving the NA cleavage structure in a site-specific manner. The 5' nuclease activity of various enzymes (see AAW24210-13) is used to cleave the target-dependent cleavage structure, thereby indicating the presence of specific NA sequence or specific variations of them.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      altered Thermus aquaticus DNA polymerase (Taq) gene in which nucleotides 875-1778 of the wild-type gene coding sequence are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 activity. The invention relates to means for the detection and characterisation of nucleic acid (NA) sequences and variations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        deleted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            acid sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Thermostable structure-specific nuclease(s) - used for detection and characterisation of nucleic acid sequences and variations in nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1997-393613/36
                                                                                                                                                                    Thermus aquaticus strain YT-1. Synthetic.
                                                                                                                                                                                                                                                                                                        02-FEB-1999
                                                                                                                                                                                                                                                                                                                                          AAV65786;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This DNA sequence, denoted clone 3F or Cleavase BB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 2; Page 245; 457pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (THIR-) THIRD WAVE TECHNOLOGIES INC
   (THIR-) THIRD WAVE TECHNOLOGIES INC
                                     24-MAR-1997;
                                                                   24-MAR-1998;
                                                                                                    01-OCT-1998
                                                                                                                                      W09842873-A1
                                                                                                                                                                                                                     DNA polymerase; nuclease; Cleavase BB; ds
                                                                                                                                                                                                                                     Nucleic acid detection; multiple sequential invasive cleavage;
                                                                                                                                                                                                                                                                     Thermus aquaticus nuclease clone 3F (Cleavase BB) DNA
                                                                                                                                                                                                                                                                                                                                                                           AAV65786 standard; DNA; 1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 LeuSer***GluLeu***IleProTyrGluGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1600 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mutant gene mutTaq (see AAT76643) was used as the starting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to means for the detection and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dahlberg JE, Prudent JR;
                                                                                                                                                                                                                                                                                                        (first entry)
                                     97US-0823516
                                                                   98WO-US05809
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                                                                                                                                                                                                                                                                                                                                                                           βĻ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  553 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kaiser MW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          acid from various viruses (e.g. human cytomegalovirus) in a sample. The method amplifies the detection molecule rather than the target itself, is less subject to contamination than exponential amplification processes, and allows many targets to be analysed in a single reaction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Thermus aquaticus (Taq). In comparison to the wild-type Taq DNAP sequence (see AAV65779), it contains an in-frame deletion of 903 nucleotides. The invention relates to means for the detection and characterisation of nuclei acid sequences, and variations in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Brow MAD,
Mast AL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of the cleavage structure by the nuclease indicates the presence of specific nucleic acid sequences or specific variants. The invention further relates to methods for the separation of nucleic acid molecules based on charge, methods for the detection of non-target cleavage products via the formation of a complete and activated protein binding region, and methods for the detection of nucleic protein binding region, and methods for the detection of nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nucleic acid sequences. It also relates to methods for forming a nucleic .cid cleavage structure on a target sequence and cleaving this structure in a site-specific manner, preferably using a thermostable structure-specific nuclease such as a modified Tag DNAP that has reduced synthetic activity (see AAV65783-86). Cleavage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Detecting target nucleic acid by sequence-specific cleavage of complex with two specific oligonucleotides - used to detect
                                                                                                                                                                                                                                                                           mutant DNA polymerase; bacteria; fungi; protozoa; RNA virus; hepatitis C virus; HCV; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1133 CTCTCCCAGGAGCTAGCCATCCCTTACGAGGAG 1165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1600 BP;
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                                26-NOV-1997;
                                                                                             04-JUN-1998
                                                                                                                                                       WO9823774-A1
                                                                                                                                                                                                                    Thermus sp.
                                                                                                                                                                                                                                                                                                                                        Clone 4D; Tag mutant gene; thermostable; structure-specific nuclease,
                                                                                                                                                                                                                                                                                                                                                                                                     Nucleotide sequence of clone 4F of the Taq gene mutant.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 LeuSer***GluLeu***IleProTyrGluGlu 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                   97WO-US21783
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AAV63407
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score
                                                                         06-JUN-1994;
07-DEC-1992;
04-JUN-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                           1133 CTCTCCCAGGAGCTAGCCATCCCTTACGAGGAG 1165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This is the nucleotide sequence of a clone of a mutant Tag gene, used in the method of the invention. In this process thermostable structure-specific nucleases are derived from mutant DAN polymerases, which can be used for detecting mutant alleles or strains of microorganisms. The structure-specific nucleases can be used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mixtures, compositions and kits to treat nucleic acid, e.g. for detection of wild type and mutant alleles of genes, for detection and/or identification of strains of microorganisms such as bacteria, fungi, protozoa, especially for detection of RNA viruses such as the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  02-DEC-1996;
29-NOV-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1600 BP; 286 A; 519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Thermostable structure-specific nuclease(s) derived from mutant DNA polymerase(s) - useful for detecting mutant allele(s) or strains of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kaiser MW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (THIR-) THIRD WAVE TECHNOLOGIES INC.
           Brow MAD,
                                                              06-JUN-1995;
                                                                                                                                                        17-NOV-1998
                                                                                                                                                                                                                          Synthetic
                                                                                                                                                                                                                                                 Thermostable DNA polymerase; nucleic acid detection; Cleavase BB thermostable 5^{\prime} nuclease; ds.
                                                                                                                                                                                                                                                                                       DNA sequence of a thermostable 5' nuclease derived from Taq polymerase.
                                                                                                                                                                                                                                                                                                                   26 JAN 1999
                                                                                                                                                                                                                                                                                                                                             AAV63407;
                                                                                                                                                                                                                                                                                                                                                                      AAV63407 standard; DNA; 1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hepatitis C virus (HCV).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 2; Page 238; 472pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 microorganisms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1998-322748/28
                                                                                                                               06-JUN-1995;
                                                                                                                                                                                   US5837450-A
                                                                                                                                                                                                          Thermus aquaticus
                                    (THIR-) THIRD WAVE TECHNOLOGIES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                         Dahlberg JE, Lyamichev VI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lyamichev VI,
                                                                                                                                                                                                                                                                                                                 (tirst entry)
                                                          92US-0986330.
93US-0073384.
95US-0471066.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96US-0758314.
96US-0757653.
                                                                                                    94US-0254359
                                                                                                                              95US-0471066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.89
44.00
81.82*
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93.62*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; 553 G; 242 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Caps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative: Mismatches:
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RESULT 8
AAQ24010
ID AAQ2
XX AAQ2
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XX 5'-3
XX 5'-3
XX Ther
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XX W091
FT 914
FT 914
FT 928-1
PR 30-1
PR 28-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alignment
                                                                                    28-SEP-1990;
28-SEP-1990;
28-SEP-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the presence of a nucleic acid molecule. The method is used for the specific detection of nucleic acid sequences, via a cleavage-based procedure, but without the need for amplification of target sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              where the 5' nuclease is capable of cleaving a linear nucleic acid duplex structure to create a single, single-stranded cleavage product. The nuclease, designated Cleavase BB, is used in a method for detecting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence represents a thermostable 5' nuclease derived from a thermostable polymerase modified to have reduced synthetic activity,
                                                                                                                                                                                                                                                                                                                  old_sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                         Mutant thermostable DNA polymerase pSPSA288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Thermostable polymerases, altered to have nuclease, but not polymerase activity are preferably used due to their specificity. The cleavage product specifically formed is detected, preferably by the use of radioactively labelled oligonucleotides. These can be used in
                  Abramson RD,
                                                                                                                                                            30-SEP-1991;
                                                                                                                                                                                             16-APR-1992
                                                                                                                                                                                                                              WO9206200-A
                                                                                                                                                                                                                                                                                                                                                                    Thermus species sps17
                                                                                                                                                                                                                                                                                                                                                                                                        5'-3'; exonuclease; PCR; amplification; SSR; sequencing; PLCK; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAQ24010;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAQ24010 standard; DNA; 1635 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    e.g. forensic testing or paternity determination.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 10; Columns 79-82; 91pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        specific detection products from oligo:nucleotide(s) and target
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Detection of target nucleic acid molecules - uses modified thermostable enzymes with specific cleavage activity to create
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1999-023438/02
                                                   (CETU ) CETUS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-OCT-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 LeuSer***GluLeu***IleProTyrGluGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTCTCCCAGGAGCTAGCCATCCCTTACGAGGAG 1165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ВP;
                  Gelfand DH;
                                                                                    90US-0590213.
90US-0590466.
90US-0590490.
                                                                                                                                                            91WO-US07035
                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                   /note=
                                                                                                                                                                                                                                                                                                   /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       286 A; 519 C;
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                                                                                                                                                                                                                                                             "nucleotides 4-861 deleted from the native sequence."
                                                                                                                                                                                                                                                                                                   ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (1-1600)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       553 G; 242 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
                               28-SEP-1990;
28-SEP-1990;
28-SEP-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               exonuclease activity than the native enzyme. Thermostable DNA polymerases are useful in many recombinant DNA techniques, esp. nucleic acid amplification by PCK, self-sustained sequence replication (SSR) and high temp. DNA sequencing. The absence of 5'-3' nuclease activity may facilitate higher sensitivity allelic discrimination in a combined polymerase ligase chain reaction (PLCR) assay. An enhanced amt. of 5'-3' exonuclease activity may be desirable in enzymes used in homogeneous assays for the amplification and detection of a target nucleic acid sequence. Mutation of the DNA enroding particular regions of the enzymes can be used to prepare a range of recombinant proteins having 5'-3' exonuclease activity to a complete lack of activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Thermostable DNA polymerases with altered 5'-3' exo nuclease activity - having conserved regions mutated or deleted, for use in e.g. PCR, sequencing and detection assays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1992-150885/18.
P-PSDB; AAR23157.
                                                                                                                                                                                                                                                             old_sequence
                                                                                                                                                                                                                                                                                                                                                 5'-3'; exonuclease;
                                                                                                                                                                                                                                                                                                                                                                                  Mutant thermostable DNA polymerase pLSG8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAQ23998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 11; Page 59; 185pp; English.
(CETU ) CETUS CORP
                                                                                                      30-SEP-1991;
                                                                                                                                       16-APR-1992
                                                                                                                                                                          W09206200-A
                                                                                                                                                                                                                                                                                                                Thermus aquaticus
                                                                                                                                                                                                                                                                                                                                                                                                                         22-OCT-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAQ23998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  See also AAQ23993-Q24013, AAQ24320-36 and AAQ24343-60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             polymerase enzyme produced to exhibit a different amt.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   has been mutated.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 LeuSer***GluLeu***IleProTyrGluGlu 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence is that of Thermus species sps17 polymerase DNA which been mutated. The mutation designated pSPSdA288 causes the vmerase enzyme produced to exhibit a different amt. of 5'-3'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTCTCCCAGGAGCTCTCCATCCCCTACGAGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             standard;
                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                               90US-0590213.
90US-0590466.
90US-0590490.
                                                                                                    91WO-US07035
                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                            /note= "nucleotides 4-867 deleted from native
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               267 A;
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44.00
81.82%
81.82%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA;
                                                                                                                                                                                                                                                                                                                                                   PCR; amplification; SSR; sequencing; PLCR; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1635
                                                                                                                                                                                                        sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Caps:
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Matches:
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DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  1168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nucleic acid amplification by PCR, self-sustained sequence replication (SSR) and high temp. DNA sequencing. The absence of 5'-3' nuclease activity may facilitate higher sensitivity allelic discrimination in a combined polymerase ligase chain reaction (PLCR) assay. An enhanced ant. of 5'-3' exonuclease activity may be desirable in enzymes used in homogeneous assays for the amplification and detection of a target nucleic acid sequence. Mutation of the DNA encoding particular regions of the enzymes can be used to prepare a range of recombinant proteins having 5'-3' exonuclease activity to a complete lack of activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The sequence is that the nutation, resulting in mutant pLSG8, causes been mutated. The mutation, resulting in mutant pLSG8, causes been mutated. The mutation of 5'-3' the polymerase enzyme produced to exhibit a different amt. of 5'-3' the polymerase enzyme produced to exhibit a different amt. of 5'-3'.
 28-SEP-1990;
28-SEP-1990;
                                                                                                                                                                                                                                                            5'-3';
                                                                                                                                                                                                                                                                                          Mutant thermostable DNA polymerase pZ05A292.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  exonuclease activity than the native enzyme. Thermostable DNA polymerases are useful in many recombinant DNA techniques, esp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 11; Page 59; 185pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Thermostable DNA polymerases with altered 5'-3' exo nuclease activity - having conserved regions mutated or deleted, for use
                                             30-SEP-1991;
                                                                                                       WO9206200-A
                                                                                                                                                                                  old_sequence
                                                                                                                                                                                                                              Thermus species Z05.
                                                                                                                                                                                                                                                                                                                          22-OCT-1992
                                                                                                                                                                                                                                                                                                                                                       AAQ24322;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1635 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                See also AAQ23993-Q24013,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P-PSDB; AAR23145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Abramson RD,
                                                                          16-APR-1992
                                                                                                                                                                                                                                                                                                                                                                                    AAQ24322 standard; DNA; 1635 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            in e.g. PCR, sequencing and detection assays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LeuSer***GluLeu***IleProTyrGluGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTCTCCCAGGAGCTAGCCATCCCTTACGAGGAG 1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1992-150885/18.
                                                                                                                                                                                                                                                           exonuclease; PCR; amplification; SSR; sequencing; PLCR; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                is that of Thermus aquaticus
                                                                                                                                                                                                                                                                                                                        (first entry)
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 90US-0590213
90US-0590466
                                             91WO-US07035
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                                                                                                                                                                                               Location/Qualifiers
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                                                                                                                                    "nucleotides 4-873 deleted from the native sequence."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAQ24320-36 and AAQ24343-60.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                564 G; 246 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No.:
                                                                                                            Key
old_sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             polymerases are useful in many recombinant DNA techniques, esp. nucleic acid amplification by PCR, self-sustained sequence replication (SSR) and high temp. DNA sequencing. The absence of 5'-3' nuclease activity may facilitate higher sensitivity allelic discrimination in a combined polymerase ligase chain reaction (PLCR) assay. An enhanced amt. of 5'-3' exonuclease activity may be desirable in enzymes used in homogeneous assays for the amplification and detection of a target nucleic acid sequence. Mutation of the DNA encoding particular regions of the enzymes can be used to prepare a range of recombinant proteins having 5'-3' exonuclease activity to a complete lack of activity.
                                                                                                                                                                                                                                                                                                                                                   1168 CTCTCCCAGGAGCTTGCCATCCCCTACGAGGAG 1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 11; Page 59; 185pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Thermostable DNA polymerases with altered 5'-3' exo nucl activity - having conserved regions mutated or deleted, in e.g. PCR, sequencing and detection assays
                         16-APR-1992.
                                                                                                                                                          Thermus
                                                                                                                                                                                5'-3'; exonuclease; PCR; amplification; SSR; sequencing; PLCR; ss
                                                                                                                                                                                                           Mutant thermostable DNA polymerase pTTHA292.
                                                                                                                                                                                                                                           22-OCT-1992
                                                                                                                                                                                                                                                                                             AAQ24328 standard; DNA; 1635 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The sequence is that of Thermus species Z05 polymerase DNA which has been mutated. The mutation designated pZ05A292 causes the polymerase enzyme produced to exhibit a different amt. of 5'-3'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Abramson RD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-SEP-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1992-150885/18
                                                W09206200-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 exonuclease activity than the native enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (CETU ) CETUS CORP.
                                                                                                                                                                                                                                                                                                                                                                             1 LeuSer***GluLeu***IleProTyrGluGlu 11
                                                                                                                                                          thermophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR23163
                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gelfand DH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ВP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90US-0590490
                                                                                                                    Location/Qualifiers
                                                                          /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           291 A; 577 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                   44.00
81.82%
81.82%
93.62%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.93
                                                                                                      ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           529 G; 238 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                              Caps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Thermostable DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         exo nuclease
                                                                                                                                                                                                                                                                                                                                                                                                                                for
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30-SEP-1991;

91WO-US07035

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AAZ29460
ID AAZ29
XX AZ29
XX AZ29
XX AZ29
XX Therm
XX Therm
XX Therm
XW INCLEASE
XW INCLEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Дb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The sequence is that of Thermus thermophilus polymerase DNA which chas been mutated. The mutation designated pTHHA292 causes the polymerase enzyme produced to exhibit a different amt. of 5'-3' complete activity than the native enzyme. Thermostable DNA complete actid amplification by pCR, self-sustained sequence replication (SSR) and high temp. DNA sequencing. The absence of complete actid amplification by pCR, self-sustained sequence complete self-sustained sequence of complete self-sustained sequence of constraintation in a combined polymerase ligase chain reaction (PLCR) complete used in homogeneous assays for the amplification and complete self-sustained sequence. Mutation of the DNA composition of a target nucleic acid sequence. Mutation of the DNA composition particular regions of the enzymes can be used to prepare composition of a complete lack of activity.

CC see also AAQ23993-Q24013, AAQ24320-36 and AAQ2433-60.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-823-649A-2 (1-11) x AAQ24328 (1-1635)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-SEP-1990;
28-SEP-1990;
28-SEP-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Thermostable DNA polymerases with altered 5'-3' exo nuclease activity - having conserved regions mutated or deleted, for use
                                                                                                                                                                       Thermostable DNA dependent polymerase; nuclease activity; Tag polymerase; mutant; Polymerase Chain Reaction; PCR; N-terminal domain; proteolytic; thermal stability, hydrophilic solution; sequencing; labeling; diagnosis; genetic disorder; primer-driven mutagenesis; identification of pathogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 11; Page 59; 185pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  in e.g. PCR, sequencing and detection assays
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (CETU ) CETUS
                                                                                      Synthetic.
                                                                                                             Thermus aquaticus
                                                                                                                                                     mutational analysis; forensic identification; ds.
                                                                                                                                                                                                                                                                               Thermostable DNA dependent mutant Taq polymerase-1 encoding DNA
                                                                                                                                                                                                                                                                                                                          14-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                            AAZ29460 standard; DNA; 1682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      No
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1635 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 LeuSer***GluLeu***IleProTyrGluGlu 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTCTCCCAGGAGCTTGCCATCCCCTACGAGGAG 1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1992-150885/18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR23168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORP
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90US-0590466.
90US-0590490.
                        8..1669
                                            Location/Qualifiers
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44.00
81.82%
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93.62%
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                                                                                                                                                                                                                                                                                                                                                                                                              ВР
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    537 G; 238 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length:
Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No.:
                                                 04-DEC-1996
                                                                                                                                                                                                                                       Mutant Taq polymerase FY2.
                                                                                                                                                                                                                                                                                    11-MAY-1997
                                                                                                                                                                                                                                                                                                                            AAT47959;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    identification.
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Claim 22; Fig 1; 32pp; English.
                                                                                                                       WPI; 2000-105869/09.
                                                                                                                                                                                                                                                                                                                                                                                                         W09964438-A1
                                                Novel enzyme, particularly useful in polymerase chain reaction
                                                                                            P-PSDB; AAY44352
                                                                                                                                                                      Wurst H, Qui Z;
                                                                                                                                                                                                                                                             11-JUN-1998;
                                                                                                                                                                                                                                                                                                            11-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                          16-DEC-1999.
                                                                                                                                                                                                                 (CLON-) CLONTECH LAB INC
                                                                                                                                                                                                                                                             98US-0096399
                                                                                                                                                                                                                                                                                                            99WO-US13305.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       from Thermus aquaticus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product= "Thermostable mutant Taq polymerase-1"
/note= "Identical at C-terminus to Taq polymerase
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The present sequence is the DNA encoding a novel, thermostable DNA dependent, mutant Taq polymerase-1 enzyme. The N-terminal domain of the polymerase includes a sequence of 9 amino acids, that has 40-50% sequence identity with residues 280-288 of native Thermus aquaticus polymerase, Taq. The residues 10-53 of encoded by this sequence is identical to residues 289-832 of Taq polymerase. This sequence has no significant nuclease activity, but good proteolytic and thermal stabilities and improved solubility in hydrophilic solutions. This sequence is used for synthesis of polymucleotides, particularly in polymerase chain reaction (PCR) based processes, like sequencing, labellng, primer-driven mutagenesis, diagnosis of genetic disorders, labellification of pathogens, mutational analysis and forensic

Sequence 1682 BP; 286 A; 567 Ç 575 G; 254 T; 0 other;

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US-09-823-649A-2 (1-11) x AAZ29460 (1-1682)
                                                                                                                                                  Percent Similarity:
Best Local Similarity:
                                                  1202 CTCTCCCAGGAGCTAGCCATCCCTTACGAGGAG 1234
AAT47959 standard; DNA; 1686 BP
                                                               1 LeuSer***GluLeu***1leProTyrGluGlu 11
                                                                                                                           44.00
81.82%
81.82%
93.62%
                                                                                                                       Gaps:
                                                                                                                                                  Conservative: Mismatches:
                                                                                                                                       Indels:
                                                                                                                                                                           Matches:
                                                                                                                                                                                       Length:
                                                                                                                           1682
9
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(first entry)
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DNA sequencing; PCR; polymerase; FY2; FY3; FY4; thermostable; SS. Thermus;

Thermus aquaticus.

EP745676-A1

30-MAY-1996; 96EP-0303880

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                                                                                                                                                                                                                                                                                                                                  RESULT 14
AAT47961
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local S
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            polymerases providing improved results in DNA sequencing reactions. FY2 is the T. aquaticus DNA polymerase lacking pref. the 271-272 N-terminal amino acids and having the amino acid at position 667 of the wild type (Phe) replaced by Tyr. FY3 contains 562 amino acids with a Met at position 1 and Ala at position 2, corresponding to the Met and Ala of positions 271 and 272, respectively, of the wild type enzyme. FY4 corresponds to the T. thermophilus DNA polymerase lacking the N-terminal 274 amino acids having a Phe to Tyr replacement at position 396 (position 669 of the wild type enzyme).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FY2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 5; Page 10-13; 36pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New enzymatically active Thermus DNA polymerase(s) - having a tyrosine at a position equivalent to 667 of Taq DNA polymerase and lacking 5' to 3' exonuclease activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P-PSDB; AAW09315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1997-013699/02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Davis
            WPI; 1997-013699/02.
P-PSDB; AAW09317.
                                                                                                                                                                                                                                                  Mutant Taq polymerase FY4.
                                                                                                                                                                                                                                                                                                                                                                         1219 CTCTCCCAGGAGCTAGCCATCCCTTACGAGGAG 1251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (AMSH ) AMERSHAM LIFE SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31-MAY-1995;
                                               Davis M,
                                                                                                                   30-MAY-1996;
                                                                                                                                                                   EP745676-A1
                                                                                                                                                                                       Thermus thermophilus.
                                                                                                                                                                                                                                                                                                                          AAT47961 standard; DNA; 1686 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1686
                                                                     (AMSH ) AMERSHAM LIFE SCI INC.
                                                                                             31-MAY-1995;
                                                                                                                                           04-DEC-1996
                                                                                                                                                                                                                 DNA sequencing;
                                                                                                                                                                                                                                                                         11-MAY-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        No
                                                                                                                                                                                                                                                                                                                                                                                              1 LeuSer***GluLeu***IleProTyrGluGlu 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FY3 and FY4 (see AAT47959 to AAT47961) are new thermostable DNA
                                                                                                                                                                                                                           polymerase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fuller C,
                                               Fuller C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ВP;
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                                                                                             95US-0455686
                                                                                                                   96EP-0303880
                                                                                                                                                                                                                 PCR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         283 A; 567 C; 578 G; 258 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       44.00
81.82%
81.82%
93.62%
                                                                                                                                                                                                                   SS
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                                                                                                                                                                                                                             FY3; FY4; thermostable; Thermus; enzyme;
                                               ß
                                                                                                                                                                                                                                                                                                                                                                                                                      (1-1686)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fuller CW,
                                                Fuller
                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative:
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                                                Moffett
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This sequence encodes a thermostable DNA polymerase of the invention. The thermostable polymerases of the invention are variants of Tag DNA polymerase having a Tyr residue at a position corresponding to Tag DNA polymerase residue 667 in its dNMP binding site, and lacking 5' to 3'
                                                                                                                                                                                                      14-MAY-1996;
31-MAY-1995;
                                                                               New thermostable DNA polymerases - having and lacking 5' to 3' exonuclease activity
                                                                                                                                 WPI; 1999-228538/19
                                                                                                                                                        Cunniff JJ,
                                                          Claim 7; Column 11-16;
                                                                                                                                                                             (AMSH ) AMERSHAM LIFE SCI INC
                                                                                                                                                                                                                                         14-MAY-1996;
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AAY00886.

27pp; English

- having 540 to 582 amino acids

Davis M,

Fuller CW,

Moffett RB

96US-0648657. 95US-0455686. 96US-0648657

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US-09-823-649A-2 (1-11) x AAT47961 (1-1686)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No.:
                                                                                                                                                                                                                                                                                                    AAX27130
                                                                                                                                                                                                                                                                                                                    RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 polymerases providing improved results in DNA sequencing reactions. FY2 is the T. aquaticus DNA polymerase lacking pref. the 271-272 N-terminal amino acids and having the amino acid at position 667 of the wild type (Phe) replaced by Tyr. FY3 contains 562 amino acids with a Met at position 1 and Ala at position 2, corresponding to the Met and Ala of positions 271 and 272, respectively, of the wild type enzyme. FY4 corresponds to the T. thermophilus DNA polymerase lacking the N-terminal 274 amino acids having a Phe to Tyr replacement at position 396 (position 669 of the wild type enzyme).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 5; Page 20-23; 36pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New enzymatically active Thermus DNA polymerase(s) - having a tyrosine at a position equivalent to 667 of Taq DNA polymerase lacking 5' to 3' exonuclease activity
                                                                                                                                                                                                                                                                                                                                                         1219 CTCTCCCAGGAGCTAGCCATCCCCTACGAAGAA 1251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1686 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FY2, FY3 and FY4 (see AAT47959 to AAT47961) are new thermostable DNA
                                   US5885813-A
                                                                                                             DNA
                                                                                                                                EY2
                                                                                                                                                                                                        27-MAY-1999
                                                                                                                                                                                                                                           AAX27130;
23-MAR-1999
                                                                      Thermus aquaticus
                                                                                                                                                                 FY2 polymerase coding sequence
                                                                                                                                                                                                                                                                              AAX27130 standard;
                                                                                                                                                                                                                                                                                                                                                                            1 LeuSer***GluLeu***IleProTyrGluGlu 11
                                                                                                         sequencing;
                                                                                                                            polymerase;
                                                                                                                                                                                                    (first entry)
                                                                                                                              EY3
                                                                                                           SS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      295 A; 593 C; 551 G; 247 T; 0 other;
                                                                                                                                                                                                                                                                              DNA; 1686 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2
44.00
81.82%
81.82%
93.62%
                                                                                                                            polymerase; FY4 polymerase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative: Mismatches:
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                                                                                                                            Taq polymerase variant;
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CC exonuclease activity as a result of an N-terminal deletion. The CC polymerases can be used for the sequencing of DNA, either by manual or CC automated means.

XX

SQ Sequence 1686 BP; 283 A; 567 C; 578 G; 258 T; 0 other;

Alignment Scores:
Pred. No.:
2
Pred. No.:
44.00
Pred. No.:
9
Percent Similarity: 81.82%
Pest Local Similarity: 81.82%
Pest Local Similarity: 81.82%
Pest Local Similarity: 93.02%
Pest Local Similarity: 93.02%
Pest Local Similarity: 93.02%
Percent Similarity: 100 Mismatches: 2
Ouery Match: 0
Ouery Match: 0
Ouery Match: 100 Gaps: 0
Ouero-923-649A-2 (1-11) x AAX27130 (1-1686)
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RESULT 2
AAB47794
ID AAB4
XX AC AAB4
XX DT 25-p
AC AAB4
XX Nat LNA
XX NAT
XX Th
X
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA polymerase's ability to incorporate dideoxynucleotides labelled with fluorescein and cyanine family dyes. The method of the invention is useful in reverse transcription/amplification reactions. The method provides improved reverse transcription efficiency at lower enzyme concentrations relative to previous high temperature reverse transcription methods, and provide a wider range of usable salt concentrations. The use of the mutant DNA polymerase provides faster reverse transcription extension rates, and consequently less time is needed for the reaction. This motif is derived from DNA polymerases from Thermus species aquaticus, thermophilus, 205 and caldophilus.
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                                                                                Reverse transcribing an RNA, comprises performing a reverse transcriptase polymerase chain reaction amplification of a mixture using a mutant thermoactive DNA polymerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA polymerase; reverse transcription; primer; divalent cation; mutant; transverse transcription reaction; fluorescein; cyanine; thermoactive; dye; amplification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-MAR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB47794;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB47794 standard; peptide; 11 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RNA, a primer, a divalent cation, and a mutant thermoactive DNA polymerase. These motifs represent a conserved region which affects the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 4; Page 3; 23pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           using a mutant thermoactive DNA polymerase
                         Claim 4; Page 4; 23pp; English
                                                                                                                                                                                                                                                                           Schoenbrunner NJ,
                                                                                                                                                                                                                                                                                                           Smith ES,
                                                                                                                                                                                                                                                                                                                                                                                                                                  18-APR-2000; 2000US-198336P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Native DNA polymerase motif #4.
                                                                                                                                                                                                                                                                                                                                                                  (HOFF ) HOFFMANN LA ROCHE & CO AG
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                                                                                                                                                                                                                                                                                                           Elfstrom CM,
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                                                                                                                                                                                                                                                                           Wang AM;
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 Mismatches

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Pred. No. 0.011;
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                                                                                                                                                                                                                                                                                                        Higuchi RG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2
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                                                                                                                                                                                                                                                                                                           Myers TW;
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CC The sequences given in AAB47791-97 and AAM48259-AAM48270 represent the CC native forms of motifs derived from DNA polymerases used in the method CC of the invention. The method for reverse transcribing an RNA, comprises treating a transverse transcription reaction mixture which comprises the CC RNA, a primer, a divalent cation, and a mutant thermoactive DNA comprises the CC polymerase. These motifs represent a conserved region which affects the CR provides and cyanine family dyes. The method of the invention is concentration and cyanine family dyes. The method of the invention is concentrations relative to previous high temperature reverse concentrations relative to previous high temperature reverse concentrations. The use of the mutant DNA polymerase provides faster creverse transcription extension rates, and consequently less time is needed for the reaction. This motif is derived from DNA polymerases of the mutant DNA polymerase alto is created for the reaction. This motif is derived from DNA polymerases and consequently less time is sequence 11 AA;
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Matches
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                                           Local Similarity
1 LSXELSIPYEE 11
               1 LSXELXIPYEE 11
                                 10;
                                  Conservative
                                          93.6%;
90.9%;
                                          Score 44;
Pred. No.
                                 0; Mismatches
                                          0.011;
                                                   DB 23;
                                                  Length 11;
                                 Indels
                                 0;
                                 Gaps
                                 0;
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gg dg

12-APR-2001; 2001EP-0109341. 18-APR-2000; 2000US-198336P

(HOFF) HOFFMANN LA ROCHE & CO AG F.

Elfstrom CM,

Gelfand DH,

Higuchi RG,

Schoenbrunner NJ, Wang AM; WPI; 2002-076891/11.

The sequences given in AAB47791-97 and AAM48259-AAM48270 represent the native forms of motifs derived from DNA polymerases used in the method of the invention. The method for reverse transcribing an RNA, comprises treating a transverse transcription reaction mixture which comprises the RNA, a primer, a divalent cation, and a mutant thermoactive DNA polymerase. These motifs represent a conserved region which affects the DNA polymerase's ability to incorporate dideoxynucleotides labelled with fluorescein and cyanine family dyes. The method of the invention is

Reverse transcribing an RNA, comprises performing a reverse transcriptase polymerase chain reaction amplification of a mixture using a mutant thermoactive DNA polymerase

Disclosure; Page 7; 23pp; English.

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RESULT 4
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                                                                                                                                                                                                                       RNA, a primer, a divalent cation, and a mutant thermoactive DNA polymerase. These motifs represent a conserved region which affects the DNA polymerase's ability to incorporate dideoxynucleotides labelled with fluorescein and cyanine family dyes. The method of the invention is useful in reverse transcription/amplification reactions. The method provides improved reverse transcription efficiency at lower enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                       The sequences given in AAB47791-97 and AAM48259-AAM48270 represent the native forms of motifs derived from DNA polymerases used in the method of the invention. The method for reverse transcribing an RNA, comprises treating a transverse transcription reaction mixture which comprises the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                          transcription methods, and provide a wider range of usable salt concentrations. The use of the mutant DNA polymerase provides faster reverse transcription extension rates, and consequently less time is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 7; 23pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Reverse transcribing an RNA, comprises performing a reverse transcriptase polymerase chain reaction amplification of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EP1152062-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-MAR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         needed for the reaction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  transcriptase polymerase chain reaction ampusing a mutant thermoactive DNA polymerase
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                                                                   needed for the reaction.
                                                                                                                                                                                                   concentrations relative to previous high temperature reverse
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nes 9; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Elfstrom CM,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of the invention.
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                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                       concentrations relative to previous high temperature reverse transcription methods, and provide a wider range of usable salt concentrations. The use of the mutant DNA polymerase provides faster reverse transcription extension rates, and consequently less time is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RNA, a primer, a divalent cation, and a mutant thermoactive DNA polymerase. These motils represent a conserved region which affects the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 7; 23pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               using a mutant thermoactive DNA polymerase
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LSQELAIPYEE 11
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                                                                                                                                                 Similarity
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81.8%;
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Pred. No. 0.011;
                                                                                                                                             Score 44; DB 23; Pred. No. 0.011;
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RESULT 7
AAM48263
ID AAM4
XX
AC AAM4
XX
AC AAM4
XX
XX
                                                                                                                                                      Query Match
Best Local Similarity
----hes 9; Conserve
                                                                                                                                                                                                                                                                                                                                                                   The sequences given in AAB47791-97 and AAM48259-AAM48270 represent the native forms of motifs derived from DNA polymerases used in the method of the invention. The method for reverse transcribing an RNA, comprises treating a transverse transcription reaction mixture which comprises the
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Reverse transcribing an \overline{x}NA, comprises performing a reverse transcriptase polymerase chain reaction amplification of a mixture using a mutant thermoactive DNA polymerase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA polymerase; reverse transcription; primer; divalent cation; mutant; transverse transcription reaction; fluorescein; cyanine; thermoactive; dye; amplification.
            25-MAR-2002
                                    AAM48263;
                                                         AAM48263 standard; Peptide; 11
                                                                                                                                                                                                                                                  transcription methods, and provide a wider range of usable salt concentrations. The use of the mutant DNA polymerase provides faster reverse transcription extension rates, and consequently less time is
                                                                                                                                                                                                                                                                                  useful in reverse transcription/amplification reactions. The method provides improved reverse transcription efficiency at lower enzyme concentrations relative to previous high temperature reverse
                                                                                                                                                                                                                                                                                                                    RNA, a primer, a divalent cation, and a mutant thermoactive DNA polymerase. These motifs represent a conserved region which affects DNA polymerase's ability to incorporate dideoxynucleotides labelled fluorescein and cyanine family dyes. The method of the invention is
                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 7; 23pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-076891/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Schoenbrunner NJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HOFF ) HOFFMANN LA ROCHE & CO AG F.
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                                                                                                                                                                                                                  Sequence
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                                                                                                                                         1 LSXELXIPYEE 11
                                                                                                                   LSQELAIPYEE 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Elfstrom CM,
                                                                                                                                                                                                                  11 AA;
                                                                                                                                                                   Conservative
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            (first entry)
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                                                                                                                                                                              93.6%;
81.8%;
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                                                                                                                                                                              Score 44; DB 23; Length 11; Pred. No. 0.011;
                                                                                                                                                                     Mismatches
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                                                                                                                                                                              RESULT 8
AAM48264
                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
"~+~hes 9; Conserva
                                                                                                                                                                                                                               Db
                                                                                                                                                                                                                                                    QΥ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Schoenbrunner NJ,
   EP1152062-A2
                                               dye; amplification.
                                                                                            Native DNA polymerase motif #13.
                                                                                                                                              AAM48264;
                                                                                                                                                                    AAM48264 standard; Peptide;
                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                          reverse transcription extension rates, and consequently less time is
                        Thermus caldophilus.
                                                         DNA polymerase; reverse transcription; primer; divalent cation; mutant; transverse transcription reaction; fluorescein; cyanine; thermoactive;
                                                                                                                     25-MAR-2002
                                                                                                                                                                                                                             1 ISORISTAKES 11
                                                                                                                                                                                                                                                    1 LSXELXIPYEE 11
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                                                                                                                                                                                                                                                                                                                         11 AA;
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                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wang AM;
                                                                                                                                                                                                                                                                                       93.6%;
81.8%;
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밁 Q

11 AA

0;

Score 44; DB 23 Pred. No. 0.011; Mismatches

DB 23;

Length 11; Indels

0 Caps

0;

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The sequences given in AAB47791-97 and AAM48259-AAM48270 represent the native forms of motifs derived from DNA polymerases used in the method of the invention. The method for reverse transcribing an RNA, comprises treating a transverse transcription reaction mixture which comprises the RNA, a primer, a divalent cation, and a mutant thermoactive DNA polymerase. These motifs represent a conserved region which affects the DNA polymerase's ability to incorporate dideoxynucleotides labelled with fluorescein and cyanine family dyes. The method of the invention is useful in reverse transcription/amplification reactions. The method provides improved reverse transcription efficiency at lower enzyme concentrations relative to previous high temperature reverse transcription methods, and provide a wider range of usable salt concentrations. The use of the mutant DNA polymerase provides faster
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Best Local
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                                                                                                                                                            dye;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The sequences given in AAH47791-97 and AAM48259-AAM48270 represent the native forms of motifs derived from DNA polymerases used in the method of the invention. The method for reverse transcribing an RNA, comprises treating a transverse transcription reaction mixture which comprises the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Reverse transcribing an RNA, comprises performing a reverse transcriptase polymerase chain reaction amplification of a mixture using a mutant thermoactive DNA polymerase
                                    18-APR-2000; 2000US-198336P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    transcription methods, and provide a wider range of usable sall concentrations. The use of the mutant DNA polymerase provides faster reverse transcription extension rates, and consequently loss time is
           (HOFF ) HOFFMANN LA ROCHE & CO AG
                                                            12-APR-2001; 2001EP-0109341.
                                                                                      07-NOV-2001
                                                                                                             EP1152062-A2
                                                                                                                                                                       DNA polymerase; reverse transcription; primer; divalent cation; mutant; transverse transcription reaction; fluorescein; cyanine; thermoactive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA polymerase's ability to incorporate dideoxynuclectides labelled with fluorescein and cyanine family dyes. The method of the invention is useful in reverse transcription/amplification reactions. The method provides improved reverse transcription efficiency at lower enzyme
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Smith ES,
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                                                                                                                                   Thermus filiformis.
                                                                                                                                                                                                           Native DNA polymerase motif #14.
                                                                                                                                                                                                                                     25-MAR-2002
                                                                                                                                                                                                                                                              AAM48265;
                                                                                                                                                                                                                                                                                     AAM48265 standard; Peptide; 11 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           concentrations relative to previous high temperature reverse
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                                                                                                                                                                                                                                                                                                                                                 1 LSQELAIPYEE 11
                                                                                                                                                            amplification
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9; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  11 AA;
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                                                                                                                                                                                                                                   (first entry)
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RESULT 10
AAR96267
ID AAR96
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Best Local
                                                                                                                                       30-AUG-1995;
09-NOV-1994;
09-MAR-1995;
07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA polymerase's ability to incorporate dideoxynuclectides labelled with fluorescein and cyanine family dyes. The method of the invention is useful in reverse transcription/amplification reactions. The method provides improved reverse transcription efficiency at lower enzyme concentrations relative to previous high temperature reverse transcription methods, and provide a wider range of usable salt concentrations. The use of the mulant DNA polymerase provides faster concentrations.
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               WP1; 1996-259862/26.
                                              Oldenburg MC, Olive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The
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N-PSDB; AAT27686
                                                                                                                                                                                                                                 09-NOV-1995;
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                                                                                                                                                                                                                                                                                                      W09615267-A1
                                                                                                                                                                                                                                                                                                                                      Thermus aquaticus.
                                                                                                                                                                                                                                                                                                                                                                          Staphylococcus; identification; detection
                                                                                                                                                                                                                                                                                                                                                                                                                                               Mutant Thermus aquaticus DNA polymerase (Clone 4F).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-NOV-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR96267 standard; Protein; 528
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                                                                     Brow MAD,
                                                                                                     (THIR-) THIRD WAVE TECHNOLOGIES INC
                                                                                                                                                                                                                                                                                                                                                                                           Escherichia; Saccharomyces; Campalalacter;
                                                                                                                                                                                                                                                                                                                                                                                                           p53; mutant; mutation; cleavage; nuclease; cleavase; Thermus;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              reverse transcription extension rates,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 LSXELXIPYER II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 LSQELSIPYEE 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequences given
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            quences given in AAB47791-97 and AAM48259-AAM48270 forms of motifs derived from DNA polymerases used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11 AA;
                                                                 Dahlberg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                       95US-0520946.
94US-0337164.
95US-0402601.
95US-0484956.
                                                                                                                                                                                                                               95WO-US14673.
                                                JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gelfand
                                                                 Fors L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 44; DB 23
Pred. No. 0.011;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ã
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DH,
                                                                 Heisler LM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Higuchi RG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and consequently less time is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            thermoactive DNA
                                                                 Lyamichev VI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          a reverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Myers TW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              in the method
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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RESULT 11
AAR23145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                   28-SEP-1990;
28-SEP-1990;
28-SEP-1990;
Abramson RD,
                                                                                                                                                                                                                                16-APR-1992
                                                                                                                                                                                                                                                                            WO9206200-A
                                                                                                                                                                                                                                                                                                                                                                    Misc-difference 1..2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5'-3'; exonuclease; PCR; amplification; SSR; sequencing; PLCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mutant thermostable DNA polymerase enzyme MET-SER 290 Taq.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-OCT-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR23145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR23145 standard; Protein; 544 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                polymerase is also referred to as the Cleavase BB enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    after the vector was digested with BstXI and BamHI. The DNA was then treated with the Klenow fragment of DNAPECH to trim both 3' overhangs to blunt ends which were then ligated together, resulting in an in frame deletion of 903 nucleotides. This mutant Trag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Thermus aquaticus (Taq) DNA polymerase was amplified using two primers (AAT27679, AAT27680). The Taq polymerase DNA was inserted into the BamiH restriction site of the expression vector pgr-3c and mutant genes we a created from that construct. This mutant was created
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          method is used for detecting mutation in the human p53 gene; for identifying strains of microorganisms, especially bacteria selected from the the group of members of the genera Campylobacter, Escherichia, Mycobacterium, Salmonella, Shigella and Staphylococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alternatively, microbial gene sequences. Cleavage products as compared to the cleavage products of reference gene sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cleavage of nucleic acids using an enzyme, especially a nuclease selected from the group consisting of Cleavage (RIM) BN enzyme, Thermus aquatious DNA polymerase, Thermus hermophilus DNA polymerase, Escherichia coli ExoIII and the Saccharomyces cerevisiae polymerase, Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 2A; Page 287-288; 433pp; English
                                       (CETU ) CETUS CORP.
                                                                                                                                                                                  30-SEP-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Thermus aquaticus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              especially hepatitis C virus and simian immunodeficiency virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The method may also be used for the identification of viruses,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     oligonucleotide containing a human p53 gene sequence or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rad1/Rad10 complex. The nucleic acid substrate is preferably an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               374 LSQELAIPYEE 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity es 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 LSXELXIPYEE 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    528 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
Gelfand DH;
                                                                                   90US-0590213.
90US-0590466.
90US-0590490.
                                                                                                                                                                                  91WO-US07035
                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                 /note= "deletion of residues 2-289 of native
                                                                                                                                                                                                                                                                                                                        sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 44; DB 1
Pred. No. 0.86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 17; Length 528;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This mutant was created and BamHI. The DNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cleavage products are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
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밁 Q

WPI; 1992-150885/18.

esp. in human p53 gene, to identify strains of microorganisms and

Thermostable DNA polymerases with altered 5'-3' exo nuclease activity - having conserved regions mutated or deleted, for use in e.g. PCR, sequencing and detection assays

Claim 11; Page 59; 185pp; English.

in enzymes used in homogeneous assays for the amplification and detection of a target nucleic acid sequence. Mutation of the DNA encoding particular regions of the enzymes can be used to prepare See also AAR23140-79 and AAR23722. a range of recombinant proteins having 5'-3' exonuclease activity discrimination in a combined polymerase ligase chain reaction (PLCR) assay. An enhanced amt. of 5'-3' exonuclease activity may be desirable sequence replication (SSR) and high temp. DNA sequencing. The absence of 5'-3' nuclease activity may facilitate higher sensitivity allelic amt. of 5'-3' exonuclease activity than the native enzyme. Thermostable DNA polymerases are useful in many recombinant DNA to a complete lack of activity. The sequence is that of a mutant of Thermus aquaticus polymerase techniques, esp. nucleic acid amplification by PCR, self-sustained MET-SER 290 Tag (the Stoffel fragment) having a different

Sequence 544 AA;

В QΥ Query Match
Best Local Similarity Matches 390 LSQELAIPYEE 400 1 LSXELXIPYEE 11 Conservative 93.6%; 0; Mismatches Score 44; DB 13; Length 544; Pred. No. 0.89; 0 Gaps 0;

XX AAR23163 RESULT 12 22-OCT-1992 (first entry) AAR23163; AAR23163 standard; Protein; 544 AA

Mutant thermostable DNA polymerase enzyme MET-ALA 292 T205.

5'-3'; exonuclease; PCR; amplification; SSR; sequencing; PLCR

Thermus species Z05 ΧX DE

WO9206200-A.

30-SEP-1991; 16-APR-1992. 91WO-US07035

28-SEP-1990; 28-SEP-1990; 28-SEP-1990; 90US-0590213. 90US-0590466. 90US-0590490.

(CETU) CETUS CORP.

Abramson RD, Gelfand DH;

N-PSDB; AAQ24322. WPI; 1992-150885/18.

in e.g. PCR, sequencing and detection assays activity - having conserved regions mutated or deleted, for use Thermostable DNA polymerases with altered 5'-3' exo nuclease

Claim 11; Page 59; 185pp; English

ΡŢ Cleavage of nucleic acids to detect mutation(s) - allows detection

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		7.		

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RESULT 13
AAR23168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local
                                                                                                                                                                                                                                                                   28-SEP-1990;
28-SEP-1990;
28-SEP-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The sequence is that of a mutant of Thermus species 205 polymerase mutant MET ALA 292 TZ05, having a different amt. of 5'-3' exonuclease activity than the native enzyme. Thermostable DNA polymerases are useful in many recombinant DNA techniques, esp. nucleic acid amplification by PCR, self-sustained sequence replication (SSR) and high temp. DNA sequencing. The absence of 5'-3' nuclease activity may facilitate higher sensitivity allelic discrimination in a combined polymerase ligase chain reaction (PLCR) assay. An enhanced amt. of 5'-3' exonuclease activity may be desirable in enzymes used in homogeneous assays for the amplification and detection of a target
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nucleic acid sequence. Mutation of the DNA encoding particular regions of the enzymes can be used to prepare a range of recombinations having 5'-3' exonuclease activity to a complete lack of
The sequence is that of a mutant of Thermus thermophilus polymerase mutant MET-ALA 292 Tth. having a different amt. of 5'-3' exonuclease activity than the native enzyme. Thermostable DNA polymerases
                                                                                        Thermostable DNA polymerases with altered 5'-3' exo nuclease activity - having conserved regions mutated or deleted, for use in e.g. PCR, sequencing and detection assays
                                                              Claim 11; Page 59; 185pp; English.
                                                                                                                                                           N-PSDB; AAQ24328.
                                                                                                                                                                         WPI; 1992-150885/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5'-3'; exonuclease; PCR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mutant thermostable DNA polymerase enzyme MET-ALA 292 Tth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR23168 standard; Protein; 544 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                        Abramson
                                                                                                                                                                                                                                                                                                                                   30-SEP-1991;
                                                                                                                                                                                                                                                                                                                                                                                              WO9206200-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-OCT-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 See also A \land R23140-79 and AAR23722.
                                                                                                                                                                                                                                    (CETU ) CETUS
                                                                                                                                                                                                                                                                                                                                                               16-APR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             390 LSCELAIPYEE 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
nes 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 LSXELXIPYEE 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      thermophilus
                                                                                                                                                                                                        RD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    544 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                      CORP.
                                                                                                                                                                                                       Gelfand
                                                                                                                                                                                                                                                                   90US-0590490
                                                                                                                                                                                                                                                                                    90US-0590213.
90US-0590466.
                                                                                                                                                                                                                                                                                                                                91WO-US07035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "residues 2-291 deleted from the native
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93.6%;
                                                                                                                                                                                                        DH.
                                                                                                                                                                                                                                                                                                                                                                                                                          sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amplification; SSR; sequencing; PLCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0.89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 544;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             . .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 14
AAR23157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCCCCCXXXXIII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Вb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best
amplification by PCR, self-sustained sequence replication (SSR) and high temp. DNA sequencing. The absence of 5'-3' nuclease activity may facilitate higher sensitivity allelic discrimination in a combine
                                               are useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Key
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in many recombinant DNA techniques, esp. nucleic

acid

exonuclease

in a combined

멍 δλ

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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-SEP-1990;
28-SEP-1990;
28-SEP-1990;
The sequence is that of a mutant of Thermus species sps17 polymerase mutant MET-ALA 288 Tsps17, having a different amt. of 5'-3' exonucles mutant MET-ALA 288 Tsps17, having a different amt. of 5'-3' exonucles activity than the native enzyme. Thermostable DNA polymerases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     regions of the enzymes can be used to prepare a range of recombinant proteins having 5'-3' exonuclease activity to a complete lack of
                                                                                                                                                                                         Thermostable DNA polymerases with altered 5'-3' activity - having conserved regions mutated or d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Thermus species
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5'-3'; exonuclease; PCR; amplification; SSR; sequencing; PLCR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mutant thermostable DNA polymerase enzyme MET-ALA 288 Tsps17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-OCT-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR23157
                                                                                                            Claim 11; Page 59; 185pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-SEP-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             W09206200-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR23157;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    See also AAR23140~79 and AAR23722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               activity.
                                                                                                                                                                in e.g. PCR, sequencing and detection assays
                                                                                                                                                                                                                                                                            N-PSDB; AAQ24010
                                                                                                                                                                                                                                                                                                                                                       Abramson RD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-APR-1992
                                                                                                                                                                                                                                                                                                                                                                                                            (CETU ) CETUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     390 LSQELAIPYEE 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
nes 9; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 LSXELXIPYEE 11
                                                                                                                                                                                                                                                                                                     1992-150885/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     standard; Protein; 545 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  544 AA;
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81.8%;
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RESULT 15
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Best Local
                                        The invention relates to a chimeric nucleic acid polymerase comprising at least two enzymatically active domains which are non-naturally associated. The polymerase is thermostable and possesses new or improved catalytic properties compared to known nucleic acid polymerases. The polymerase eliminates the need to specifically develop multi-enzyme reaction mixtures, which are often difficult to optimise and expensive to use. The polymerase facilitates rapid, efficient and accurate generation of nucleic acid molecules, particularly in regard to PCR protocols. The polymerase is also useful for nucleic acid polymerisation which is useful in genetic engineering techniques and molecular biology.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          polymerase ligase chain reaction (PLCR) assay. An enhanced amt. of 5'-3' exonuclease activity may be desirable in enzymes used in homogeneous assays for the amplification and detection of a target nucleic acid sequence. Mutation of the DNA encoding particular regions of the enzymes can be used to prepare a range of recombinant proteins having 5'-3' exonuclease activity to a complete lack of
                                                                                                                                                                                                                                                                    Chimeric nucleic acid polymerase for nucleic acid polymerization and generation of nucleic acids, comprises two enzymatically active domains which are non-naturally associated .
                                                                                                                                                                                                                                     Claim 12; Page 46-49; 93pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Thermus aquaticus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             genetic engineering.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Thermus aquaticus; Taq; DNA polymerase; polymerisation; PCR protocol;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAE09304;
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                              The present protein sequence is Thermus aquaticus (Taq) DNA polymerase
                                                                                                                                                                                                                                                                                                                                         WPI; 2001-536571/59
                                                                                                                                                                                                                                                                                                                                                                         Loeffert D,
                                                                                                                                                                                                                                                                                                                                                                                                                                           17-FEB-2000; 2000US-0506153.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-FEB-2001; 2001WO-EP01790.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Thermus aquaticus (Taq) DNA polymerase #1.
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Pred. No. 0.89;
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Query Match Best Local

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552 AA;

Matches

Similarity9; Conserve

Conservative

93.6%;

Score 44; DB 22; Pred. No. 0.9; 0; Mismatches 2

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398 LSQELAIPYEE 408
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Search completed: January 15, Job time: 30.2857 secs 2003, 11:20:14

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Result
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Maximum DB seq
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     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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    protein search, using sw model

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length: 2000000000
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47
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Match
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     Issued_Patents_AA:*
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Copyright (c) 1993 - 2003 Compugen Ltd.
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/cgn2_6/ptodata/1/iaa/5B_comB.pep:*
/cgn2_6/ptodata/1/iaa/6A_comB.pep:*
/cgn2_6/ptodata/1/iaa/6B_comB.pep:*
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US-08-520-946-990
US-08-520-946-990
US-09-96-399-2
US-08-021-6-32C-6
US-09-96-399-4
PCT-US95-14418-4
PCT-US95-14418-4
PCT-US95-14418-4
PCT-US95-1537-4
US-09-777-538-2
US-09-777-538-2
US-09-777-538-2
US-09-777-538-6
US-08-4819-6
US-08-4819-6
US-08-4819-65-5
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US-08-4819-65-5
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US-08-957-653-5
US-08-959-491-5
US-08-823-516-5
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(without alignments)
34.855 Million cell updates/sec
Sequence 2, Appli
Sequence 4, Appli
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Sequence 90, Appl
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US-08-484-956-90
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APPLICATION NUMBER: US 08/254,359
FILING DATE: 06-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/073,384
FILING DATE: 04-JUN-1993
                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 08/402,601
FILING DATE: 09-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/337,164
FILING DATE: 09-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: DAHLBERG, JAMES E. APPLICANT: LYAMICHEV, VICTOR I. APPLICANT: BROW, MARY ANN D.
                                                                              FILING DATE: 07-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: CARRPOLL ], PETER G.
                                                                                                                                                   PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
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                 TELEPHONE: (415) 705-8410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: DETECTION OF NUMBER OF SEQUENCES: 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: OLDENBURG, MARY C. APPLICANT: HEISLER, LAURA
                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC COMPUTER: 1008/MS-DOS

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY:
STATE:
                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: HAVERSTOCK, MEDLEN & CARROLL STREET: 220 MONTGOMERY STREET, SUITE 2200 CLITY: SAN FRANCISCO
                                                  REFERENCE/DOCKET NUMBER: FO
                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
               TELEPHONE:
                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
   TELEFAX: (415) 397-8338
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US-08-758-314-5
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US-08-520-946-5
US-08-156-020-2
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US-08-156-020-1
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US-08-433-043-4
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US-08-438-619-2
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US-08-438-956-4
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Sequence 90, Application US/08520946
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 90:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Kaiser, Michael W.
APPLICANT: Lyamichev, Victor I.
APPLICANT: Lyamichev, Natasha
TITLE OF INVENTION: Cleavage Of Nucleic Acid Using
TITLE OF INVENTION: Thermostable FEN-1 Endonucleases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                            MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 705-8410
                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Ingolia, Diane E.
REGISTRATION NUMBER: 40,027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                              374 LSQELAIPYEE 384
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Local Similarity 81.8%;
nes 9; Conservation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/757,653 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 94104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH:
                                                                                                             1 LSXELXIPYEE 11
                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 LSXELXIPYEE 11
                                                                                                                                                                                                                                                                                             LENGTH:
                                                                                                                                                                                                                                                                          amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         San Francisco.
California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5843669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Application US/08757653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                220 Montgomery Street, Suite 2200
                                                                                                                                                                                                                                                                                          528 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          United States Of America
                                                                                                                                                                                                                                                                                                                                               (415) 397-8338
                                                                                                                                                                                                                                             linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Medlen & Carroll, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                              435
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81.8%;
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                                                                                                                                                                                                                                                                                                                                                                                               FORS-02565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                             Score 44; DB 2; Length 528; Pred. No. 0.34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 44; DB 2;
Pred. No. 0.34;
                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Indels
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                                                                                                                                              Indels
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; OTHER INFORMATION: Recombinantly engineered mutant \ensuremath{\text{US-09-096-399-2}}
                                                                                                                                                                                                                                                                                                                                                        ; GENERAL INFORMATION:
; APPLICANT: Wurst, Helmut
; APPLICANT: Qui, Zhi-Hao
                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 4
US-09-096-399=2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ъ
                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 2, Application US/09096399A
; Patent No. 6130045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-520-946-90
Query Match
Best Local Similarity 81.0
                                                                                                                                                                                                   SEQ ID NO 2
LENGTH: 553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 93.6%;
Best Local Similarity 81.8%;
Matches 9; Conservative
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                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/096,399A CURRENT FILING DATE: 1998-06-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Thermostable Polymerase
                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: CLON-007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
                                                                                                                                            ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                   TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: BROW, MARY ANN D.
APPLICANT: LYAMICHBY, VICTOR I.
APPLICANT: OLIVE, DAVID M.
TITLE OF INVENTION: RAPID DETECTIVE OF INVENTION: PATHOGENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: 11 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: FO TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         374 LSQHLAIPYHH 384
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: CARROLL, PETER G. REGISTRATION NUMBER: 32,837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: PC-DOS/MS-DOS
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STATE: CALIFORNIA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 LSXELXIPYBE 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/520,946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           528 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                Helmut
                      93.6%; Score 44; DB 4; Length 553;
81.8%; Pred. No. 0.36;
ative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RAPID DETECTION AND IDENTIFICATION OF PATHOGENS
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Pred. No. 0.34;
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US-08-021-623C-6
                                                                                                                                                                                                                                   US-09-096-399-4
                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-021-623C-6
                                                                                                                                                                                                                                                    RESULT 6
                             SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 4
                                                                                                                                                                                                 Sequence 4, Application US/09096399A Patent No. 6130045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 6, Application US/08021623C Patent No. 5436149
                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                           CURRENT APPLICATION NUMBER: US/09/096,399A
CURRENT FILING DATE: 1998-06-11
NUMBER OF SEQ ID NOS: 4
                                                                                                                            APPLICANT: Wurst, Helmut
APPLICANT: Qui, Zhi-Hao
TITLE OF INVENTION: Thermostable Polymerase
                                                                                                               FILE REFERENCE: CLON-007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
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TYPE: PRT
                 ENGIH: 559
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin 1.0, v1.25; EDIX; Wordperfect.
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk, 5.25",
                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                     400 LSQELAIPYEE 410
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 33,650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Blosser, G. Harley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/021,623C FILING DATE: 19-FEB-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                  Local Similarity es 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE:
                                                                                                                                                                                                                                                                                                                                    1 LSXELXIPYEE 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: Senninger, Powers, Leavitt and Roedel
One Metropolitan Square, 16th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   554 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Barnes Ph.D., Wayne M.
WENTION: Thermostable DNA polymerase with
WENTION: enhanced thermostability and enhanced length and
WENTION: efficiency of primer extension
                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         314/231-4342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
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                                                                                                                                                                                                                                                                                                                                                                                    93.6%;
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                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                    Score 44; DB 1
Pred. No. 0.36;
                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              360 kb
                                                                                                                                                                                                                                                                                                                                                                                                     DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                     Length 554;
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                                                                                                                                                              RESULT 8
                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                     Best
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RESULT 7
PCT-US95-14418-5
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US-09-096-399-4
                                                                                                                                                              PCT-US95-15327-5
                                                                                                                                                                                                                                                                                                                                                                                 PCT-US95-14418-5
                                                                                                                           Sequence 5, Application PC/TUS9515327 GENERAL INFORMATION:
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Best Local Similarity 81.8%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                             TITLE OF INVENTION: Bio-
TITLE OF INVENTION: The:
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Gass, David A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
                                                                                                                                                                                                                                   406 LSQELAIPYEE 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       405 LSQELAIPYEE 415
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                        Local Similarity
nes 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Chicago
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: PCT/US95/14418
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312/474-0448
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81.8%;
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                                                                   Biologically Active Fragments
Thermus Flavus DNA Polymerase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             38, 153
                                                                                                                                                                                                                                                                                                      0; Mismatches
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Pred. No. 0.37;
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Pred. No. 0.37;
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South Wacker Drive
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                             TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 597 amino acids
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SEQUENCE CHARACTERISTICS:
LENGTH: 560 amino acid
                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Gass, David A.
REGISTRATION NUMBER: 38,153
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NAME: GASS, DAVID A.
REGISTRAT: ION UNDBER: 38,153
REFERENCE TOCKET NUMBER: 28003/31716
                                                                                                                    TELECOMMUNICATION INFORMATION: TELEPHONE: 312/474-6300
                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
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MEDIUM TYPE: Floppy disk
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TYPE: ami
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CLASSIFICATI
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TELEX: 25-3856
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STATE: Illinois
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CLASSIFICATION:
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                amino acid
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81.8%;
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Pred. No. 0.37;
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PCT-US95-14418-4
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SOFTWARE:
SEQ ID NO 2
                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                      Sequence 2, Application US/09587856 Patent No. 6214557
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Matches 9; Conserv
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                    CURRENT APPLICATION NUMBER: US/09/587,856
CURRENT FILING DATE: 2000-06-06
NUMBER OF SEQ ID NOS: 9
SOFTMARE: Patentin Ver. 2.1
                                                                                        APPLICANT: Washington University TITLE OF INVENTION: COLD SENSITIFILE REFERENCE: WSHU 2009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acids
TYPE: amino acid
TOPOLOGY: ]in--
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LENGTH: 597 amino acid
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SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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                                                                                                    COLD SENSITIVE MUTANT DNA POLYMERASES
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    Mismatches

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Pred. No. 0.39;
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; TYPE: PRT
; ORGANIZM: Thermus aquaticus
US-09-777-538-2
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SEQ ID NO 2
LENGTH: 810
TYPE: PRT
ORGANISM: Thermus aquaticus
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                                                                              Query Match
                                                                                                                                                                               SEQ ID NO 2
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                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/777,538
CURRENT FILING DATE: 2001-02-06
PRIOR APPLICATION NUMBER: 09/587,856
PRIOR FILING DATE: 2000-06-06
NUMBER OF SEQ ID NOS: 9
                                                                                                                                                                                                                                                                                       APPLICANT: Barnes, Wayne M
APPLICANT: Kermekchiev, Milko B
TITLE OF INVENTION: USE THEREOF
FILE REFERENCE: WSHU 2009.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT FILING DATE: 2001-02-06
PRIOR APPLICATION NUMBER: 09/587,856
PRIOR FILING DATE: 2000-06-06
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CURRENT FILING DATE: 2001-02-06
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TITLE OF INVENTION: NUCLEIC ACIDS ENCODING COLD SENSITIVE MUTANT DNA
TITLE OF INVENTION: POLYMERASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE:
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Local Similarity 81.8%;
hes 9; Conservative
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                 1 LSXELXIPYEE 11
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                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WSHU 2009.1
                                                                93.6%;
                                               Score 44; DB 4;
Pred. No. 0.55;
0; Mismatches
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Pred. No. 0.55;
0; Mismatches
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                                                                                 DB 4;
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                                                                                Length 810;
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RESULT 14
US-07-977-434-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 6,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: WordPerfect 2.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
TELEPHONE: (510) 814-2972
                                                                    ATTORNEY/AGENT INFORMATION: NAME: Luann Cserr
                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 22-AUG-
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 17-JUN-
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 5: FILING DATE: 15-MAY-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 5 FILING DATE: 28-SEP-1990
                               REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: Case No.
                                                                                                                                                    APPLICATION NUMBER: FILING DATE: 02-NOV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 143,441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 28-SEP-1990
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                                                                                                                                                    02-NOV-1990
                                                                                                                                                                                                                                                     20-SEP-1990
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                                                                                                     24-JUL-1990
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5' TO 3' EXONUCLEASE MUTATIONS OF THERMOSTABLE DNA POLYMERASES
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                                                                                                                   US 557,517
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US-08-458-819-6
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                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: (
FILING DATE: 15-AUG-)
                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 01
FILING DATE: 17-JUN-1987
                                                                                                                                                                                                                                                          APPLICATION NUMBER: 15-MAY-
FILING DATE: 15-MAY-
PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US,
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Gelfand, David H.
APPLICANT: Abramson, Richard D.
TITLE OF INVENTION: 5' TO 3' EXONUCLEASE MUTATIONS OF
TITLE OF INVENTION: THERMOSTABLE DNA POLYMERASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
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APPLICATION NUMBER:
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PRIOR APPLICATION DATA:
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                              APPLICATION NUMBER: WO PCT/US90/07641 FILING DATE: 21-DEC-1990
                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 590,466 FILING DATE: 28-SEP-1990
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APPLICATION NUMBER:
                                                                                                                             FILING DATE: 22-AUG-1986
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                                                                                                                                             APPLICATION NUMBER:
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07110-1199
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9; Conserv
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amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       340 Kingsland Street
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                                                                                                                                                                                                                                                                                                                                                                                                                                         23-FEB-1993
UMBER: US 590,490
                                                                            15-AUG-1991
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US 585,471
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Search completed: January 15, 2003, 12:38:22 Job time : 11.2857 secs

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Query Match
Best Local Similarity
Matches 9; Conserve
 В
                          γΩ
                                                                                                              ; MOLECULE TYPE: US-08-458-819-6
                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO:
                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 830 amino acid
                                                                                                                                                                                                                                                                                   FILING DATE: 24-JUL-1990 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 1
                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 22-DEC-1989 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 20-SEP-PRIOR APPLICATION DATA:
                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION: TELEPHONE: (510) 814-2972
676 LSQELSIPYEE 686
                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 31,822
                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
                          1 LSXELXIPYEE 11
                                                                                                                                                      amino acids
                                                                                                                                                                                                                                                                       Luann Cserr
                                                       Conservative
                                                                                                                                          linear
                                                                                                                           protein
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81.8%;
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                                                                                                                                                                                                                                           Case No. 5795762 8753
                                                       0;
                                                                   Score 44; DB 1;
Pred. No. 0.56;
                                                       Mismatches
                                                                                Length 830;
                                                       Indels
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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq
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                                                                                                                                                                                                                                                                                                                                                                                            and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed.
                                                                                                                                                                                                                                                                                                                   Score
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47
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                                                                                                                                                                                                                                                                                                                   Match
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                                                                                                                                                                                                                                                                                                                                  Query
   Published_Applications_AA: *
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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/cgin2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
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/cgin2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
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/cgin2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
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US-10-033-297-4
US-10-033-297-4
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US-10-071-505-1
US-10-081-806-4
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US-10-033-297-71
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US-09-823-649A-4
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US-09-823-649A-13
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US-09-823-649A-11
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US-09-823-649A-3
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ALIGNMENTS

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: Sequence 4, Application US/09823649A; Patent No. US20020012970A1; GENERAL INFORMATION:
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; Patent No. US20020012970A1
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APPLICANT: Elfstrom, Carita
APPLICANT: Gelfand, David
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APPLICANT: Wang, Alice
TITLE OF INVENTION: HIGH TEMPERATURE REVERSE TRANSCRIPTION USING MUTANT DNA POLYME
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Myers, Thomas
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Query Match
Best Local Similarity
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     Sequence 9, Application US/09823649A
                                                                                                                                                                                                                                                                               SEQ ID NO 8
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Patent No. US20 20012970A1
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CURRENT FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: US 60/198,336
PRIOR FILING DATE: 2000-04-18
NUMBER OF SEQ ID NOS: 21
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CURRENT ETLING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: US 60/198,336
PRIOR FILING DATE: 2000-04-18
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                                                                                                                                                                                                                           TYPE: PRT ORGANISM: Thermus aquaticus
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Elfstrom, Carita
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Schoenbrunner, Nancy
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Higuchi, Russell
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Pred. No. 0.0021;
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                                                                                RESULT 6
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APPLICANT: Smith, Edward
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US-09-823-649A-11
; Sequence 11, Application US/09823649A
; Patent No. US20020012970A1
                                                                                                                                                                         Query Match
Best Local Similarity
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SOFTWARE: PatentIn version 3.0
SEQ ID NO 10
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PRIOR FILING DATE: 2000-04-18
NUMBER OF SEQ ID NOS: 21
SOFTWARE: BATCH.
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APPLICANT:
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PRIOR APPLICATION NUMBER: US 60/198,336
PRIOR FILING DATE: 2000-04-18
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CURRENT APPLICATION NUMBER: US/09/823,649A
CURRENT FILING DATE: 2001-03-30
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APPLICANT: Elfstrom, Ca.
APPLICANT: Gelfand, Dav
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CURRENT APPLICATION NUMBER: US/09/823,649A
CURRENT FILING DATE: 2001-03-30
                                                                                                                                                                                                                                                                                                    LENGTH: 11
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: HIGH TEMPERATURE REVERSE TRANSCRIPTION USING MUTANT DNA POLYME
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Gelfand, David
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Gelfand, David
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milarity 81.8%;
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Pred. No. 0.0021;
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US-09-823-649A-13; Sequence 13, Application US/09823649A; Patent No. US20020012970A1
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: Sequence 12, Application US/09823649A

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                                                                GENERAL INFORMATION:
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LENGTH: 11
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APPLICANT:
APPLICANT:
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CURRENT FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: US 60/198,336
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APPLICANT:
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                             APPLICANT: Smith, Edward APPLICANT: Elfstrom, Car
                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 21 SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Elfstrom, Carita
APPLICANT: Gelfand, David
APPLICANT: Higuchi, Russell
APPLICANT: Myers, Thomas
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                                                                                                                                                                                                                                                                                                                               TYPE: PRT ORGANISM: Thermus sp. sps17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: RPA1006
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Gelfand, David
Higuchi, Russell
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Gelfand, David
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81.8%;
                                 Carita
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81.8%;
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Pred. No. 0.0021;
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Query Match
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US-10-033-297-5
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                                                                                                                                    Sequence 5, Application US/10033297 Publication No. US20020187486A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 14
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CURRENT APPLICATION NUMBER: US/09/823,649A
CURRENT FLIING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: US 60/198,336
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TITLE OF INVENTION: HICH TEMPERATURE REVERSE TRANSCRIPTION USING MUTANT DNA POLYMETILE REFERENCE: REALOGE
FILE REFERENCE: REALOGE
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                                                                      GENERAL INFORMATION:
GENERAL INFORMATION:
Hall, Jeff G.
Lyamichev, Victor I.
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NUMBER OF SEQUENCES: 163
                                TITLE OF INVENTION:
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Schoenbrunner, Nancy
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Gelfand, David
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                                                                 Mast, Andrea L.
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            Mary Ann D.
ON: Detection Of Nucleic Acids By Multiple
Sequential Invasive Cleavages
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Pred. No. 0.0021;
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Pred. No. 0.0021;
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US-10-081-806-5
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INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                        677 LSGELSIPYEE 687
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                                                       CORRESPONDENCE ADDRESS:
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TELEPHONE: (415) 705-8410
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                                                                                NUMBER OF SEQUENCES:
                                                                                               Lyamichev, Victor I.
TITLE OF INVENTION: Invasive Cleavge Of Nucleic Acids
                                                                                                                                       APPLICANT: Prudent, James R. Hall, Jeff G.
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ADDRESSEE: Medlen & Carroll, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                          9; Conserva
STREET: 220 Montgomery Street, Suite 2200 CITY: San Francisco
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                      ADDRESSEE: Medlen & Carroll, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 08/682,853 FILING DATE: 12-JUL-1996
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FILING DATE: 12-No. US20020187486A1-2001
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STATE: California
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APPLICATION NUMBER: US 08/758,314
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Sequence 4, Application US/10033297 Publication No. US20020187486A1 GENERAL INFORMATION:
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Matches 9; Conserv
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             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/033,297
FILING DATE: 12-No. US20020187486A1-2001
                                                                                                                                                                     COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Hall,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein SEQUENCE DESCRIPTION: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: <Unknown> PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                       STREET: 220 Montgomery Street, Suite 2200 CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Ingolia, Diane E. REGISTRATION NUMBER: 40,027
CLASSIFICATION: <Unknown>
                                                                                SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                COUNTRY: United States Of America
                                                                                                                                                                                                                                          STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 08/599,491 FILING DATE: 24-JAN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 08/682,853 FILING DATE: 12-JUL-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 22-Feb-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: California
COUNTRY: United States Of America
                                                                                                                                              MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                     ADDRESSEE: Medlen & Carroll, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 831 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (415) 705-8410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: FORS-02564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/756,386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/10/081,806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                      Mast, Andrea L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               yamichev, Victor I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Jeff G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                   Mary Ann D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      397-8338
                                                                                                                                                                                                                                                                                                                                                                        Sequential Invasive Cleavages
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ 1D NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
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Pred. No. 0.22;
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FILING DATE:

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Sequence 2, Application US/09972834
Publication No. US20020192663A1
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                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-TOS/MS-DOS
OPERATING SYSTEM: PC-TOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/09/972,834
FILING DATE: 04-Oct-2001
CLASSIFICATION: GUNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS: NO. US20020187486A1 Relevant
TOPOLOGY: NO. US20020187486A1 Relevant
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
3-297-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                           PRIOR APPLICATION DATA
                                                                                                                                                                                                                             COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Thermostable Polymerases Having Altered Fidelity and Methods of Identifying and Using Same
                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Loeb, Lawrence A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 08/682,853
FILING DATE: 12-UUL-1996
APPLICATION NUMBER: US 08/599,491
FILING DATE: 24-JAN-1996
  APPLICATION NUMBER: 08/978,806 FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                    COUNTRY: United States
                                                                                                                                                                                                                                                                                     STATE: California
                                                                                                                                                                                                                                                                                                                              ADDRESSEE: CAMPBELL & FLORES LLP
STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 832 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: FORS-02736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Ingolia, Diane E. REGISTRATION NUMBER: 40,027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 08/756,386 FILING DATE: 29-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 02-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 08/758,314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 08/759,038 FILING DATE: 02-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: PCT/US97/01072 FILING DATE: 21-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/09/350,597 FILING DATE: 09-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/823,516
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81.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
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Pred. No. 0.22;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 832;
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                                                                                                                                                                                                       US-10-081-806-4
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                                                                                                                                          Sequence 4, Application US/10081806 Publication No. US20020197623A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 93.6%;
Best Local Similarity 81.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Flick, Parke
TITLE OF INVENTION: "FAQ DNA Polymerase Having an Amino Acid Substitution at
TITLE OF INVENTION: E681 and Homologs Thereof Exhibiting Improved Salt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Davis, Maria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: ENTITLE OF INVENTION: TO FILE REFERENCE: PB9944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 60/148,012 PRIOR FILING DATE: 1999-08-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/10/071,505
CURRENT FILING DATE: 2002-02-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT ORGANISM: Thermus aquaticus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             678 LSQELAIPYEE 688
                                                                                                                                                                                                                                                                                         678 LSQELAIPYEE 688
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-UW 2873
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619)535-9001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION: NAME: Campbell, Cathry
                                    Lyamichev, Victor I.
TITLE OF INVENTION: Invasive Cleavge Of Nucleic Acids
NUMBER OF SEQUENCES: 69
                     CORRESPONDENCE ADDRESS:
                                                                                                   APPLICANT: Prudent, James R. Hall, Jeff G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
ADDRESSEE: Medlen & Carroll, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nelson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 832 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Finn, Patrick J.
Nampalli, Satyam
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kumar,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                           93.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2002-02-08
                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                         Score 44; DB 9
Pred. No. 0.22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
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Pred. No. 0.22;
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                                                                                                                                                                                                                                                                                                                                                                                                                 DB 9; Length 832;
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678 LSQELAIPYEE 688

Matches Query Match

Local Similarity nes 9; Conserv 1 LSXELXIPYEE 11

Conservative

TYPE: amino acid

US-09-972-834-2 RESULT 13

GENERAL INFORMATION:

NUMBER OF SEQUENCES:

CITY: San Diego

```
STREET: 220 Montgomery Street, Suite 2200
CTTY: San Prancisco
STREE. California
COMPUTER CALIFORNIA
COMPUTER RAMABLE PORN:
COMPUTER RAMABLE PORN:
COMPUTER: 18 Me Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM:
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Result
No.
                                                                                                                                                                                                                                                                                                                                                                                              Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                  Minimum DB
Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                Database :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Title:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OM protein - protein search, using sw model
  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                 Score
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  length: 2000000000
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Gapop 10.0 , Gapext 0.5
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Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            283224 seqs, 96134422 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-823-649A-2
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  PIR_73:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LSXELXIPYEE 11
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pir3:*
pir4:*
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259
857
457
474
1451
149
327
327
3381
7381
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3363
                  JQ0494
T41581
G84529
AC1431
AI1804
H98220
                                                                    S25321
S75715
G64312
T40331
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C;Date: 03-May-1994 #sequence_revision 20-Feb-1995 #text_change 18-Jun-1999
C;Accession: $26675; $24929
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45	44	43	42	41	40	39	38	37	36	35	4	S S	32	31	30
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ALIGNMENTS

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A;Molecule type: DNA
A;Residues: 1-831 <ISH>
C:Superfamily: DNA-directed DNA polymerase
C;Keywords: nucleotidyltransferase
                                                                                                                                                                                            R:Ishino, Y.; Ueno, T.; Miyagi, M.; Uemori, T.; Imamura, M.; Tsunasawa, S.; Kato, I.
3. Biochem. 115, 1019-1024, 1994
A:Title: Overproduction of Thermus aquaticus DNA polymerase and its structural analys A:Reference number: JX0359; MUID:95204371; pMID:7896728
A;Accession: JX0359
                                                                                                                                                                                                                                                                                                                 DNA-directed DNA polymerase (EC 2.7.7.7) - Thermus aquaticus C:Species: Thermus aquaticus C:Date: 04-Sep-1998 #sequence_revision 04-Sep-1998 #text_change 07-May-1999
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C;Superfamily: DNA-directed DNA polymerase I
C;Keywords: DNA binding; nucleotidyltransferase
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A; Note: the source is designated
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A;Title: Molecular cloning and nucleotide sequence of the DNA polymerase gene from A;Reference number: S26675; MUID:93087201; PMID:1454544
                                                                                                                                                                        A; Status: preliminary
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R; Ishino, Y.; Ueno,
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                      Score 44; DB 2;
Pred. No. 0.46;
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Pred. No. 0.46;
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conserved hypothetical protein aq_367 - Aquifex aeolicus
C;Species: Aquifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 05-Nov-1999
C;Accession: G70332
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                                  A; Title: The complete genome of the hyperthermophilic bacterium A; Reference number: A70300; MUID:98196666; PMID:9537320
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A;Title: Isolation, characterization, and expression in Escherichia coli of the A;Reference number: A33530; MUID:89197950; PMID:2649500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein YHR071w - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein H8025.1
C;Species: Saccharomyces cerevisiae
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A; Residues: 1-832 < LAW>
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C;Date: 29-Jan-1990 #sequence_revision 29-Jan-1990 #text_change
A;Status:
                  A; Accession: G70332
                                                                       Nature 392,
                                                                                                      R; Deckert, G.; Warren, P.V.;
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A; Cross-references: EMB
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                                                    Aquifex aeolicus
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C; Superfamily: n
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-474 <KUR>
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                                                                                                                                                                                                                                                                                                                                                    alpha-galactosidase (melibiase) [imported] - Agrobacterium tumefaciens (strain
C;Species: Agrobacterium tumefaciens
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 17-May-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; M.; Karp, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001
                                                                                                                                                                                                                  A; Reference number:
A; Accession: D98157
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A; Molecule type: DNA
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R;Wood, D.W.; Setuba
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C; Species: Agrobacterium tumefaciens
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A; Residues: 1-850 < AQF>
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F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas,
94, 2323-2328, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         l Similarity
7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity 54.5
6; Conservative
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                                                                                                                                                                                                                                     uence of the Plant Pathogen and Biotechnology Agent Agrobacterium
A97359; PMID:11743194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Y.; Biddle, P.;
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63.6%;
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"Cloning of rat alpha-2-B-adrenergic receptor gene
rat submandibular gland.";
Shigahu 80:317-326(1992).
-!- FUNCTION: ALPHA-2 ADRENERGIC RECEPTORS MEDIATE
                                                                                                                                                      SEQUENCE
                                                                                                                                                                         CONFLICT
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PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
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PIR; S13023; S13023.
PIR; A40392; A40392.
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EMBL; X57659; CAA40861.1; -.
EMBL; M62371; AAA42033.1; -.
EMBL; D00819; BAA00700.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entities requires a license agreement (See http://www.isb-sib.ch/announce/
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TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=95340540; PubMed=7615550; Johnson E.S., Ma P.C.M., Ota T.M., Varshavsky
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nelson M.K., Kurihara T., Silver P.A.; "Extragenic suppressors of mutations in the cytoplasmic C SEC63 define five genes in Saccharomyces cerevisiae."; Genetics 134:159-173(1993).
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                                                                     InterPro; IPR000822; znf_C2H2.
Pfam; PF00096; zf-C2H2; 2.
SMART; SM00355; ZnF_C2H2; 1.
PROSITE; PS50157; ZINC_FINGER_C2H2_2;
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PIR; S30806; S30806.
PIR; S41986; S41986.
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                                                                                                                                                                                                                                                                                                                                      use by non-profit institutions as long a modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Saccharomyces cerevisiae."; FEBS Lett. 423:149-154(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     signal.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Andre B., Vissers S., Urrestarazu L.;
Submitted (FEB-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Pungi; Ascomycota; Saccharomycotina; Saccharomycetes;
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"Sonip is a component of the 26S proteasome of the yeast
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHARACTERIZATION.
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                                                         Proteasome;
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01-007-1993 (Rel. 27, Last sequence update)
16-007-2001 (Rel. 40, Last annotation update)
265 proteasome regulatory subunit RPN4 (Nuclear protein SON1)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION: MAY PLAY A ROLE IN NUCLEAR INTEGRITY, IS REQUIRED FOR NORMAL GROWTH AT LOW TEMPERATURES. SONI MUTANTS GROW SLOWLY AT LOW TEMPERATURES AND SHOW PARTIAL MISLOCALIZATION OF NUCLEAR ANTIGENS. PROBABLY INTERACTS MITH SEC63. COMPONENT OF 26S PROTEASOME.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PubMed=9512348;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PubMed-8514125;
ASP/GLU-RICH (ACIDIC).
ASP/GLU-RICH (ACIDIC).
NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
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SEQUENCE

531

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60152 MW;

4316281AC09FBE7F CRC64;

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RESULT 12
VG12_BPPH2
ID VG12_BPP 2
                                                                                                                                                            RESULT 13
VG12_BPP2A
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                                                                                                     _BPPZA
VGI2_BPPZA
VGI2_BPPZA
P07537;
P07537;
P07537;
P0858 (Rel. 07,
P1991 (Rel. 07,
P1991 (Rel. 1)
                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local
                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                            Viruses; dsDNA viruses, no phi-29-like viruses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-FEB-1991
01-FEB-1991
SEQUENCE FROM N.A.
MEDLINE-87031573; PubMed=3095188;
Paces V., Vicek C., Urbanek P.;
Pucleotide sequence of the late region of Bacillus subtilis phage
                                                                                                                                                                                                                                                                                                                              entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                  the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                     "Nucleotide sequence of the late region of Bacillus phage phi completes the 19,285-bp sequence of phi 29 genome. Comparison the homologous sequence of phage PZA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Viruses; dsDNA virus
phi-29-like viruses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-FEB-1991
                                                                                 Bacteriophage PZA.
                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Vlcek C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=87106857; PubMed=3803926;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P20345;
                                                   NCBI_TaxID=10757
                                                                                                   Pre-neck appendage protein
                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                         Late protein
                                                                                                                                                                                                                                                                                                            EMBL; M14782; AAA32285.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                            Gene 46:215-225(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10756;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteriophage phi-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pre-neck appendage protein (Late protein GP12).
                                                                                                                                                                                                     587 LTSSSSKTSSE 597
                                                                                                                                                                                                                                         Local Similarity tes 2; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94 LITTISFTISE 104
                                                                                                                                                                                                                      1 LXXXXXXXXX 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
2; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            dsDNA viruses, no RNA stage; Caudovirales; Podoviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Paces V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                l (Rel. 17,
l (Rel. 17,
l (Rel. 17,
                                                                                                                                                                                                                                                                                854 AA;
                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                    WMBP22
                                                                                                                                                   STANDARD;
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. 07, Last
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                                                                                                                                                                                                                                                                                92102 MW;
                                                                                                                                                                                                                                                   44.48;
18.28;
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18.2%;
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Last annotation updat
                                                                                                                                Created)
                                                                       RNA stage; Caudovirales; Podoviridae;
                                                                                                   (Late protein GP12).
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                                                                                                                                                                                                                                          0;
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Pred. No. 9.8e-07;
                                                                                                                                                                                                                                                    Pred. No.
                                                                                                                                                                                                                                                            Score 8;
                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                373D4F4275D73EED CRC64;
                                                                                                                                                                                                                                          Mismatches
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                                                                                                             update)
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                                                                                                                                                                                                                                                           DB 1;
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                                                                                                                                                                                                                                                                                                                                                   Usage
                                                                                                                                                                                                                                                           Length 854;
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YM8G_YEAST
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Best Local
                                                                                                            Hypothetical
TRANSMEM 1
TRANSMEM 1
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01-NOV-1997
                             TRANSMEM
TRANSMEM
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TRANSMEM
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                                                                      TRANSMEM
                                                                              FRANSMEM
                                                                                         PRANSMEM
                                                                                                  FRANSMEM
                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                           Saccharomycetales;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 LXXXXXXXXXE 11
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2; Conserva
                                                                                                                                                                                                                            non-profit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               854 AA;
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EMBL; Z49260; CAA89249.1; -. SGD; S0004879; YMR266W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1997 (Rel. 35, Last sequence update)
01-WOV-1997 (Rel. 35, Last sequence update)
Hypothetical 107.7 kha protein in TSP3-IPP2 intergenic region.
YMR256W OR YM8156.08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PZA, a close relative of phi 29.";
Gene 44:107-114(1986).
                                                                                                                                                                                                                                                                       InterPro; IPR003864; D
Pfam; PF02714; DUF221;
                                                                                                                                                                                                                                                                                                                                                                         or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                         modified and this statement is not removed. entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lye G., Churcher C.M., Barrell B.G., Rajandream M.A.;
Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases.
-I- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-i- SIMILARITY: BELONGS TO THE YLL005C/YMR256W/YOL084W FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                          IPR003864; DUF221.
                                                                                                                                                                                                               1 protein;
23 43
103 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAA88489.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Saccharomycetaceae; Saccharomyces
                                      43
123
168
367
412
455
455
560
560
560
662
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  107672 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                            rmatics Institute. There are no restrictions on institutions as long as its content is in no
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                                                                                                                                                                                                                                                       Transmembrane
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Pred. No. 1.3e-06;
                    POTENTIAL
                                      POTENTIAL
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F6F7BA2B3F3AD44B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                953 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Usage
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RESULT 15
E4412_MOUSE
ID 2412_M
AC 070318
DT 15-JUN
DT 1
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Best Local Similarity
"~+~hes 2; Conserva
                                                                                                                                                             Qy
Search completed: January 15, 2003, 11:21:14 Job time: 13.2857 secs
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Best Local Similarity 18.2%;
Matches 2; Conservative
                                                                                                                                                                                                                                                                                                                                                    Structural protein; CDOMAIN 208 42
DOMAIN 489 652
DOMAIN 652 83
DOMAIN 838 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E412_MOUSE STANDARD; PRT; 988 AA.

670318;
15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
Band 4.1-11ke protein 2 (Generally expressed protein 4.1) (4.1G).

EPB41L2 OR EPB4.L12.

Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBI, outstation the European Bioinformatics Institute. There are no restrictions on its
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AF044312; AAC40083.1; -. MGD; MGI:103009; Epb4.112. InterPro; IPR000299; Band_4.1. Pfam; PF00373; Band_41; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Brain;
MEDLINE=98198473; PubMed=9531554;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                           720 LSSESSSSSSE 730
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                                                                                                                                                                                                                                                                                                                           988 AA;
                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                           109833 MW; B0367A16C5A2EC05 CRC64;
                                                                                                                                                                                                                                                                                                                                                    422
651
837
988
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18.28;
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                                                                                                                                                                                                                                              Score 8; DB 1;
Pred. No. 1.4e-
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                                                                                                                                                                                                                                                                                                                                            HYDROPHILIC.
SPECTRIN--ACTIN-BINDING.
CARBOXYL-TERMINAL (CTD).
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                                                                                                                                                                                                                     Mismatches
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                                                                                                                                                                                                               9; Indels
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Database :
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Scoring table:
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Perfect score:
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                                                                                                                                                                                                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                   Score
             protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     length: 2000000000
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Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gapop 10.0 , Gapext 0.5
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             SPTREMBL_21:*
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                                                                                                                                                                                                                                                                                                                                                  sp_rodent:*
sp_virus:*
sp_vertebrate:*
sp_unclassified:*
sp_unclassified:*
sp_bacteriap:*
sp_bacteriap:*
sp_archeap:*
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             101
274
303
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326
4466
639
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                                                                                                                              2 Q9J1A0
Q9VNY3
0 O81807
0 Q9ZUS8
0 Q9FH69
0 Q9H0C7
Q9H0C7
                                    Q9U0V2
Q9VC00
Q9UMS8
Q9UL43
             Q9NMB8
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Q9VYY9
Q60288
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                                                                                                                                                                                                                                                                          SUMMARIES
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                                                                                  Q9vyy9 drosophila 060288 homo
            Q9ums8 homo sapien
Q91143 trebouxia j
Q9nmb8 leishmania
Q8wzw6 neurospora
                                                                                                                              Q9h0c7
Q96t25
                                                               Q9vc00
                                                                            Q9u0v2
                                                                                                                                                                               Q9vny3 drosophila
081807 arabidopsi
                                                                                                                                                                                                                                   Description
                                                                                                                                                        Q9zus8 arabidopsis
Q9fh69 arabidopsis
                                                                                                                                                                                                         Q9j1a0 pseudorabie
                                                                          homo sapien
leishmania
                                                               drosophila
                                                                                                                              homo sapien
                                                                                                                                          homo sapien
                                                                                                                                                                               arabidopsis
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     RESULT 2
Q9VNY3
ID Q9V)
AC Q9V
DT 01
DT 01
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Q9JIA0
ID Q9JIA1
AC QPIA1
AC QPIA
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Best Local Similarity 18.2
Matches 2; Conservative
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Q9VNY3;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
                                                                                                                                                                                                                                                                              STRAIN=PSEUDOKABIES VIRUS STRAIN EA;
Fang L.R., Xiao S.B., Xu J.X., Hong W.Z., Chen H.C.;
"Cloning and expression of IE180 gene of pseudorables virus
                                                                                                                                                                                                                                                                                                                                                                                                                            09JIAO;
01-CCT-2000 (TrEMBLrel. 15, Created)
01-CCT-2000 (TrEMBLrel. 15, Last seq
01-CCT-2000 (TrEMBLrel. 15, Last ann
                                                                                                                                                                                                                  Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases. EMBL; AF218842; AAR43385.1; -. NON_TER 101 101 SEQUENCE 101 AA; 10187 MW; 6E45D3887C53CA94 CRC64;
                                                                                                                                                                                                                                                                                                                                                 Viruses; dsDNA viruses, no RNA stage; Alphaherpesvirinae; Varicellovirus. NCBI_TaxID=10345;
                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                        Pseudorabies virus.
                                                                                                                                                                                                                                                                                                                                                                                                              IE180 (Fragment).
                                                                                                                                                                                                                                                                         strain."
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18.2%;
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| Q9R1L2
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Q8UES5
Q9UHA6
Q8TD05
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Q9G0C8
Q942X0
Q9VPS9
Q9VPS8
Q9VPS8
Q87741
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Q9RWJ6
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Last annotation update)
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Q9NZH6
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Q8TD04
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                                                                                                                                                                Score 9; DB 12; Le Pred. No. 5.7e-14; 0; Mismatches 9;
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Q9A9K6
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                                                                                                                                                                                                                                                                                                                                                                           Herpesviridae,
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                                                                                                                                                                                         Length 101;
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Q9a9%6 caulobacter
Q8sbb5 oryza sativ
Q9h1c6 homo sapien
Q9nh6 homo sapien
Q9nh6 homo sapien
Q9vnm9 drosophila
Q8szpl drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9vps9 drosophila
Q9vps8 drosophila
Q87741 chimpanzee
Q641145 rattus sp.
Q8td04 homo sapien
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Q9vtl6 drosophila
Q9amw4 bradyrhizob
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Q8td05 homo sapien
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Q9w3s3 drosophila
Q8ues5 agrobacteri
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Q9rwj6 deinococcus
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Q9g0c8 lactococcus
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Q9r112 microtus oc
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Result No.

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RESULT 3
081807
1D 0818
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OS Arab
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Best Local
             01-NOV-1998 (TrEMBLrel. 08, Cr
01-NOV-1998 (TrEMBLrel. 08, La
01-OCT-2000 (TrEMBLrel. 15, La
Hypothetical 32.8 kDa protein.
FBD20,270 OR AT4G35760.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L., Nelson E.A., Nixon K., Nusskern D.R., Pacleb J.M., Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., Palazzolo M., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Swirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Walliams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zhong L., Zhong Y.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Xhu X., Smith H.O., Gibhs R.A., Weers E. W. Ribin G.M., Venter T.C., Xhu X., Smith H.O., Gibhs R.A., Weers E. W. Ribin G.M., Venter T.C., Xhu X., Smith H.O., Gibhs R.A., Weers E. W. Ribin G.M., Venter T.C., Xhu X., Smith H.O., Gibhs R.A., Weers E. W. Ribin G.M., Venter T.C., Xhu X., Smith H.O., Gibhs R.A., Weers E. W. Ribin G.M., Venter T.C., Xhu X., Smith H.O., Gibhs R.A., Weers E. W. Ribin G.M., Venter T.C., Xhu X., Smith H.O., Gibhs R.A., Weers E. W. Ribin G.M., Venter T.C., Xhu X., Xhu X., Smith H.O., King R., Xhu X., X
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Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottlier P.,
Burtis K.C., Busam D.A., Butler H., Cadieu B., Center A., Chandra I.,
Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
de Pablos B., Delcher A., Deng Z., Mays A.D., Dew J., Dietz S.M.,
Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.
Durbin K.J., Evangelista C.C., Ferrac C., Ferriera S., Fleischmann W.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfelffer B.D.,
Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
Abril J.F., Agbayani A., An H.-J., Andrews-Pfankkoch C., Baldwin D.,
  Arabidopsis
                                                                                                                                       081807;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ephydroidea;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster (Fruit fly). Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CG14564
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                                                                                                                                                                                                                                                                                                                                                             Similarity
2; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                             Conservative
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(Mouse-ear cress).
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Last annotation updat
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9.7e-14
                                                                 update)
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Query Match
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Best Local
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MEDLINE-2008 4487; PubMed-10617197;

Lin X., Kaul S., Kounsley S.D., Shea T.P., Benito M.-I., Town C.D.,

Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,

Buell C.R., Ketchum K.A., Lee J.J., Konning C.M., Koo H., Moffat K.S.,

Cronin L.A., Shen M., Vanaken S.B., Umayam L., Tallon L.J., Gill J.E.,

Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,

Copenhaver G.P., Freuss D., Nierman W.C., White O., Eisen J.A.,

Salzberg S.L., Fraser C.M., Venter J.C.;

Salzberg S.L., Fraser C.M., Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-1999 (TrEMBLrel. 10, 01-MAY-1999 (TrEMBLrel. 10, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
Rose M., Hempel S.,
Submitted (MAR-2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids_II; Brassicales; Brassicaceae; Arabidopsis.
                                                                SEQUENCE
                                                                                 EMBL;
                                                                                              Submitted (MAR-2000)
                                                                                                                Lin X.;
                                                                                                                              STRAIN-CY.
                                                                                                                                                                        Nature 402:761-768(1999).
                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     At2g37380 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8SUZ60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     92US8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Koetter P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=3702;
                                                                                                                                           SEQUENCE FROM N.A.
    Local Similarity
les 2; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 LSSSSSSTSE 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 LXXXXXXXXX 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  abidopsis sequencing projected (MAR-2000) to the EM AL031135; CAA20046.1; -. AL161588; CAB81485.1; -.
                                                                            ted (MAR-2000) to the EMBL/GenBank/DDBJ databases AC005896; AAC98057.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (JUL-1998)
                                                                321 AA;
                                                                                                                             COLUMBIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        303 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vos P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hempel S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         S., Entian K.-D., Hoheisel Mewes H.W., Mayer K.F.X.,
                                                               34973 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Entian K.-D.,
                 50.0%;
18.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32828 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       50.0%;
18.2%;
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   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last annotation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL/GenBank/DDBJ
                   Pred. No.
                                Score 9;
                                                               7E76DD64A49CBAEB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AF301B0FE04AF13C CRC64;
 Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 321
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1e-13;
                                DB 10;
                   .le-13
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Schueller
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
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databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  databases
                                Length 321;
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   Indels
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   0;
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Gaps
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RESULT 5
Q9FH69
ID Q9FH 69
ID Q9FH
AC Q9FH
DT 01-M
DT 01-M
DT 01-M
DT 01-D
DE Geno
OX Arab
OC Euka
OC Euka
OC Euka
OC Sperr
OX NCBLI
RN [1]
RN [1]
RN [1]
RN [1]
RN SEQU
RC STRA
RX MEDLI
RA Taba
RX MEDLI
RX 
                                                                                                                            RESULT 6
Q9HCT 1
Q9HCT 1
D Q9HCT 1
AC 09H0
DT 01-M
DT 101-M
DT 
                                                    Query Match
Best Local :
                               Matches
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Best Local
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01-MAR 2001 (TIEMBLIFE1. 16, Last sequence update)
01-DEC-2001 (TIEMBLIFE1. 19, Last annotation update)
01-DEC-2001 (TIEMBLIFE1. 19, Last annotation update)
Genomic DNA, chromosome 5, TAC clone:K16E1.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatcophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                Wiemann S., Weil B., Wellenreuther R., Gassenhuber J., Glass! SANSOTGE W., Becher M., Bloecker H., Bauersachs S., Blum H., Lauber J., Duesterhoeft A., Beyer A., Kohrer K., Strack N., Mewes H.W., Ottenwaelder B., Obermaier B., Tampe J., Heubner D. Wambutt R., Korn B., Klein M., Poustka A.; "Towards a Catalog of Human Genes and Proteins: Sequencing and Analysis of 500 Novel Complete Protein Coding Human cDNAs."; Genome Res. 11:422-435(2001).
                                                                                                                                 SEQUENCE
                                                                                                                                                   EMBL; AL136851; CAB66785.1; Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteis
Mammalia; Eutheria; Primates; Catarrnini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Hypothetical 51.6 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9H0C7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9H0C7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA Res.
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MEDLINE-20181125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9FH69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9FH69
                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=21154917; PubMed=11230166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DKFZP434B0535.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR004345; TB2_DP1_HVA22. Pfam; Pr03134; TB2_DP1_HVA22; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sato
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Structural analysis of Arabidopsis thaliana chromosome 5. X. Seque features of the regions of 3,076,755 bp covered by sixty P1 and TAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tabata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=3702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              212 LSSSSSSSSE 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 LXXXXXXXXX 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LASSSSTAATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AB022210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           l Similarity
2; Conserva
                             Similarity 2; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7:31-63(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20181125; PubMed=10718197;
Nakamura Y., Kaneko T., Katoh T., Asamizu E., Kotani H.,
                                                                                                                                 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    326 AA;
                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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                                                                                                                              AA;
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                                                                                                                              51621 MW;
                                                    50.0%;
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18:2%;
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Pred. No. 1.1e
0; Mismatches
                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                             Pred. No. 1.30
0; Mismatches
                                                                            Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata; Buteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                              8B54AD1F940CBE24 CRC64;
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                                                                               9;
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o. 1.1e-13;
9;
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                                                                            DB 4;
                                                          1.3e-13
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                                                                         Length 466;
                               9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 326;
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                               Indels
                                                                                                                                                                                                                                                                                                                                                                                    Glassi S.,
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                               0;
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                               Gaps
                             0;
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Best Local
Best Local Similarity
                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9BHY3;
Q1-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Hypothetical 80.2 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-DEC-2001 (TrEMBLrel. 19, Created)
01-JDEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Zinc family member 5 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q96T25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gou D.M., Li W.X., Gao L., Sun Y.;
"A novel human zine finger gene, hkic5.";
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ
EMBL; AF378304, AAK55418.1;
InterPro; IPR000822; Znf_C2H2.
Pfam; PF00096; zi-C2H2; 4.
                                                                            SEQUENCE
                                                                                                                                                                                                                        MEDLINE=98146435; PubMed
Ivens A.C., Lewis S.M.,
                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. STRAIN-FRIEDLIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                098473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human)
                                                                                                    Hypothetical
                                                                                                                    "A physical map of the Leishmania major Friedlin Genome Res. 8:135-145(1998).
EMBL: AL583932; CAC32257.1; -.
                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                       Submitted (APR-2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Huglenozoa;
NCBI_TaxID-5664;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00028; ZINC_FINGER_C2H2_1; PROSITE; PS50157; ZINC_FINGER_C2H2_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PR01582; KV33CHANNEL. ProDom; PD000003; Znf_C2H2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID-9606;
                                                                                                                                                                                                        Smith D.F.;
                                                                                                                                                                                                                                                                               STRAIN-FRIEDLIN;
                                                                                                                                                                                                                                                                                                                                                    Zimmermann W., Ivens A.C., Quail M., Rajandream M.A., Barrell B.G.;
Sübmitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Leishmania major
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          261
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2; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g; Zinc-finger.
639 AA; 65849
                                                                         761 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          271
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                                                                                                                                                                                                                                                     PubMed=9477341;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             65849 MW;
                                                                         80172 MW;
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18.2%;
18.2%;
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                                                                                                                                                                                                                           Bagherzadeh
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rane, h&ic5.";
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Score 9;
Pred. No.
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Pred. No. 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FB1E966ED28D38BF CRC64;
                                                                         3D21A6BA5E01109D CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 4;
  1.7e-13;
                     DB 5;
                                                                                                                                                                                                                        Zhang L., Chan H.M.
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                  Length 761;
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RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Amanatides P.G., Scherer S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Chang Q., Chen L.X.,
RA George R.A., Lewis S.E., Richards R.G., Chang Q., Chen L.X.,
RA George R.A., Lewis S.F., Yandell M.D., Zhang Q., Chen L.X.,
RA Barlon R.C., Rogers Y.-H.C., Blazej R.G., Nelson C.R., Miklos G.i.G.,
RA Hann K.H., Doyle C., Baxter E.G., Hell G., Nelson C.R., Miklos G.i.G.,
RA Abril J.F., Adbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Beallew R.M., Basu A., Bexendale J., Bayraktaroglu L., Beasley E.M.,
Beallew R.M., Basu A., Bexendale J., Bayraktaroglu L., Beasley E.M.,
Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
Burtis K.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra I.,
RA Burtis K.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies S.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dorlor G., Evangelista C.C., Ferriera S., Fleischmann W.,
RA Dorlor G., Carley S., Calbart W. G., Sterickann W.,
RA Dorlor G., Carley S., Calbart W. G., Sterickann W.,
             Query Match
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                                                                                                                                                                                                                                                                                                                                                               Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Smith H.O., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;

"The genome sequence of Drosophila melanogaster.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibogwam C.,
Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai z.,
Liasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPhorson D.,
Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
Mount S.M., My M., Murphy B., Murphy L., Muzny D.M., Nelson D.I.,
Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Packeb J.M.,
Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
Shue B.C., Siden Kiams I., Simpson M., Skupski M.P., Smith T.,
Shiper R., Stradling A.C., Stableton M., Strapski M.P., Smith T.,
                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischma Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-JUN-2001 (TrEMBLrel. 17, CG11777 prototo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Spier E., Sp
Svirskas R.,
                                                                                                                                                                                                                                                                       FlyBase; FBqn0030299; CG11727.
                                                                                                                                                                                                                                                                                                         EMBL; AE003486; AAF48044.1;
                                                                                                                                                                                                                                                                                                                                       Science 287:2185-2195(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=BERKELEY;
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9YYY9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                 nterPro;
                                                                                                                                                                                                                                         nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             682 LSTTTTTTTE 692
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                                                                                                                                                                         PF00566; TBC; 1.
                                                                                                                                              SM00164; TBC; 1.
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                                                                                                               PS00402;
                                                                                                                                                                                                       IPR000515; BPD_transp.
IPR000195; RabGAP_TBC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Spradling A.C., Stapleton M., Strong R., Sun E., R., Tector C., Turner R., Venter E., Wang A.H., W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11
                                                                                 BPD_TRANSP_INN_MEMBR; UNKNOWN_1; 92352 MW; 204F968E447D021E C
                    50.0%;
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Last annotation update)
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                Score 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                             204F968E447D021E CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          803 AA
                DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wang X.,
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GN L6342

GN CBLA

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RN [1]

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RA Massy

RA Massy

RA Submil

RN SUBMIL

RP STRAIL

RR MEDLILL

RR MEDLILL

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Best Local
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01-DEC-2001
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01-AUG-1998 (TrEMBLrel.
01-MAY-2000 (TrEMBLrel.
01-DEG-2001 (TrEMBLRE).
                                        STRAIN-PRIEDLIN;
MEDLINE-98146435; PubMed=9477341;
IVens A.C., Lewis S.M., Bagherzad
Smith D.F.;
                                                                                                                                                                                                                               Masuy D., Purnelle B., Goffeau A., Ivens A.C., Lawson D., Quail Rajandream M.A., Barrell B.G.; Submitted (DMC-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                             STRAIN-FRIEDLIN
                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=5664;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Leishmania major.
Eukaryota; Euglenozoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Possible MUS308 homolog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9U0V2;
01-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9U0V2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000409; Beige_BEACH
Pfam; PF02138; Beach; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Prediction of the coding sequences of unidentified human genes. I The complete sequences of 100 new cDNA clones from brain which can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KIAA0540 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     060288
"A physical map of the Leishmania major Friedlin genome.";
                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ProDom; PD007848; Beige_BEACH; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AB011112; BAA25466.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  code
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ohara O.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=98290545; PubMed=9628581;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID~9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KIAA0540
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA Res.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nagase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS50197; BEACH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 LXXXXXXXXXX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LAAAAAAAAAE 693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LTTTTTASSAE 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LXXXXXXXXX 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  T., Ishikawa K., Miyajima N., Tanaka A., Kotani H., Nomura N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
2; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
2; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5:31-39(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (TremBlrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (Fragment).
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18.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chordata; Craniata; Vertebrata; Eutele Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     125533 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kinetoplastida; Trypanosomatidae; Leishmania.
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13, Last sequence update)
19, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .2%;
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                                                                Bagherzadeh A.,

    Last sequence update)
    Last annotation updat

                                                                                                                                                                                                                           EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 9;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 1.7e-13; 0; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7B460C2D0211B884 CRC64;
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                                                            Zhang L., Chan H.M.
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Length 1133; Indels

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                                                                                                                                                                                                                                                                                                                                                                                                                         RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Dodson K., Doup L.B., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferriac C., Ferriac S., Fleischmann W.,
ROSIEr C., Gabriellan A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeywan C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kinmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Kinmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Markulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
Merkulov G., Milshina N.V., Mobarry C., Morris J., Woshrefi A.,
Merkulov G., Milshina N.V., Mobarry C., Morris J., Woshrefi A.,
Merkulov G., Milshina N.V., Mobarry C., Morris J., Woshrefi A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local
                                                                                                    Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L., Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M., Pathazzolo M., Pittnan G.S., Pan S., Pollard J., Puri V., Reese M.G. Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Sylrskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Wang Z.-Y., Wassarman D. Weinstock G.M., Weissenbad J., Walliams S., M. Wooden D. M., Weinstock G.M., Weissenbad J., Walliams S., M. Wooden D. M., Weinstock G.M., Weissenbad J., Weiliams S., M. Wooden D. M., Weinstock G.M., Weissenbad J., Weiliams S., M. Wooden D. M., Weinstock G.M., Weissenbad J., Weiliams S., M. Wooden D. M., Weinstock G.M., Weissenbad J., Weiliams S., M. Wooden D. M., Weinstock G.M., We
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Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Asburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Sutton R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
Wash K. H. C., Blazej R.G., Champe M., Pfeiffer B.D.,
Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Beesor K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ephydroidea; Drc
NCBI_TaxID=7227;
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01-MAY-2000 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAY-2000
01-MAY-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00271;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=_ )196006; PubMed=10731132;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genome Res. 8:135-145(1998).
EMBL; AL122012; CAB58415.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001410; DEAD InterPro; IPR001650; Helio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     980
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P.G., Scherer S.E., Li P.W.,
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EMBL; AE003750; AAF56376.1; -. FlyBase; FBgn0039257; CG13648.
Kroken S., Taylor J.W.;

"Phylogenetic species, reproductive mode, and forming lichens with the fungal genus Letharia submitted (MAR-2000) to the EMBL/GenBank/DDBJ EMBL; AF242472; AAF78028.1; -.
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Pfam; PF00093; vwc; 1.
SMART; SM00214; VWC; 4.
                                                                                                                                                                           Eukaryota; Viridiplantae; Microthamniales; Trebouxia
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Kroken S., Taylor
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01-JUN-2001
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                                                                                                                                                        NCBI_TaxID=53267;
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Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databa
EMBL; AJ010196; CAB50862.1; -.
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Pred. No.
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STRAIN-FRIEDLIN;

Murphy L., Quail M., Harris D., Rajandream M., Ivens A., Barrell B.;

Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AL160493; CAB97.2921; -.

Hypothetical protein.

NON_TER 60 60
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Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
NCBI_TaxID=5664;
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Pfam; PF00022; actin; 1.
NON_TER 1.
NON_TER 56 56
SEQUENCE 56 AA; 6357 MW; 64F701537B21BD32 CRC64;
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-DB-GenEmbl -QFWT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPGI=0 -LOOPEXT=0
-UNITS-bits -START=1 -END=-1 -MATRIX=blosum62 -TRANGS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pet -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
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-NO_XLPXY -NO_MAPA -LARGEQUERY -NGE_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPEXT=7
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18
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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Derived from rice genomic sequences generated from the Monsanto Rice Genome Sequencing project. Please see http://www.rice-research.org for more information. The sequence data were produced primarily in the laboratories of Dr. Leroy Hood at the University of Washington in Seattle.
              Direct Submission Submitted (10-JAN-2001) Genomics, Monsanto, 800 North Lindbergh
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AY022695
                                                  Tao, N., Barbazuk, W.B., Liu, J., Wu, K. and Barry, G.F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tao, N., Barbazuk, W.B., Liu, J., Wu, K. and Barry, G.F. Simple sequence repeats from Monsanto rice genomic
 Blvd.,
                                                                                     Unpublished
                                                                                                      Simple sequence repeats from Monsanto rice genomic sequences
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
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                                                                                                                      N., Barbazuk, W.B., Liu, J., Wu, K. and Barry, G.
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Creve Coeur, MO 63167, USA
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                                                                                                                                                                                                                                                                         http://www.rice-research.org for more information. data were produced primarily in the laboratories o at the University of Washington in Seattle.
                                                                                                                                                                                                                                                                                                                        Submitted (10-JAN-2001) Genomics, Monsanto, 800 North Lindbergh Blvd., Creve Coeur, MO 63167, USA Derived from rice genomic sequences generated from the Monsanto Rice Genome Sequencing project. Please see
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bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                                                                                                                                       227 bp DNA linear PLN 07-FEB-200: Oryza sativa microsatellite MRG5574 containing (GGA)X9, closest to marker RZ272, genomic sequence.
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                                                                      Oryza sativa.
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Primer A: AGATCGCGCCATTGCACTC
Primer B: TTTCTGGCTACTGCCGCCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (10-JAN-2001) Genomics, Monsanto, 800 North Lindbergh Blvd., Creve Coeur, MO 63167, USA
Derived from rice genomic sequences generated from the Monsanto
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1 (bases 1 to 227)

Tao.N., Barbazuk, W.B., Liu, J., Wu, K. and Barry, G.
                                                                                                                                                                                                                                                          sequence tagged sites from the human genome Unpublished (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              marker; sequence tadged site; tetranucleotide repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STS; PCR primer; STS sequence;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.30260.1 61:605306
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                                                                                                     End to Label: Primer B
                                                                                                                                                                                 Salt Lake City, UT 84112
                                                                                                                                                                                                 Utah, Dept. of Human Genetics
2160 Eccles Institute of Human Genetics
                                                                                                                                                                                                                                        Submitted by:
                                                                                                                                                                                                                                                                                                  Genetic and physical mapping of simple sequence repeat containing
                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryola: Metazoa; Chordala; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                      PCR Profile:
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/db_xref="taxon:4530"
      Denaturation Annealing
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0 sec. 72 C 20 sec. Mg++:
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and Brygoo, Y.

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nitrogen deprivation.
AL110710
AL110710.1 GI:5824997
CDNA library; nitrogen deprivation
                                                                         Botrytis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kassam,A., Reinhard,C., Randazzo,F., Kennedy,G.C., Pot,D.,
Lamson,G., Drmanac,R., Crkenjakov,R., Drmanac,S., Dickson,M.,
Labat,I., Leshkowitiz,D., Kita,D., Garcia,V. and Strache-Crain,B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1755 from Patent W00102568.
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1 'bases 1 to 352)
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The cDNA library to be analyzed within the framework of this project was created using a Botrytis cinerea strain which was grown under conditions of nitrogen deprivation, which is the normal situation for B. cinerea during its development on its host plant. The library was produced in an oriented direction, in the pBSII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The cDNA library to be analyzed within the framework of this project was created using a Hotzytis cinerea strain which was grown under conditions of nitrogen deprivation, which is the normal situation for B. cinerea during its development on its host plant. The library was produced in an oriented direction, in the pBSII
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Botryotinia fuckeliana
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Leotiomycetes;
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Botryotinia fuckeliana.
Botryotinia fuckeliana
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1 (bases 1 to 420)
Bitton, F., Levis, C., Fortini, D., Pradier, J.M.
                                                                                                                        Submitted (01-SEP-1999) Genoscope - Centre National de Sequencage : CP 5706 91057 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
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AL115282.1 GI:5829901
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    Web : www.genoscope.cns.fr)

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/note="Genoscope sequence ID : W30B091"
100 c 135 g 92 t
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Conservative: Mismatches: Indels:

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Submitted (25-DEC-1999) Lab of Animal Virology, College of Animal Science and Veterinary Medicine, Huazhong Agricultural University, Wuhan, Hubei 430070, China
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 (bases 1 to 560) Fang, L.R., Xiao, S.B., Xu, J.X., Hong, W.Z. and Chen, H.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cloning and expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fang,L.R., Xiao,S.B., Xu,J.X., Hong,W.Z. and Chen,H.C. Cloning and expression of IE180 gene of pseudorables virus
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Viruses; dsDNA viruses,
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See DNA linear Pseudorables virus IE180 (IE180) gene, partial cds.
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/db_xref="GI:7243655"
/db_xref="GI:7243655"
/translation="MADDLEDBTETERNESQULAAAAAAAAAEEEGTAAGSDGGSQGS
/translation="MADDLEDBTETERNESQULAAAAGATRPPRPPSAQQQQQQQPRR"
                                                                                                                                                                                                                                                                                        /gene="IE180"
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/db_xref="taxon:10345"
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21918426
       Machado, C.A., Kliman, R.M., Markert, J.A. and Hey, J.
Inferring the History of Speciation from Multilocus DNA Sequence
Data: The Case of Drosophila pseudoobscura and Close Relatives
Mol. Biol. Evol. 19 (4), 472-488 (2002)
                                                                                Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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Machado,C.A., Kliman,R.M., Markert,J.A. and Hey,J.
Direct Submission
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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/note="3002 locus"
/so c 125 g
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/strain="MSH42"
/db_xref="taxon:7234"
/chromosome="3"
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21918426
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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Machado,C.A., Kliman,R.M., Markert,J.A.
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/strain="Flagstaff16"
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Location/Qualifiers
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/note="3002 locus"
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/strain="AFC3"
                                                                                                                                                                                                           'chromosome="3"
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CNS01DLJ/c
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            cDNA library; nitrogen deprivation.
Botryotinia fuckeliana.
Botryotinia fuckeliana
Eukaryota; Fungi; Ascomycota; Peziz.
Helotiales; Sclerotiniaceae; Botryo
1 (bases 1 to 660)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      project was created using a Botrytis cinerea strain which was grown under conditions of nitrogen deprivation, which is the normal situation for B. cinerea during its development on its host plant. The library was produced in an oriented direction, in the pBSII
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Bitton, F., Levis, C., Fortini, D., Pradier, J.M.
                                                                                                                                                                  CNSOLBJR 660 bp mRNA linear PIN 02-1
Botrytis cinerea strain T4 CDNA library under conditions of
                                                                                                                 AL114319.1 GI:5828938
                                                                                                                                       nitrogen deprivation.
AL114319
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AL116975.1 GI:5832191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:40559"
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                                                Pezizomycotina;
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0090236

Leotiomycetes;

PLN 02-SEP-1999

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BASE COUNT
ORIGIN
Search completed: January 16, 2003, 11:02:10 Job time: 1537.14 secs
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TITLE
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JOURNAL
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                                                                          387 CTCTCCACCACCACGTCCACCGCGGCCACCGAA 355
                                                                                                            Submitted (01-SEP-1999) Genoscope - Centre National de Sequencage : CE 5706 91057 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
The cDNA library to be analyzed within the framework of this project was created using a Botryti3 cinerea strain which was grown under conditions of nitrogen deprivation, which is the normal situation for B. cinerea during its development on its host plant. The library was produced in an oriented direction, in the pBSII
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Submitted (01-SEP-1999) Phytopathologie, INRA, route de St Cyr, 78026 Versailles, France
2 (bases 1 to 660)
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Direct submission
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                                                                                                                                                                                                                                                                                                                                           /organism="Botryotinia fuckeliana"
/strain="74"
/db_xref="taxon:40559"
/notc="Genoscope sequence ID : W58F091"
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/SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

07-FEB-2002

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n genome-deri	17	robe #5178 used	#15464	#13340 used	#11420 for	#9395	bone	bone marrow	brain e	uman brain expre	robe #12098 for	e #10080	n foetal live	n foetal li	n breast ce	n breast cell	ide f	qonucleotide f	dopsis thali	prostate	state e	Oligonucleotide fo	nucleotide	genon	#101 used	be #104 usec	#102	bone marrow	brain exp	#95 for gen	foetal	breast	breast	Human breast cance	tagard de	no income	2000	Arachidonic acid m	hidonic		uman secreted	lone DM293	secreted pr	∌ .	ption

ABN37254 RESULT 1 Human; mouse; rat; splice transcript; detection; RNA transcript; splice variant; transcriptome; oligonucleotide library; ss. WO200210449-A2 Human spliced transcript detection oligonucleotide SEQ ID NO:10002. 15-JUL-2002 (first entry) ABN37254; ABN37254 standard; DNA; 60 BP. Homo sapiens

ALIGNMENTS

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RESULT 2
AACO4346/c
ID AACO437
XX AACO437
AC AACO43
XX A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the genome, which encodes one or more messenger RNA splice variants. CC The oligonuclectide libraries are useful for detecting mRNAs from a CC biological sample, in expression profiling studies, in qualitatively or Quantitatively characterising the corresponding transcriptome, and in CC detecting RNA transcripts and splice variants of human or animal cC transcriptomes. The libraries may also be used as specialised mini CC libraries to detect transcripts of a sub-transcriptome under a particular biological, or pathological state, and so allowing the CC detection of tissue- and pathology-specific genes such as those genes CC only expressed in specific tissue under a specific pathological condition; to detect developmental specific genes; and to detect RNA CC transcripts and splice variants of a transcriptome of a patient suffering CC oligonuclectide sequences from rats, humans and mice, which are used in CC the exemplification of the present invention.

CC N.B. The sequence data for this patent did not form part of the printed CC specification, but was obtained in electronic format directly from WIPO CC at fip.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
                  Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
gene therapy; chromosome mapping; ss.
                                                                                Human secreted protein 5' EST, SEQ ID NO: 8421
                                                                                                                                 06-0CT-2000
                                                                                                                                                                           AAC04346;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 60 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           several oligonucleotides, each capable of hybridising selectively to
set of messenger RNAs transcribed from a given transcription unit of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (sub-)transcriptome comprises messenger RNAs transcribed from multiple transcription units that populate a genome. The library comprises
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1; SEQ ID 10002; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New oligonucleotide libraries comprising oligonucleotides which selectively hybridize to mRNAs transcribed from a transcription unit of a genome, useful for detecting tissue-, pathology-, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-257383/30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Shoshan A, Wasserman A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-JUL-2000; 2000US-221607P.
02-MAY-2001; 2001US-287724P.
                                                                                                                                                                                                                    AAC04346 standard; cDNA; 261 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              messenger RNAs that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention describes oligonucleotide libraries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           developmental-specific genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-JUL-2001; 2001WO-IB01903.
                                                                                                                                                                                                                                                                                                          23
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                                                                                                                                                                                                                                                                                                          TTAGCAGCAGCAGCAGCAGCGGCATCGGAG 55
                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14 A; 20 C;
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Best Local Similarity:
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15-OCT-1998
                                                                                                                        gene therapy;
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                                                                                                                                                                                                                                                                                                                            AAV90423;
                                                                                                                                                                                                                                                                                                                                                                 AAV90423 standard; cDNA; 280 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 261 BP;
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                                         W09845436-A2
                                                                              Homo sapiens
                                                                                                                                                                                                                                       EST clone DM293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         No.:
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                                                                                                                                                                                                                                                                                (first entry)
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US-09-823-649A-1 (1-11) x AAC04346 (1-261)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mrna's encoding secreted proteins. No ORF has yet been conclusively identified within the present sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mrnah because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mrnahs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mrnahs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures \frac{1}{2}
                                                                   Human; secreted protein; expressed sequence tag; EST; haematopoiesis; tissue growth; activin; inhibin; chemotaxis; chemokinesis; haemostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. No ORF has yet been conclusively
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID 8421; 71pp + CD-ROM; English
receptor; ligand; thrombolytic; anti-inflammatory; cadherin; anti-tumour; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62 TYAGCTIGCCACATICCTCTTCCTCTTCCTCCGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Duclert A, Giordano J;
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RESULT 4
AAC17532
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Query Match:
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                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                 Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence represents a human expressed sequence tag (EST). The polynucleotide, which is a secreted EST, and the encoded protein are predicted to have useful biological activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and animals, although no supporting data is given. Suggested activities include nutritional activity, immune setimulating or suppressing activity, haematopolesis regulating activity, tissue growth activity, activin/inhibin activity.
 Dumas Milne Edwards J,
                                                                                                                                                                                                                                                                                                                                           Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                      activity, receptor/ligand activity, anti-inflammatory activity, cadherin/tumour invasion suppressor activity, tumour inhibition activity. The polynucleotide may also be useful for gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New polynucleotides encoding human secreted proteins - derived from e.g. human blood, kidney, foetal lung, placenta, tesles, brain, ovary, pituitary, retina and colon cDNA libraries.
                                     26-FEB-1999;
                                                                                                                                   gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 536; 618pp; English.
                                                         21-FEB-2000; 2000EP-0200610
                                                                             06-SEP-2000
                                                                                                                                                                 Human secreted protein 5' EST,
                                                                                                                                                                                                        AAC17532;
                                                                                                                                                                                                                         AAC17532 standard; cDNA; 343 BP
                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 280 BP;
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                                                                                               EP1033401-A2
                                                                                                                 Homo sapiens
                                                                                                                                              Human; 5' EST;
                                                                                                                                                                                    06-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                         No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     chemotactic/chemokinetic activity, haemostatic and thrombolytic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Agostino MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (GEMY ) GENETICS INST INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10-APR-1997;
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                                                                                                                                                                                                                                                                150 TIGTCATCCTCTTCCTCCTCTICATCATCAGAG 118

    Jacobs K,
Spaulding V,

                                                                                                                                                                                   (first entry)
                                                                                                                                    ; expressed sequence tag; secreted protein; cDNA isolation; chromosome mapping; ss.
                                     99US-0122487
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                                                                                                                                                                                                                                                                                                                                                                                                109 A; 60 C;
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                                                                                                                                                                                                                                                                                                                                                                                                      65 G; 46 T; 0
                                                                                                                                                                 SEQ ID NO: 21607
                                                                                                                                                                                                                                                                                                                                 Mismatches: Indels:
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Matches:
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 Giordano J;
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NPI; 2000-500381/45.

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New nucleic acid that is a 5' expressed sequence tag (5' EST) for pT obtaining chas and genomic DNAs that correspond to 5'ESTs and for pT obtaining chas and genomic DNAs that correspond to 5'ESTs and for pT diagnostic, forensic, gene therapy and chromosome mapping procedures - XX

Claim 1; SEQ ID 21607; 71pp + CD-ROM; English.

XX

The present sequence is one of a large number of 5' ESTs derived from CC mRNAs encoding screeted proteins. No ORF has yet been conclusively correspond mainly to the 3' untranslated region (UTR) ctdal human RNAs or polyA+ RNAs derived from 30 different Lissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) cf the mRNA because they are often obtained from 01igo-dT primed cDNA 1 ibraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer CDNA sequences have been obtained, the full 5' UTR is rarely included. CC 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. CC expression and secretion vectors.
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Sequence 343 BP; 73 A; 84 C; 79 G; 106 T; 1 other;

Alignment Scores: Pred. No.: AAF65999 RESULT 5 US-09-823-649A-1 (1-11) x AAC17532 (1-343) Query Match: Best Local Similarity: Percent Similarity: Williams LT,
Reinhard C, R
Crkenjakov R, 11-JAN-2001 WO200102568-A2 09-APR-2001 Kita D, 02-JUL-1999; 30-JUN-2000; 2000WO-US18374. Homo sapiens breast cancer; lung cancer; cancer detection; ss Human; Novel human polynucleotide, SEQ ID NO: 1755. AAF65999; AAF65999 standard; No.: (CHIR) CHIRON CORP. (HYSE-) HYSEQ INC. 02-JUL-1999; 18 1 Leu*************************Glu 11 TTAGCAGCAGCAGCAGCAGCAGCACCATCGGAG 50 cytostatic; gene therapy; colon cancer; prostate cancer; Garcia V, Randazzo F,
R, Drmanac S, (first entry) 99US-0142310. 99US-0142311. 17.7 9.00 18.18% 18.18% 50.00% CDNA; Jones Kennedy GC,
Dickson M, 352 LW, ВP nis MA, Garcia PD, nedy GC, Pot D, Lau ckson M, Labat I, Strache-Crain B; Gaps: Conservative: Mismatches: Matches: Indels: Lamson G, 0 0 9 0 2 4 3 Leshkowitiz Klinger J, J, Kassam A; Drmanac R;

WPI; 2001-091805/10

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match:
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               WPI; 2000-571881/53.
                                                                                                                                                                                                                                                                                                     Human; biallelic marker; arachidonic acid metabolism; genotyping; detection; hybridisation; phenotype; haplotype; SNP; polymorphic base; single nucleotide polymorphism; hybridisation assay; sequencing assay; specific amplification assay; identification; ERBM; 12-LO-RBM; eicosanoid-related biallelic marker; 12-LO-related biallelic marker; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            preventive interventions. The polynucleotides, polypeptides and antibodies against them can be used in pharmaceutical composition treat the cancers and proliferative disorders such as neoplasia, dysplasia and hyperplasia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         to produce probes for detection of mRNA and to produce additional copies of the polynuclectides. The probes can be used for chromosome mapping of the polynuclectide and for detection of transcription levels. Ribozymes or antisense oligonuclectides can be generated. The polynuclectides and their gene products are used as genetic or biochemical markers (e.g. in blood or tissues) that will detect the earliest changes along the
                                          Blumenfeld M, Bougueleret L,
                                                                                                              07-MAY-1999;
                                                                                                                                                                                                             17-AUG-2000.
                                                                                                                                                                                                                                           WO200047771-A2
                                                                                                                                                                                                                                                                           Homo
                                                                                                                                                                                                                                                                                                                                                                                                       Arachidonic acid metabolism related genomic biallelic marker #223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAC57589;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAC57589 standard; DNA; 362 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 352 BP; 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence is one of 3351 sequences in a library of human polynucleotides. The library is used to detect differentially expressed genes correlated with a cancerous state of a mammalian cell and can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Library of polynucleotides for diagnosing a cancerous state of a mammalian cell and detecting cancer, particularly of the colon or prostate, comprises 3351 human polynucleotide sequences -
                                                                            (GEST ) GENSET
                                                                                                                                                                            11-FEB-2000; 2000WO-IB00184
                                                                                                                                                                                                                                                                                                                                                                                                                                       25-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               carcing jenesis pathway and/or monitor the efficacy of therapies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 9;
                                                                                                                             23-MAR-1999;
                                                                                                                                           12-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             detect colon, prostate, breast and lung cancer. The library can be used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Мо.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                          99US-0119917.
99US-0275267.
99US-0133200.
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                                               Chumakov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps:
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RESULT 7
AAC57590
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WPI; 2000-571881/53
                              Blumenfeld M,
                                                                                                                                                                                                                                                                                                        detection; hybridisation; phenotype; haplotype; SNP; pólymorphic base; single nucleotide polymorphism; hybridisation assay; sequencing assay; specific amplification assay; identification; ERBM; 12-LO-RBM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 predict responses to treatment with drugs. The polynucleotides may be used in hybridisation assays, sequencing assays and specific amplification assays for identifying an eicosanoid-related biallelic marker, and for amplifying a marker (ERBM) or 12-LO-related biallelic marker, and for amplifying a
                                                                                                             12-FEB-1999;
23-MAR-1999;
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                                                                                                                                                                                                                                                                                          eicosanoid-related biallelic marker; 12-LO-related biallelic marker; ds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    exemplification of the present invention.

N.B. Polymorphic bases (single nucleotide polymorphisms also known
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel biallelic markers useful for detecting conditions and genotypes associated with arachidonic acid metabolism - \,
                                                                                                                                                            11-FEB-2000; 2000WO-IB00184
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                                                                                                                                                                                                                                                             Homo sapiens.
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                                                             (GEST ) GENSET
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                                                                                            99US-0119917.
99US-0275267.
99US-0133200.
                              Bougueleret L,
                                                                                                                                                                                                                                                                                                                                                                                         metabolism related genomic biallelic marker #224.
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RESULT 8
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                                                                                                                                         12-FEB-1999;
23-MAR-1999;
07-MAY-1999;
                                                            Blumenfeld M, Bougueleret
                                                                                                                                                                                                                                                                                                                                                                                                            detection; hybridisation; phenotype; haplotype; SNP; polymorphic base; single nucleotide polymorphism; hybridisation assay; sequencing assay; specific amplification assay; identification; ERBM; 12-LO-RBM;
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                   WPI; 2000-571881/53
                                                                                                    (GEST ) GENSET.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                predict responses to treatment with drugs. The polynucleotides may be used in hybridisation assays, sequencing assays and specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention describes polynucleotides including biallelic markers derived from genes involved in arachidonic acid metabolism and from genemic regions flanking those genes. Methods from the present invention may be used to select individuals for clinical trials and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel biallelic markers useful for detecting conditions and genotypes associated with arachidonic acid metabolism -
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99US-0275267.
99US-0133200.
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                                                            Chumakov I;
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exemplification of the present invention.

N.B. Polymorphic bases (single nucleotide polymorphisms also known as N.B. Polymorphic bases (single nucleotide polymorphisms also known as N.B. Polymorphic bases (single nucleotide polymorphisms also known as N.B. Polymorphic bases).
                                                                                                                                                                                  segment of nucleotides containing an ERBM. The polynucleotides are useful in diagnostic kits. The markers may be used to detect conditions and genotypes associated with arachidonic acid metabolism. AAC57367 to AAC58018 and AAB24019 and AAB24020 represent sequences used in the
                                                                                                                                                                                                                                                                                                  amplification assays for identifying an eicosanoid-related biallelic marker (ERBM) or 12-10-related biallelic marker, and for amplifying a
                                                                                                                                                                                                                                                                                                                                                         predict responses to treatment with drugs. The polynucleotides may be used in hybridisation assays, sequencing assays and specific
                                                                                                                                                                                                                                                                                                                                                                                                           markers derived from genes involved in arachidonic acid metabolism a from genomic regions flanking those genes. Methods from the present invention may be used to select individuals for clinical trials and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel biallelic markers useful for detecting conditions and genotypes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention describes polynucleotides including biallelic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 13; Page 423; 802pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         associated with arachidonic acid metabolism
                                                    given as their corresponding degenerate bases e.g. a polymorphic of C or T has been given as Y.
                                                 T has been given
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      metabolism and
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Sequence 362 BP; 51 A; 101 C; 99 G; 101 T; 10 other;

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                                                             RESULT 9
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                                                                                                                      US-09-823-649A-1 (1-11) x AAC57591 (1-362)
                                                                                                                                                     Query Match:
                                                                                                                                                                                                         Alignment Scores:
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 13-FEB-2002
                     AAS84547;
                                        AAS84547
                                                                                                                                                                                               No.:
                                                                                56 TTAGCAGCAGCAGCAGCAGCAGCATCGGAG
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                                       standard; cDNA; 436 BP
(first entry)
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DNA encoding moves human diagnostic protein #20351.

Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss

Homo sapiens.

WO200175067-A2

11-OCT-2001

30-MAR-2001; 2001WO-US08631

31-MAR-2000; 23-AUG-2000; 2000US-0540217 2000US-0649167

(HYSE-) HYSEQ INC

Drmanac RT, Liu C, Tang YT;

2001-639362/73

P-PSDB; ABG20360,

New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess

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0 other;

for

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RESULT 10
AAL17
XX AAL17
XX AAL17
XX O7-DE
XX Human
XX Human
XX Homo
XX Homo
XX Homo
XX 19-JU
XX 12-JA
PR 14-MA
PR 29-MA
PR 15-MA
PR 15-MA
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14-MAR-2000;
24-MAR-2000;
29-MAR-2000;
15-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The
                                                                  (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC
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                                                                                                                  2000US-0220534.
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The invention relates to human breast cancer expressed polynucleotides (AAL07544-AAL026789) and methods of assessing whether a patient is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         detecting, diagnosing, monitoring, characterising treating and potentially preventing breast cancer. The polynucleotides and encoded polypeptides are also useful for isolating compounds with cytostatic
                                                                         Claim 1; Page 1867; 3695pp; English.
                                                                                                                                                                                                                                                                                                                                                 15-MAY-2000;
09-JUN-2000;
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                                                                                                                         New peptide useful as a marker for the
                                                                                                                                                                            WPI; 2001-451856/48
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29-MAR-2000;
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14-MAR-2000; 2000US-0189167.

24-MAR-2000; 2000US-0192999.

29-MAR-2000; 2000US-0193480.

15-MAY-2000; 2000US-0219315.

09-JUN-2000; 2000US-021933.
                                                                                                            The invention relates to human breast cancer expressed polynucleotides (AALO7544-AALZ6789) and methods of assessing whether a patient is afflicted with breast cancer by examining the correlation between the expression of certain markers and the cancerous state of breast cells. The polynucleotides and encoded polypeptides are potential markers for detecting, diagnosing, monitoring, characterising treating and potentially preventing breast cancer. The polynucleotides and encoded potentially preventing breast cancer. The polynucleotides and encoded
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Sequence 442 BP; 116 A;

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122 T; 0 other,

Query Match:

Best Local Similarity: Percent Similarity:

19.6 9.00 18.18% 18.18% 50.00%

Conservative: Mismatches: Indels:

452 0 0

Matches:

Gaps:

Score:

Alignment Scores: Pred. No.:

Sequence 452

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117 A;

97 Ç

113

G; 125 T;

0 other;

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RESULT 13
AAL10819
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Best Local Similarity:
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15-MAY-2000;
09-JUN-2000;
                                           expression of certain markers and the cancerous state of breast cells. The polynucleotides and encoded polypeptides are potential markers for detecting, diagnosing, monitoring, characterising treating and potentially preventing breast cancer. The polynucleotides and encoded
                                                                                          The invention relates to human breast cancer expressed polynucleotides (AAL07544-AAL26789) and methods of assessing whether a patient is afflicted with breast cancer by examining the correlation between the
                      polypeptides are also useful for isolating compounds with cytostatic activity.
                                                                                                                                              Claim 1; Page 604; 3695pp; English.
                                                                                                                                                                     New peptide useful as a marker for the diagnosis of breast cancer
                                                                                                                                                                                                                                                                                                                         14-MAR-2000;
24-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; breast cancer; cell marker; cytostatic; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human breast cancer expressed polynucleotide 3276.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-DEC-2001
                                                                                                                                                                                                                          Lillie
                                                                                                                                                                                                                                                (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
                                                                                                                                                                                                                                                                          25-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                            10-JAN-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Leu************************Glu
                                                                                                                                                                                                                          Xu Y,
                                                                                                                                                                                                                                                                       ; 2000US-0193480.
; 2000US-0205230.
; 2000US-0211315.
; 2000US-0220534.
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2000US-0192099
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RESULT 14
ABA51801/c
ID ABA518
XX ABA5180
XX ABA518
XX Human 1
XX Human 1
XX Human 2
XX Human 3
XX Human 3
XX Human 3
XX Homo si
XX WO2001
XX WO2001
XX O9-AUG
PR 03-AUG
PR 26-MAY
PR 30-JUN
PR 30-JUN
PR 30-JUN
XX WPI 27-SEP
PR 21-SEP
R 27-SEP
R 04-OCT
XX WPI; 2
XX Human 1
XX Human 1
XX Human 2
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XX Human 1
XX Human 1
XX Human 1
XX Human 2
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XX Human 3
X
RESULT 15
ABA21629/c
                                                                                                                                              US-09-823-649A-1 (1-11) x ABA51801 (1-462)
                                                                                                                                                                                            Query Match:
DB:
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21-SEP-2000;
27-SEP-2000;
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26-MAY-2000;
30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human
                                                                                                                                                                                                                                                                                                                                                                 Sequence 462 BP;
                                                                                                                                                                                                                                                                                                                                                                                                       Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format direfrom WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              analyzing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-483447/52.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     fetal liver. The present sequence is a single exon nucleic acid probe of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-JAN-2001;
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                                                              288 CTGACAGCAGCCTCTTCCACATCAAGTGAA 256
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                                                                                                      1 Leu******************************Glu 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           genome-derived single exon nucleic acid probes useful zing gene expression in human fetal liver -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               foetal liver; gene expression; single exon nucleic acid probe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hanzel DK,
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2000US-0234687.
2000US-0236359.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2000GB-0024263.
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2000US-0608408.
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                                                                                                                                                                                                                                                                                                                                                               131 A; 124 C;
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                                     Search completed: January 15, 2003, 12:55:20 Job time : 135.143 secs
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                                                                                                                                                                                                                                                                                          Percent Similarity:
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26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascues. Gradiovascular disease, hypertension, cardiac arrhythmias
                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 462 BP; 131 A; 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      measuring human gene expression in a sample derived from human heart. The present sequence is one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to single exon nucleic acid probes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID No 95; 530pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Single exon nucleic acid probes for analyzing gene expression in human hearts -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               congenital heart disease.
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Sequence Sequence Sequence

94, Appl 18, Appl 94, Appl 17, Appl 3, Appl

876, App
43, Appl
49, Appl
3, Appl
107, App
1107, App
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Result
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-QC_PG9n2_1/USPTO_Spool/USS9823649/runat_14012003_151002_29127/app_query.fasta_1.1393
-QC_PG9n2_1/USPTO_Spool/USS9823649/runat_14012003_151002_29127/app_query.fasta_1.1393
-DB=Issued_Patents_Na -OFMT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=blts -START=1 -END=-1 -MATXIX=blosum62 -TRANS=hunan40.cdi
-LOOPEXT=0 -UNITS=blts -START=1 -END=-1 -MATXIX=blosum62 -TRANS=hunan40.cdi
-LIST=45 -DCOALIGN=200 -THR_SCORE-pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE-LOCAL -OUTFMT=pto -NORM-ext -HEAPSIZE-S0 -MINLEN=0 -MAXLEN-200000000
-USER-USO9823649_eCGN_1_1_35_@runat_14012003_151002_29127 -NCPU-6 -ICPU-3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPDXT=0.5 -FGAPOP=6 -FGAPEXT=7
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Maximum Match 100%
Listing first 45 summaries
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Ygapop 10.0 ,
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                                                                                                                                                                                   Query
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Copyright (c) 1993 - 2003 Compugen Ltd.
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/cgn2_6/ptodata/1/ina/5B_COMB.seq: *
/cgn2_6/ptodata/1/ina/5A_COMB.seq: *
/cgn2_6/ptodata/1/ina/6A_COMB.seq: *
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/cgn2_6/ptodata/1/ina/backfiles1.seq: *
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 US-09-641-638-877

US-09-641-638-23

US-09-641-638-223

US-09-641-638-224

US-09-641-638-225

US-09-641-638-225

US-08-597-495B-23

US-09-068-051A-23

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Sequence 877, App
Sequence 878, App
Sequence 223, App
Sequence 225, App
Sequence 225, App
Sequence 23, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 29, Appli
Sequence 31, Appl
Sequence 31, Appl
Sequence 38, Appl
                                                                                                                                                                    Description
                                       : OTHER INFORMATION: 10-87-74 : polymorphic base US-09-641-638-877
             Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 877, Appl Patent No. 6432648
                                                                                                                                                                PRIOR APPLICATION NUMBER: US 60/133,200
PRIOR FILING DATE: 1999-05-07
PRIOR FILING DATE: 1999-03-23
PRIOR FILING DATE: 1999-03-23
PRIOR PILING DATE: 1999-03-23
PRIOR PILING DATE: 1999-03-23
PRIOR FILING DATE: 1999-02-12
NUMBER: OF SEQ ID NOS: 1304
                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: 05/09/641.538
CURRENT FILING DATE: 2000-08 16
PRIOR APPLICATION NUMBER: US 09/502,330
PRIOR FILING DATE: 2000-02-11
                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: BIALLELIC MAKKERS DERIVED FROM GENOMIC REGIONS CARRYING TITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM FILLE REFERENCE: GENESET 05100H
                                                              NAME/KEY: allele
LOCATION: 24
                                                                                                   ORGANISM: Homo Sapiens
                                                                                                                 TYPE: DNA
                                                                                         FEATURE:
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PCT-USS-09-167-615-107
PCT-USS-09816A-107
US-08-207-481-4
PCT-USS-0289-51
US-08-594-031-146
US-09-129-637A-242
US-09-129-637A-242
US-09-128-155-10
US-08-207-481-3
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US-09-199-637A-240

US-09-219-625-1

US-08-207-481-25

PCT-US95-02689-25

US-09-222-939-24

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US-08-207-481-38

PCT-US95-02689-40
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US-08-623-428D-3
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PCT-US95-08501-3
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Sequence

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Sequence

10, Appl 32, Appl 6, Appl 6, Appl 20, Appl 20, Appl 21, Appl 25, Appl 25, Appl 24, Appl 24, Appl 24, Appl

CURRENT FILING DATE:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: 10-87-80 ; polymorphic base A or US-09-641-638-878
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                                                                                                                              GENERAL INFORMATION: APPLICANT: Blumenfo
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CURRENT APPLICATION NUMBER: US/09/641,638
CURRENT FILING DATE: 2000-08-16
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APPLICANT: Cohen, Annick
TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING
TITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM
FILE REFERENCE: GENSET.051CP1
CURRENT APPLICATION NUMBER: US/09/641,638
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PRIOR APPLICATION NUMBER: US
PRIOR FILING DATE: 1999-03-23
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PRIOR FILING DATE: 2000-02-11
PRIOR APPLICATION NUMBER: US 60/133,200
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PRIOR FILING DATE: 1999-02-12
NUMBER OF SEQ ID NOS: 1304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
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Matches:
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Indels:
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US-09-641-638-224
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PRIOR FILING DATE: 2000-02-11
PRIOR PELICATION NUMBER: US 60
PRIOR RELING DATE: 1999-05-07
PRIOR APPLICATION NUMBER: US 09
PRIOR FILING DATE: 1999-03-23
PRIOR FILING DATE: 1999-02-12
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                Sequence 224, Application US/09641638 Patent No. 6432648
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PRIOR APPLICATION NUMBER: US 09/502,330
PRIOR FILING DATE: 2000-02-11
PRIOR APPLICATION NUMBER: US 60/133,200
PRIOR FILING DATE: 1999-05-07
PRIOR APPLICATION NUMBER: US 09/275,267
PRIOR FILING DATE: 1999-03-23
                                                                                                                     CURRENT APPLICATION NUMBER: US/09/641,638
CURRENT FILING DATE: 2000-08-16
                                                                                                                                                              TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING TITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM FILE REFERENCE: GENEET.051Cp1
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OTHER INFORMATION: downstream amplification primer, complement
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LOCATION: 73
OTHER INFORMATION: 10-87-74 : polymorphic base A or
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OTHER INFORMATION: 10-87-74.mis1, polential
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Chumakov, Ilya
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BER: US 09/502,330
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SOFTWARE: P SEQ ID NO 224

Patent.pm

ENGTH:

362

NAME/KEY: allele FEATURE: LOCATION: 79

PRIOR FILING DATE: 19
NUMBER OF SEQ ID NOS:

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US-09-823-649A-1 (1-11) x US-09-641-638-224 (1-362)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 225, Application US/09641638 Patent No. 6432648
                                                                                                                                                               PRIOR FILING DATE: 2000-02-11
PRIOR APPLICATION NUMBER: US 60/133,200
PRIOR FILING DATE: 1999-05-07
PRIOR APPLICATION NUMBER: US 09/275,267
                                                                                                          PRIOR APPLICATION NUMBER: US 60/119,917 PRIOR FILING DATE: 1999-02-12
                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/641,638
CURRENT FILING DATE: 2000-08-16
PRIOR APPLICATION NUMBER: US 09/502,330
PRIOR FILING DATE: 2000-02-11
                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING TITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM FILE REFERENCE: GENSET.051CP1
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ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: downstream amplification primer, complement
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: 10-87-80 : polymorphic base A or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               56 TTAGCAGCAGCAGCAGCAGCAGCATCGGAG 88
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Chumakov, Ilya
                                                                                                                                                                                                                                                                                                                                                                                    Cohen, Annick
                                                                                                                                                                                                                                                                                                                                                                                                                                               Blumenfeld, Marta
                                                                                                                                                    1999-03-23
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Best Local Similarity:
Query Match:
DB:
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US-08-597-495B-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Old, Lic
APPLICANT: Simpson
APPLICANT: Catimel
APPLICANT: Heath,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 23, Application US/08597495B Patent No. 5712369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: 126..150
OTHER INFORMATION: 10-87-140 potential probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature LOCATION: 172..174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: downstream amplification primer, complement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: primer_bind LOCATION: 345..362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KBY: primer_bind LOCATION: 1..18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: 10-87-140.mis2, potential complement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc_binding LOCATION: 139..158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: 10-87-140.mis1, potential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_binding LOCATION: 118..137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: 138
OTHER INFORMATION: 10-87-140 : polymorphic base C or T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: upstream amplification primes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM:
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                     APPLICATION NUMBER: 08/511,876
FILING DATE: 04-Aug-1995
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 5712369man D
                                                                                                                                                                                       SOFTWARE: Wordperfect CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                    PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                THTLE OF INVENTION: Associated Nucleic Acid Molecules, Protein And Peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                  STREET:
NAME: Hanson, No. 5 REGISTRATION NUMBER:
                                                                                                                                             APPLICATION NUMBER: US/0 FILING DATE: 02-Feb-1996
                                                                                                                                                                                                                              COMPUTER: IBM PS/2
OPERATING SYSTEM: 1
                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                              STATE:
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1: 805 Third Avenue
New York City
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                                                                                                                                                                                                                                                                                                                                                            New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Old, Lloyd J.; Welt, Sydney; Ritter, Gerd; Simpson, Richard J.; Nice, Edouard; Moritz, R. L.; Catimel, B.; Ji, Hong; Burgess, Anthony W.; Heath, Joan K.; White, Sara J.; Johnstone, Cameron WERNTION: Colon Cell And Colon Cancer Cell
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Indels:
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Best Local Similarity:
Query Match:

Percent Similarity:

Pred. No.: Alignment Scores: US-09-641-638-224

NAME/KEY: primer_bind LOCATION: 345..362

US-09-641-638-225 RESULT 5

APPLICANT:
APPLICANT:

APPLICANT:

GENERAL INFORMATION:

NUMBER OF SEQ ID NOS: SOFTWARE: Patent.pm SEQ ID NO 225

TYPE: DNA

362

PRIOR FILING DATE:

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GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                  INFORMATION FOR SEQ ID NO: 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: 1BM PS/2
OPERATING SYSTEM: PC-DOS
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/068,051A
FILING DATE: 10-Dec-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Old, Lloyd J.; Welt, Sydney; Ritter, Gerd;
Simpson, Telchard J.; Nice, Edouard; Moritz, R. L.;
Catimel, B.; Ji, Hog; Burgess, Anthony W.;
Heath, Joan K.; White, Sara J.; Johnstone, Cameron
TITLE OF INVENTION: Colon Cell And Colon Cancer Cell
Associated Nucleic Acid Molecules, Protein And Peptides
                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
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COMPUTER READABLE FORM:
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ADDRESSEE: Fulbright & Jaworski LLP
STREET: 666 Fifth Avenue
SEQUENCE DESCRIPTION: SEQ ID NO: 23
                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: LUD 5316.2 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
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                                      LENGTH: 960 nucleotides TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 08/597,495
FILING DATE: 02-Feb-1996
APPLICATION NUMBER: 08/511,876
FILING DATE: 04-Aug-1995
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STATE: New York
                                                                                                                                                   TELEFAX: (212)
                                                                                                                                                                                                                                                   NAME: Hanson, No. 6291235man D. REGISTRATION NUMBER: 30,946
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
                                                                                                                                                       TELEPHONE: (212) 318-3168
TELEFAX: (212) 752-5958
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Best Local Similarity:
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Best Local Similarity:
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                                                                        Pred. No.:
                                                                                       Alignment Scores:
                                                                                                                    US-08-959-011-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
                                                                                                                                TOPOLOGY: linea
IMMEDIATE SOURCE:
LIBRARY: CRBLNC
CLONE: 676592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Hillman, Jennifer L.
APPLICANT: Shah, Purvi
APPLICANT: Coricy, weil C.
TITLE OF INVENTION: VACUOLAR ATPASE SUBUNIT AC45
NUMBER OF SEQUENCES: 3
                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: PATELECOMMUNICATION INFORMATION: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
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                                                                                                                               CLONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version
                                                                                                                                                                                                      TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                NAME: Billings, Lucy J. REGISTRATION NUMBER: 36,749
                                                                                                                                                                                        STRANDEDNESS: single
                                                                                                                                                                                                                                                                              TELEFAX: 650-845-4166
                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: FILING DATE: Herew
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US-09-823-649A-1 (1-11) x US-08-959-011-2 (1-2156)

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US-09-068-051A-31
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                  Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                  Alignment Scores:
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                                                               Patent No. 6291235
GENERAL INFORMATION:
                                                                                                        Sequence 31, Application US/09068051A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 29, Application US/08597495B Patent No. 5712369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION: APPLICANT: Old, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                             . No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 2565 nucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 688-9200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Simpson, Richard J.; Nice, Edouard; Moritz, R. L.;
APPLICANT: Catimel, B.; Ji, Hong; Burgess, Anthony W.;
APPLICANT: Heath, Joan K.; White, Sara J.; Johnstone, Cameron
TITLE OF INVENTION: Colon Cell And Colon Cancer Cell
TITLE OF INVENTION: Associated Nucleic Acid Molecules, Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 04-Aug-1995
ATTORNEY/AGENT INFORMATION:
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CORRESPONDENCE ADDRESS:
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OPERATING SYSTEM: PC-
SOFTWARE: Wordperfect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Hanson, No. 5712369man D. REGISTRATION NUMBER: 30,946
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 08/511,876
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APPLICANT: Old, Lloyd J.; Welt, Sydney; Ritter, Gerd; Simpson, Richard J.; Nice, Edouard; Moritz, R. L.; Catimel, B.; Ji, Hong; Burgess, Anthony W.;
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US-09-336-536-68
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Query Match:
                                                                                                                                                                                                                                                                         /S-09-330; Sequence 68, Appilon; Sequence 68, Appilon; 6406884
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                                        SEQ ID NO 68
LENGTH: 2793
                                                                                SOFTWARE:
ORGANISM: Homo sapiens
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TELEFAX: (212) 752-5958
INFORMATION FOR SEQ ID NO: 31
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SOFTWARE: Wordperfect
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CORRESPONDENCE ADDRESS: Heath, Joan K.; White, Sara J.; Johnstone, Cameron TITLE OF INVENTION: Colon Cell And Colon Cancer Cell NUMBER OF SEQUENCES: Associated Nucleic Acid Molecules, Protein And Peptides

STREET: 666 Fifth Avenue ADDRESSEE: Fulbright & Jaworski LLP

STATE: New York COUNTRY: USA CITY: New York City

COMPUTER READABLE FORM: MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage COMPUTER: IBM PS/2

PRIOR APPLICATION DATA CURRENT APPLICATION DATA: APPLICATION NUMBER: 08/597,495 FILING DATE: 02-Feb-1996 FILING DATE: 10-Dec-1998 CLASSIFICATION: 435 APPLICATION NUMBER: US/09/068,051A

APPLICATION NUMBER: 08/511,876 FILING DATE: 04-Aug-1995 ATTORNEY/AGENT INFORMATION: TELECOMMUNICATION INFORMATION: NAME: Hanson, No. 6291235man D. REGISTRATION NUMBER: 30,946 REFERENCE/DOCKET NUMBER: LUD 5316.2

SEQUENCE DESCRIPTION: SEQ ID NO: US-09-068-051A-31 SEQUENCE CHARACTERISTICS: TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear LENGTH: 2565 nucleotides 31

189 9.00 18.18% 18.18% 50.00% Caps: Conservative: Mismatches: indels: Matches:

US-09-823-649A-1 (1-11) x US-09-068-051A-31 (1-2565)

Application US/09336536

GENERAL INFORMATION:
APPLICANT: Leiby, K.
APPLICANT: MCKBY, C.
APPLICANT: BOSSONE, S.
TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF
FILE REFERENCE: 7853-144

CURRENT APPLICATION NUMBER: US/09/336,536 CURRENT FILING DATE: 1999-06-18 NUMBER OF SEQ ID NOS: 75 Patentin Ver. 2.0

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Query Match:
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 33:
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FILING DAFF: 02-Fcb-1996
APPLICATION NUMBER: 08/511,876
FILING DAFF: 04-Auq-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage COMPUTER: IBM PS/2

OPERATING SYSTEM: PC-DOS SOFTWARE: Wordperfect

CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 318-3168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/09/068,051A
FILING DATE: 10-Dec-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Old, Lloyd J.; Welt, Sydney; Ritter, Gerd; Simpson, Richard J.; Nice, Edouard; Moritz, R. I..; Catimel, B.; Ji, Hong; Burgess, Anthony W.; Heath, Joan K.; White, Sara J.; Johnstone, Cameron TITLE OF INVENTION: Colon Cell And Colon Cancer Cell
                                                                                                                                                                                       SEQUENCE DESCRIPTION: SEQ ID NO: 33:
                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 2803 nucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 33
                                                                                                                                                                                                                                                                                                                                                             NAME: Hanson, No. 6291235man D. REGISTRATION NUMBER: 30,946 REFERENCE/DOCKET NUMBER: LUD 5316.2
                                                                                                                                                                                                                    STRANDEDNESS: single
                                                                                                                                                                                                                                           TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 666 Fifth Avenue CITY: New York City
                                                                                                                                                                                                                                                                                                           TELEPHONE: (212) 318-31
TELEFAX: (212) 752-5958
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Best Local Similarity:
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US-08-474-633A-94
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                Sequence 18, Application US/08737524B Patent No. 5912414 CENERAL INFORMATION:
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TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
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MEDJIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MICROSOFT WORD VERSION 2.0C
CURRENT APPLICATION DATA:
APPLICANT: CARL SAVERIO FALCO
                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: 302-992-4931
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1007 MARKET STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        302-773-0164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            U.S.A.
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44.44%
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8.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    METHODS FOR INCREASING INCREASING THE LYSINE AND THREONINE CONTENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHIMERIC GENES AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      107
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                                                                                                                                                                                                                                 Gaps:
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                                                                                                                                                                                                                                                                                   Conservative:
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                                                                                                                                                                                                                                                                                                                      Length:
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                                                                                                                                                                                                                                                                                    US-08-823-771-94
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-737-524B- ∂
                                                                                                                                                                                                                Sequence 94, Application US/08823771
Patent No. 6459019
GENERAL INFORMATION:
APPLICANT: E. I. DU PONT DE N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: BB-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-92-5481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS*
LENGTH: 43 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: LYNNE M. CHRISTENBURY
REGISTRATION NUMBER: 30,971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: DISKETTE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MICROSOFT WINDOWS 95
SOFTWARE: MICROSOFT WORD FOR WINDOWS 95 (7.0)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: 302-773-0164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: WILMINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/737,524B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                    1 CTAGAAGCCTCGGCAACGTCACCAACGGCGGAA 33
                                                                                               NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                 TITLE OF INVENTION: CHIMERIC GENES AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19898
CITY: WILMINGTON STATE: DELAWARE COUNTRY: U.S.A.
                                                AND COMPANY
STREET: 1007 MARKET STREET
                                                                                 ADDRESSEE: E. I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DELAWARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E: E. I. DU PONT DE NEMOURS AND COMPANY
1007 MARKET STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMINICK ANTHONY GUIDA, JR. MARY ELIZABETH HARNETT LOCKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
                                                                                                                                                                                                    COMPANY
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GENES AND METHODS FOR INCREASING
THE METHIONINE CONTENT OF THE SEEDS
OF PLANTS
                                                                                                                                                                                                                  DU PONT DE NEMOURS AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27
                                                                                                                                                METHODS FOR INCREASING INCREASING THE LYSINE
                                                                                                                                  AND THREONINE CONTENT
                                                                                                                    107
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                                                                                 DU PONT DE NEMOURS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative:
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Qy
                                                                                                                                       US-09-823-649A-1 (1-11) x US-08-823-771-94 (1-43)
Search completed: January 15, 2003, 12:58:36 Job time : 30 secs
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                                                                                                                                                                                                                  Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                 US-08-823-771-94
                                                                                                                                                                                                                                                           Score:
                                                                                                                                                                                                                                                                            Pred. No.:
                                                                                                                                                                                                                                                                                              Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 94:
SEQUENCE CHARACTERISTICS:
LENGTH: 43 base pairs
TYPE: nucleic acid
                                                                                                      1 Leu****************************Glu 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 08/474,633
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: 1EM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: MICROSOFT WORD VERSION 2.0C CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                    SEQUENCE DESCRIPTION: SEQ ID NO: 94:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
                                                                   CTAGAAGCCTCGGCAACGTCAGCAACGGCGGAA 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/823,771 FILING DATE: 24-Mar-1997 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 30,684
REFERENCE/DOCKET NUMBER: BB-1037-C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: 835420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: 302-992-4931
TELEFAX: 302-773-0164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: BARBARA C. SIEGELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 19898
                                                                                                                                                                                                 18.18%
18.18%
44.44%
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8.00
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Matches:
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Result
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Searched:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Title:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                             Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-823-649A-2
                                                                                                                                                                                                                                           Match
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                                                                                                                                                                                                                                                               Query
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 908470 seqs, 133250620 residues
    Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         January 15, 2003, 09:02:09;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                             SIDS2/gcgdata/geneseq/geneseqp-embl/AA199.DAT:
SIDS2/gcgdata/geneseq/geneseqp-embl/AA2000.DAT:
SIDS2/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:
SIDS2/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LSXELXIPYEE 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /SIDS2/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1982.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1983.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /SIDS2,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1984.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1985.DAT:*
                                                                                                                                                                                                                                           Length
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/gcgdata/geneseq/geneseqp-embl/AA1987.DAT:*
/gcgdata/geneseq/geneseqp-embl/AA1988.DAT:*
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  AAM48262
AAM48263
AAM48264
AAM48265
AAR96267
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AAB47794
AAM48259
AAM48260
AAM48261
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(without alignments)
52.083 Million cell updates/sec .
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                                                                                                                                                                                                                                        Description
                      Native
                                      DNA polymer
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Thermus aqu
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polymer
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AAR23154	AAR23141	316	AAR23161	315	AAR23143	AAE15569	AAE15568	AAE15565	AAR23167	AAR23162	AAR23156	AAR23144	AAU00575	57	620	AAR99543	AAE09310	AAE09305	AAY00887	AAW09316	AAY00888	AAY00886	AAW09317	AAW09315	AAR96205	AAR99544	35		AAY44352	93	315	316	AAR23163	w
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ALIGNMENTS

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RESULT 1
AAB47793
ID AAB4
XX
AC AAB4
XX
DT 25-)
XX
NAT DN LY
KW DN/
KW DN/
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KW dy
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DR PD 0
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PPD 0
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PPI
Reverse transcribing an RNA, comprises performing a reverse transcriptase polymerase chain reaction amplification of a r
                                                    WPI; 2002-076891/11.
                                                                             Smith ES, Elfstrom CM, Ge Schoenbrunner NJ, Wang AM;
                                                                                                                                                                                              12-APR-2001; 2001EP-0109341.
                                                                                                                                                                                                                                 07-NOV-2001
                                                                                                                                                                                                                                                              EP1152062-A2
                                                                                                                                                                                                                                                                                              Thermus sp.
                                                                                                                                                              18-APR-2000; 2000US-198336P.
                                                                                                                              (HOFF ) HOFFMANN LA ROCHE & CO AG
                                                                                              Gelfand DH,
                                                                                              Higuchi RG,
                                                                                            Myers TW;
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of a mixture

dye; amplification.

Native DNA polymerase motif #3

25-MAR-2002 AAB47793;

(first entry)

AAB47793 standard; peptide;

11 AA

DNA polymerase; reverse transcription; primer; divalent cation; mutant; transverse transcription reaction; fluorescein; cyanine; thermoactive;

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US-08-180-524-8
; Sequence 8, Application US/08180524
; Patent No. 5849537
; Patent No. 5849537
                                                                                                                                                                                                                                                                                                                                                                                   ga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Pseudopleuronectus americanus US-08-180-524-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 66-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (414) 277-5707
TELEFAX: (414) 277-5591
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: p
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acids TYPE: amino acids STRANDEDNESS: single TOPOLOGY: linear 40150000
                                                                                                                                                                                                                               APPLICANT:
                                             CORRESPONDENCE ADDRESS:
                                                             TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: MSWORD Version 5.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                               APPLICANT:
                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/409,217
FILING DATE: 19-SEP-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                               APPLICANT:
                                                                                                                                                APPLICANT:
                                                                                                                                                                APPLICANT:
                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                 APPLICANT:
CITY: Milwaukee
             ADDRESSEE: Thad Kryshak, Quarles & Brady STREET: 411 East Wisconsin Avenue
                                                                                                                                                                                                                                                                                                                                                                                   12 LTAANAKAAAE 22
                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 18.2 les 2; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 411 East
CITY: Milwaukee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 35,433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/180,524
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                                                    Chicoye, Etzer
Chicoye, Etzer
Barney, Michael C.
Bower, Patricia A.
Bower, Patricia A.
Cronan, Charles L.
Cronan, Charles L.
NYENTION: METHOD OF EXPRESING ANTIFREEZE PROTEINS
INVENTION: IN YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E: Thad Kryshak, Quarles & Brady
411 East Wisconsin Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
                                                                                                                                                                                          Rhodes, Thomas
Huige, Nick
                                                                                                                                                                                                                               Tripp, Matthew
Lusk, Lance
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NO
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                                                                                                                                                                              Edward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                38.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US 07/486,333
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 7; DB 2; 1
Pred. No. 4.5e+02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     66-005-9234-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 37;
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; MOLECULE TYPE: I
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-180-524-8
                                                Query Match
Best Local Similarity
Watches 2; Conserve
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                                                                                                                                                                                                                                                                                           TELEFAX: (414) 277-5591
INFORMATION FOR SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 66-005-9234-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (414) 277-5707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 37 amino acids
                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Kryshak, Thad
                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: US 07/486,333
APPLICATION NUMBER: US 07/486,333
FILING DATE: 28-FEB-1990
PRIOR APPLICATION DATE: 05 07/466,317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: MSWORD Version 5.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: ISBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
12 LTAANAKAAAE 22
                                                                                                                                                                                                                                        TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                              NAME: Kryshak, Thad REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 07/409,217 FILING DATE: 19-SEP-1989
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: Wisconsin
                                                                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/07/917,216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                          TOPOLOGY:
                                1 LXXXXXXXXXE 11
                                                                  Conservative
                                                                                                                                                                                                          linear
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                                                                                                                                                                                    protein
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                                                                                 38.9%;
18.2%;
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                                                                 0,
                                                                               Score 7; DB 2; I
Pred. No. 4.5e+02;
                                                                  Mismatches
                                                                                               Length 37;
                                                                 Indels
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Search completed: January 15, 2003, 12:38:20 Job time: 11.2857 secs

0; Gaps

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OM protein - protein search, using sw model
       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
          Published_Applications_AA:*

1: /cgn2_6/ptodata/2/pubpaa/P

2: /cgn2_6/ptodata/2/pubpaa/U

3: /cgn2_6/ptodata/2/pubpaa/U

4: /cgn2_6/ptodata/2/pubpaa/U

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9: /cgn2_6/ptodata/2/pubpaa/U

10: /cgn2_6/ptodata/2/pubpaa/U

11: /cgn2_6/ptodata/2/pubpaa/U

11: /cgn2_6/ptodata/2/pubpaa/U
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length: 2000000000
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18
1 LXXXXXXXXX 11
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Match
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Gapop 10.0 , Gapext 0.5
       120991 seqs, 19878514 residues
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: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
1: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
1: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
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Copyright (c) 1993 - 2003 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
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/cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
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     $ 9 US-10-095-407-11
9 US-10-095-407-7
5 9 US-09-965-528-25
9 US-10-095-407-2
19 US-10-139-833-11
9 US-10-139-833-13
9 US-10-063-547-142
12 US-10-066-667-142
10 US-09-788-963-6
10 US-09-738-963-2
10 US-09-738-963-2
10 US-09-738-963-2
10 US-09-788-963-2
10 US-09-788-963-6
10 US-09-788-781-6
9 US-09-788-781-6
9 US-09-788-626-6186
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                             Sequence 25, Appli
Sequence 27, Appli
Sequence 11, Appli
Sequence 11, Appli
Sequence 142, Appli
Sequence 142, Appli
Sequence 6397, Appli
Sequence 12, Appli
Sequence 1264, Appli
Sequence 1264, Appli
Sequence 87, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 6, Appli
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Sequence 4316, Ap
Sequence 6186, Ap
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Sequence 7, Appli
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US-10-095-407-7
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LENGTH: 136
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Best Local
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1493	1400	1302	1034	911	892	834	672	628	610	610	610	586	496	483	475	441	430	391	356	345	300	196	194	191	175
10	10	12	10	10	9	10	10	10	10	9	9	2	9	9	10	12	10	10	9	10	9	10	10	9	9
US-09-858-754-3	US-09-764-176-7	US-10-000-864-2	US-09-858-754-5	US-09-745-763-140	US-09-738-626-5307	US-09-826-752-4	US-09-858-754-2	US-09-881-752A-144	US-09-852-118-2	US-10-138-713-2	US-09-738-626-6657	US-10-071-751-30	US-10-108-605-51	US-09-738-626-5097	US-09-826-752-14	US-10-115-406-4	US-09-815-242-11250	US-09-866-562-62	US-09-738-626-6416	US-09-858-718-4	US-09-938-269-1	US-09-858-664A-16	US-09-811-284-140	US-09-738-626-3880	US-09-989-919-84
ω	7,	N		Sequence 140, App	Sequence 5307, Ap	Sequence 4, Appli	Sequence 2, Appli	Sequence 144, App	Sequence 2, Appli	Sequence 2, Appli	Sequence 6657, Ap	e G	Sequence 51, Appl	Sequence 5097, Ap	14	Sequence 4, Appli	Sequence 11250, A	Sequence 62, Appl	Sequence 6416, Ap	Sequence 4, Appli	Sequence 1, Appli	Sequence 16, Appl	Sequence 140, App	3880	Sequence 84, Appl

ALIGNMENTS

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; ORGANISM: Homo sapiens US-10-095-407-11
             Sequence 7, Application US/10095407
Patent No. US20020164330A1
GENERAL INFORMATION:
APPLICANT: Pan, Yang
TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: 09404/552001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
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Patent No. US20020164330A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/10/095,407
CURRENT FILING DATE: 2002-03-11
PRIOR APPLICATION NUMBER: US 60/091,650
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: US 60/054,646
PRIOR APPLICATION NUMBER: US 60/054,646
PRIOR FILING DATE: 1997-08-04
NUMBER OF SEO ID NOS: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Pan, Yang
TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: 09404/052001
CURRENT APPLICATION NUMBER: US/10/095,407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                      12 LASSLSSASAE 22
                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 18.28; es 2; Conservative
                                                                                                                                                                                                                                                                                                                                                        1 LXXXXXXXXXX 11
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Pred. No. 45;
                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 136;
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Query Match
Best Local Similarity
Thes 2; Conserve
                                      US-10-095-407-2
                                                                                                                                                                                                                                                    ; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20020187523A1 4365383CD1
US-09-965-528-25
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-095-407-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-965-528-25
   Sequence 2, Application US/10095407 Patent No. US20020164330A1
                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 55
SOFTWARE: PERL Program
SEQ ID NO 25
LENGTH: 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: INCYTE GENOMICS, INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 7
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PRIOR APPLICATION NUMBER: US 60/091,650
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: US 60/054,646
PRIOR FILING DATE: 1997-08-04
                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR FILING DATE: 1999-10-04
                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR FILING DATE: 1999-07-30
PRIOR APPLICATION NUMBER: 60/157,508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 60/134,949
PRIOR FILING DATE: 1999-05-19
PRIOR APPLICATION NUMBER: 60/144,270
PRIOR FILING DATE: 1999-07-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/965,528
CURRENT FILING DATE: 2001-09-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: LJ Dyung Aina M.
APPLICANT: PATTERSON, Chandra
TITLE OF INVENTION: EXTRACELLULAR SIGNALING MOLECULES
FILE REFERENCE: PF-0701 USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 60/146,700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
                                                                                                         52 LASSISSASAE 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               43 LASSLSSASAE 53
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                                                                                                                                              1 LXXXXXXXXX 11
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BANDMAN, Olga *
BAUGHN, Mariah R.
AZIMZAI, Yalda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YUE, Henry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TANG, Y. Tom
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                                                                                                                                                                                              18.2%;
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Pred. No.
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Pred. No.
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RESULT 6
US-10-139-833-13
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                                                                                                                                                                                                                  SEQ ID NO 11
LENGTH: 178
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2
                                                                                     Matches
                                                                                                                       Query Match
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Matches 2; Conservative
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                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 60/795,910
PRIOR FILING DATE: 2000-04-10
PRIOR APPLICATION NUMBER: 09/724,583
PRIOR FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 37
SOFTWARE: Patentin Ver: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/095,407
CURRENT FILING DATE: 2002-03-11
PRIOR APPLICATION NUMBER: US 60/091,650
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: US 60/054,646
PRIOR FILING DATE: 1997-08-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/10/139,833
CURRENT FILING DATE: 2002-05-06
PRIOR APPLICATION UNMBER: 60/170,191
PRIOR FILING DATE: 1999-12-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Craveiro, Roger
TITLE OF INVENTION: Interleukin-1 Receptor Antagonist-Related Molecules and
TITLE OF INVENTION: Uses Thereof
FILE REFERENCE: 00-1213-E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Saris, Christiaan M. APPLICANT: Giles, Jennifer
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TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: 09404/052001
                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 60/194,521 PRIOR FILING DATE: 2000-04-04
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TYPE: PRT
      54 LASSLSSASAE 64
                                                                               Local Similarity nes 2; Conserv
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                                                                                   Conservative
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18.28;
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Pred. No.
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Pred. No. 51;
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51;
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; TYPE: PRT; ORGANISM: Homo Sapien US-10-063-547-142
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                               Query Match 44.4%;
Best Local Similarity 18.2%;
Matches 2; Conservative
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LENGTH: 193
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Publication No. US20030004106A1
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                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/10/063,547
CURRENT FILING DATE: 2002-05-02
                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME
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APPLICANT: Craveiro, Roger
TITLE OF INVENTION: Interleukin-1 Receptor Antagonist-Related Molecules and
TITLE OF INVENTION: Uses Thereof
FILE REFERENCE: 00-1213-E
                                                                                                                                                                                                  Prior Application removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 170
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                                                                                                                                                                                                                                                                                FILE REFERENCE: P3230R1C1
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RIOR APPLICATION NUMBER: 60/194,521
RIOR FILING DATE: 2000-04-04
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PRIOR FILING DATE: 1999-12-10
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URRENT FILING DATE: 2002-05-06
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 1 LXXXXXXXXX 11
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Gerritsen, Mary E.
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Pred. No.
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CURRENT FILING DATE: 2001-12-06
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APPLICATION NUMBER: 60/091628
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APPLICATION

NUMBER: 60/096012

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PRIOR FILING DATE: 1998-09-24
PRIOR APPLICATION NUMBER: 60/102570
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IN FILING DATE: 1998-09-17
OR APPLICATION NUMBER: 60/101279
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APPLICATION NUMBER: 60/108807
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APPLICATION NUMBER: 60/105002
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FILING DATE: 1998-10-08
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FILING DATE: 1998-10-08
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A) PLICATION NUMBER: 60/103449
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APPLICATION NUMBER: 60/101738
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APPLICATION NUMBER: 60/100683
FILING DATE: 1998-09-17
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APPLICATION NUMBER: 60/100662
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FILING DATE: 1998-09-10
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Similarity 18.:
2; Conservative
                                             NUMBER: 09/380142
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        Score 8;
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RESULT 9 US-09-788-963-6 ; Sequence 6, Application US/09788963

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US-09-738-626-6397
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RESULT 11
                                                                                                            Best Local Similarity 18.2%; Score 8; DB 9;
Matches 2; Conservative 0; Mismatches
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PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PATENTIN VET. 3.0
SEQ ID NO 6397
LENGTH: 206
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Publication No. US20020197605A1
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CURRENT FILING DATE: 2001-02-20
PRIOR APPLICATION NUMBER: 09/293,625
PRIOR FILING DATE: 1999-04-16
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APPLICANT: MCDONNELL, PETER C.
APPLICANT: KUMAR, SANJAY
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PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
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CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
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OCHIAI, KEIKO
YOKOI, HARUHIKO
TATEISHI, NAOKO
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; Sequence 12, Application US/10139833
; Publication No. US20030004106A1
                                                                                                                 ; ORGANISM: HOMO SAPIENS US-09-788-963-2
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US-09-788-963-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Homo sapiens US-10-139-833-12
                                                                                                                                                                                                SEQ 1D NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/788,963
CURRENT FILING DATE: 2001-02-20
                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
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PRIOR APPLICATION NUMBER: 60/170,191
PRIOR FILING DATE: 1999-12-10
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TITLE OF INVENTION: Interleukin-1 Receptor Antagonist-Related Molecules and
TITLE OF INVENTION: Uses Thereof
FILE REFERENCE: 00-1213-E
CURRENT APPLICATION NUMBER: US/10/139,833
CURRENT FILING DATE: 2002-05-06
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                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 09/293,625 PRIOR FILING DATE: 1999-04-16
                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 09/452,140 PRIOR FILING DATE: 1999-12-01
                                                                                                                                                                                                                                                                                                                                                                           FILE REFERENCE: GP-70607-1C1
                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: INTERLEUKIN-1 HOMOLOGUE, MAT IL-1H4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 60/188,053
PRIOR FILING DATE: 2000-03-09
PRIOR APPLICATION UMBER: 60/194,521
PRIOR FILING DATE: 2000-04-04
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                                                                                                                                                      LENGTH: 21
TYPE: PRT
                                                                                                                                                                                                                SOFTWARE: FastSEQ for Windows Version 3.0
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                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 60/195,910
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1 LXXXXXXXXX 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bass, Michael B.
                                   Conservative
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                                                   44.48;
18.28;
                                 Score 8; DB 1
Pred. No. 56;
0; Mismatches
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Pred. No. 56;
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94 LASSLSSASAE 104

RESULT 13 US-09-925-301-1264

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US-09-864-761-35469 ; Sequence 35469, Application US/09864761
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                                                                                                                                                                                                                                              ; TYPE: PRT ; ORGANISM: Rattus norvegicus US-10-047-542-87
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-047-542-87
                                                                                                                                         Query Match
Best Local Similarity 16.4
"~* hes 2; Conservative
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Best Local Similarity 18.2
Thes 2; Conservative
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Patent No. US20020052308A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 87, Application U Patent No. US20020168367Al
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CURRENT FILING DATE: 2001-10-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: NOVEL IMMUNOADHESINS FOR TREATING AND PREVENTING VIRAL TITLE OF INVENTION: AND BACTERIAL DISEASES FILE REFERENCE: 030905.0004.CIP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE RETERBNCE: PA106
                                                                                                                                                                                                                                                                                                                                                        PRIOR FILING DATE: 2000-04-28
NUMBER OF SEQ ID NOS: 101
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PRIOR FILING DATE: 2001-04-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 60/124,270 PRIOR FILING DATE: 1999-03-12
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TYPE: PRT
ORGANISM: Homo sapiens
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                                                                                              282 LVATATATASE 292
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18.28;
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Pred. No.
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Pred. No.
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9;
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Best Local
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TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Acomica-X-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
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CURRENT FILING DATE: 2001-05-23
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NUMBER OF SEQ 10 NOS: 49117
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PRIOR FILING DATE:
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PRIOR FILING DATE: 2001-01-30
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PRIOR FILING DATE: 2001-01-30
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                                                                                                                                                                                                                         OTHER INFORMATION: KXPRESSED IN BONE MARROW, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.3
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.2
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.2
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.3
OTHER INFORMATION: EXPRESSED IN HELACENTA, SIGNAL = 1.3
OTHER INFORMATION: EXPRESSED IN BLACENTA, SIGNAL = 1.3
OTHER INFORMATION: EXPRESSED IN BLACENTA, SIGNAL = 0.98
OTHER INFORMATION: EXPRESSED IN HELACENTA, SIGNAL = 0.98
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PRIOR APPLICATION NUMBER: PCT/US01/00669
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapieus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
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40 LRAAAQTSSAE 50
                                                    1 LXXXXXXXXXX 11
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                                                                                                  . Similarity
2; Conserv
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                                                                                                  Conservative
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18.2%;
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Pred. No.
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Search completed: January 15, 2003, 12:39:50 Job time : 11.8571 secs

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                     Score
US-09-823-649A-1
18
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                                                                                                                                                                                                                                                                                                                                                                                               283224 segs, 96134422 residues
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Copyright (c) 1993 - 2003 Compuc
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T04681
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R; Bevan, M.; Rose,
                                                                                                                                                                                                                                                                                                                                                                          C; Genetics:
                                                                                                                                                                                                                        A84792
         Query Match
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ALIGNMENTS

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                                                                                 C;Genetics:
A;Gene: At2g37380
A;Map position: 2
A;Map position: 2
C;Superfamily: Arabidopsis thaliana hypothetical protein At2g39370
                                                                                                                                                                                                                                                                                                                                                                                                                                  R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter Nature 402, 761-768, 1999

A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Map position: 4
A;Introns: 33/3; 129/1; 141/3; 179/2; 228/3; 274/3
A;Note: F8D20.270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein F8D20.270 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 21-May-1999
                                                                                                                                                                                                                                                                                                                                                                  A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A;Reference number: A84420; MUID:20083487; PMID:10617197 A;Accession: A84792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Mar-2001
C;Accession: A84792
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A; Cross-references: EMBL: AL031135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Reference number: 215381
A; Accession: T04681
                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-321 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein At2q37380 [imported] - Arabidopsis thaliana C; Species: Arabidopsis thaliana (mouse-ear cress)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Experimental source: cultivar Columbia; BAC clone F8D20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
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                                                                                                                                                                                                                                      A;Cross-references: GB:AE002093; NID:g4056491; PIDN:AAC98057.1; GSPDB:GN00139
                                                                                                                                                                                                                                                                                                                                  A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 50.0%;
Best Local Similarity 18.2%;
Matches 2; Conservative
   Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 LSSSSSSSTSE 71
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             M.; Nempel, S.; Entian, K.D.; Jesse, T.; Heijnen, L.; Vos, P.; Mewrotein Sequence Database, July 1998
   18.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 9; DB 2; Length 303; Pred. No. 5.3e-l1; 0; Mismatches 9; Indels
   Pred. No. 5.4e-11;
                                   Score 9;
                                   DB 2; Length 321;
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Gaps

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J.D.; Dodson, R.J

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N;Alternate names: morphogenetic protein
C;Species: Pisolithus tinctorius
C;Date: 10-Apr-1996 #sequence_revision 24-May-1996 #text_change 18-Jul-2001
C;Accession: JC4607; PC4145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein F4B14.30 - Alabidopsis thaliana C; Species: Arabidopsis thaliana /m.....
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A; Note: KIAA0540
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A; Residues: 1-1113 < NAG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Reference number: Z14086; MUID:98290545; PMID:9628581
A;Accession: T00271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Homo sapiens (man)
C;Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 11-Jan-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Bevan, M.; Rose, M.; Hempel, S.; Entian, K.D.; Hoheisel, J.; Mewes, H.W.; Mayer, K.F.X submitted to the Protein Sequence Database, October 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 21-May-1999
C;Accession: T04686
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                                         R; Tagu,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Experimental source: cultivar Columbia; BAC clone F4B14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-463 <BEV>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Accession: T04686
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A;Title: Cloning and characterization of hydrophobins-encoding cDNAs from the ectomycord
                                                                                                                                                                                              JC4607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: EMBL:AB011112; NID:d1185382; PIDN:BAA25466.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary; translated from GB/EMBL/DDHJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Title: Prediction of the coding sequences of unidentified human genes. IX. The complet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R; Nagase,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein KIAA0540 - human (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Map position: 4
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                                                                                                                                                                 hydrophobin 1 precursor - Pisolithus tinctorius
                                                                                                                                                                                                                   RESULT 5
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                                                                                                                                                                                                                                                                                           683 LAAAAAAAAE 693
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                  D.; Nasse, B.; Martin, F.
8, 93-97, 1996
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                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
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les 2; Conserv
                                                                                                                                                                                                                                                                                                                                        1 LXXXXXXXXXX 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ishikawa, K.; Miyajima, N.; Tanaka, A.; Kotani, H.; Nomura, N.; Ohara,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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18.2%;
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18.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 9;
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9.5e-11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , M.; Shen, M.; Vamathovan, J.J.; Lam, P.; S.; Smith, H.O.; Venter, J.C.; Fraser, C.M. Science 286, 1571-1577, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: protein A; Residues: 115-140 <TA2>
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R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
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E;1-18/Domain: signal sequence #status predicted <SIG>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Reference number: JC4607; MUID:96186962; PMID:8626073 A;Accession: JC4607
                    A; Experimental source: cv. Haisa,
                                    A;Cross-references: EMBL:AJ222779; NID:e1203989; PIDN:CAA10984 1; PID:e1203990
                                                                   A; Molecule type: mRNA
A; Residues: 1-181 <HES>
                                                                                                                A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                            A; Reference number: Z15411
A; Accession: T05925
                                                                                                                                                                                      A; Title: Analysis of randomly selcelted cDNAs reveals the expression of stress- and d
                                                                                                                                                                                                                   Plant Sci. 133, 191-201, 1998
                                                                                                                                                                                                                                       C:Accession: T05925
R;Hess, W.R.; Golz, R.R.; Boerner, T.
                                                                                                                                                                                                                                                                                      C:Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 08-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Map position: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Gene:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-169 <WHJ>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein - Deinococcus radiodurans (strain R1)
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                                                                                                                                                                                                                                                                                                                C;Species: Hordeum vulgare (barley)
                                                                                                                                                                                                                                                                                                                                   hypothetical protein - barley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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Best Local Similarity
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les 2; Conservative
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18.2%;
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C;Species: Agrobacterium tumefaciens
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 11-Jan-2002
C;Accession: C97562
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-189 <KUR>
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A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz,
Science 294, 2323-2328, 2001
Дb
                                    QV
                                                                                                                                                                    C; Superfamily: peptidylprolyl isomerase; cyclophilin homology
                                                                                                                                                                                             A; Map
                                                                                                                                                                                                               A; Gene: ppiB
                                                                                                                                                                                                                                                          A; Experimental source: strain C58 (Dupont)
                                                                                                                                                                                                                                                                             A;Cross-references: GB:AE008688; PIDN:AAL42680.1; PID:g17740114; GSPDB:GN00186
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Science 294, 2317-2323, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, 1 erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell
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A;Reference number: A97359; PMID:11743194
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                                                                                                                                                                                                                                                                                                                                                                                        A; Reference number: AB2577; PMID:11743193
                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Accession: C97562
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R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, R;Nierman, W.C.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Ko
                                                                                                                                                                                                                                                                       homeobox and LIM domain protein lim-6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 **sequence_revision 29-Oct-1999 **text_change 31-Mar-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein YHR143w - yeast (Saccharomyces cerevisiae)
C;Species: Saccharomyces cerevisiae
C;Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 19-Apr-2002
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n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser,
Proc. Natl. Acad. Sci. U.S.A. 98, 4186-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
                                                                                                                                                             R;Latreille, P.; Gattung, S. submitted to the EMBL Data Library, April 1996
A;Description: The sequence of C. elegans cosmid K03E6
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A; Residues: 1-325 < MAC>
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A; Accession: S46760
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A;Accession: B87370
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C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
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A; Uross-references:
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A;Cross-references: EMBL:U55375; PIDN:AAC69042.1; GSPDB:GN00028; CESP:K03E6.1
                                  A; Molecule type: DNA
A; Residues: 1-334 <LAT>
                                                                                A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                             A; Accession: T34326
                                                                                                                                         A; Reference number: 221506
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein CC0974 [imported] - Caulobacter crescentus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 2; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           225 LASSSSTSAVE 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               90 LSTSAASAAIE 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 LXXXXXXXXXX 11
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                                                                                                                                                                                                                                                      T34326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SGD:S0001186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             44.48;
18.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     44.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 8; DB 2;
Pred. No. 4e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 8;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .3e-07;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
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A; Experimental source: strain Bristol N2; clone K03E6

В

227 LAAAASSSSLE 237

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A; Introns: 15//5; 54:C; Superfamily: actin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein T25C8.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein APE1409 - Aeropyrum pernix (strain K1)
C:Species: Aeropyrum pernix
C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Introns: 29/2; 65/3; 106/2; 149/3; 238/3
C;Superfamily: homeotic protein mec-3; homeobox homology; LIM metal-binding repeat homol C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              D
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                                                                                                                                                                                                                                                                                                A; Residues: 1-375 <WIL>
A; Residues: 1-375 <WIL>
A; Cross-references: EMBL: Z83241; PIDN: CAB05817.1; GSPDB: GN00021; CESP: T25C8.2
                                                                                                                                                                                                                                                                                                                                                                                                      A; Reference number: Z20008
A; Accession: T25272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Accession: T25272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Superfamily: Aeropyrum pernix hypothetical protein APE1409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr A; Reference number: A72450; MUID:99310339; PMID:10382966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA Res. 6, 83-101, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takabawa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Accession: H72618
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                                                                                                                                                                                                                           A; Gene:
                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                        A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                      submitted to the EMBL Data Library, December 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Gene: APE1409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Experimental source: strain Kl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-336 < KAW>
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                                                                                                                                                                                                A; Map position:
                                                                                                                                                                                                                                                                           A; Experimental source: clone T25C8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: DDBJ:AP000061; NID:g5104821; PIDN:BAA80406.1; PID:g5105092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary
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                                                Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              123 LASTTASSLTE 133
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les 2; Conserv
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1 LXXXXXXXXX 11
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                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      44.4%; Score 8; DB 2;
18.2%; Pred. No. 4.1e-0
                                                                     44.4%; Score 8; DB 2; I
18.2%; Pred. No. 4.3e-07;
                                                  0;

 Mismatches

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                                                  Mismatches
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                                                                                             Length 375;
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Job time : 20.1429 secs

Search completed: January 15, 2003, 12:37:06

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A; Accession: D97521
A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                              A;Molecule type: DNA
A;Residues: 1-387 <KUR>
A;Cross-references: GB:AE007869; PIDN:AAK87125.1; PID:g15156389; GSPDB:GN00169
C;Genetics:
   뭉
                                                                                                                                                                                                                                                       A;Map position: circular chromosome C;Superfamily: aspartate transaminase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldm
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz,
Science 294, 2323-2328, 2001
                                                                                                                                                                                                                                     C; Keywords: aminotransferase
                                                                                                                                                                                                                                                                                                                        A;Gene: AGR_C_2460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Reference number: A97359; PMID:11743194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                probable aspartate transaminase (EC 2.6.1.1) aspB (similarity) [imported] - Agrobacte
C;Species: Agrobacterium tumefaciens
C;Late: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 11-Jan-2002
C;Accession: D97521
                                                                                                                  Matches
                                                                                                                                                                          Query Match
276 LAATAAFSAAE 286
                                                                                                               Local Similarity hes 2; Conserv
                                                       1 LXXXXXXXXX 11
                                                                                                               Conservative
                                                                                                                                        44.48;
18.28;
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                                                                                                                                        Score 8; DB 2; Length 387; Pred. No. 4.3e-07;
                                                                                                               Mismatches
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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Sequence:
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   pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Scor
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   SwissProt_40:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GenCore version 5.1.3 Compugen Ltd.
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HYP1_P1STI
Y65L_HORVI
Y103_YEAST
OXYR_MOUSE
OXYR_RAT
YXEK_BACSU
SWP1_ENCCU
A2AC_MOUSE
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VRIAL JEPPLA
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E412 HUMAN
ALAB ARATH
MOZ HUMAN
SENL YEAST
WDR9 HUMAN
ANPA PSEAM
Y507 METTH
FKB2 MOUSE
SSI_STRVL
OPRJ. NEIMC
PYRE PSEAE
SSI_STRVL
OPRJ. NEIMC
PYRE PSEAE
SWSI_MOUSE
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ALIGNMENTS

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	RP Watt RA Wat RA Nak RA Nak RT "NE RC CC -! CC -!		RESULT 1 VAS1_HUMAN ID VAS1_ OL150 AC Q150 AC Q151 AC Q151 AC Q151
-i- SUBCRILULAR LOCATION: Integral membrane protein. Vacuolar (By similarity)i- TISUE SPECIFICITY: UBIQUITOUSi- TISSUE SPECIFICITY: UBIQUITOUS. -i- TISS	SEQUENCE OF 128-470 FROM N.A. Watanabe K., Kumaqai A., Itakura S., Yamazaki M., Tashiro H., Ota T., Watanabe K., Kumaqai A., Nishi T., Shibahara T., Tanaka T., Suzuki Y., Obayashi M., Nishi T., Shibahara T., Tanaka T., Nakamura Y., Isogai T., Sugano S.; NNBDO human cDNA sequencing project."; Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases. -i- FUNCTION: VACUOLAR APPASE IS RESPONSIBLE FOR ACIDIFYING A VARIETY OF INTRACELLULAR COMPARTMENTS IN EUKARYOTIC CELLS (BY SIMILARITY). -i- CATALYTIC ACTIVITY: ATP + H(2)O + H(+)(In) = ADP + phosphate + H(+)(Out).	SEQUENCE FROM N.A. MEDLINE-96311563; PubMed-8733135; Chen E.Y., Zollo M., Mazzarella R.A., Ciccodicola A., Chen CN., Chen E.Y., Zollo M., Mazzarella R.A., Ciccodicola A., Chen CN., Zuo L., Heiner C., Burough F.W., Ripetto M., Schlessinger D., Zuo L., Heiner C., Burough F.W., Ripetto M., Schlessinger D., Zuo L., Heiner C., Burough F.W., Ripetto M., Schlessinger D., Zuo L., Heiner C., Burough F.W., Ripetto M., Schlessinger D., Ziong-range sequence analysis in Xq28: thirteen known and six Candidate genes in 219.4 kb of high GC DNA between the RCP/GCP and GGEND loci.", GGEND loci.", GGEND loci.", GGEND loci.", FISULE OF 97-470 FROM N.A. TISSUE-Brain, MEDLINE-94307726; PubMed-8034313; MEDLINE-94307726; PubMed-8	HUMAN STANDARD; PRT; 470 AA. VASI_HUMAN STANDARD; PRT; 470 AA. Q15904; 16-OCT-2001 (Rel. 40, Created) 16-OCT-2001 (Rel. 41, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Vacuolar ATP synthase subunit S1 precursor (EC 3.6.3.14) (V-ATPase S1 subunit) (V-ATPase S1 accessory protein) (V-ATPase Ac45 subunit) (XAP-3). ATP6IP1 OR ATP6S1 OR VATPS1 OR XAP3. Homo sapiens (Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBL_TaxID=9806;

DB 1;

Length 140;

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  SEQUENCE
                                                           PROSITE; PS00956; Cell wall; Signal.
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                                                                                                                                                                                                  entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                           use by non-profit institutions as long a modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                  Gene 168:93-97(1996).
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Tagu D., Nasse B., Martin F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-441
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Boletales; Sclerodermataceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AK026519; -; NOT_ANGenew; HGNC:868; ATP6IP1.
                                             SIGNAL
                                                                                                                                                                                                                                                                              the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                   "Cloning and and characterization of hydrophobins-encoding cDNAs from
the ectomycorrhizal basdiomycete Pisolithus tinctorius.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=37468;
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SIMILARITY: BELONGS TO THE FUNGAL HYDROPHOBIN FAMILY.
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                                                                                HYDROPHOBIN;
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      HYDROPHOBIN-1.
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RESULT 3
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DT 15-DEC
DT 15-DEC
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DE YC165-
OS HOZGEN
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Commatonhyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Analysis of randomly selected cDNAs reveals the expression of stress-
and defence-related genes in the barley mutant albostrians.";
Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
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Hess W.R., Golz R., Boerner T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Y65L_HORVU
O48609;
                                                                  Saccharomycetales;
NCBI_TaxID=4932;
                                                                                                                                                                                             precursor.
                                                                                                                                                                                                                       Hypothetical
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15-DEC-1998 (Rel. 37, Last sequence up. 16-OCT-2001 (Rel. 40, Last annotation)
STRAIN=S288c / AB972;
                    SEQUENCE FROM N.A.
                                                                                                                     Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                          Saccharomyces cerevisiae (Baker's yeast)
                                                                                                                                                                      YHR143W.
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                                                                                                                                                                                                                    . 31, Created)
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19865 MW;
                                                                                            Saccharomycetaceae;
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Last annotation update)
protein in RPL44B-RPC10
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CHLOROPLAST (POTENTIAL).
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Pred. No.
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(POTENTIAL).

Glycoprotein

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RESULT 5
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DT 16-JUL
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                                                              between the Swiss Institute of Bioinformatics and the I
the European Bioinformatics Institute. There are no rest
use by non-profit institutions as long as its content
modified and this statement is not removed. Usage by ar
entities requires a license agreement (See http://www.isb
or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                 "Structure and expression of the mouse oxytocin receptor gene.";
Mol. Cell. Endocrinol. 124:25-32(1996).
-!- FUNCTION: RECEPTOR FOR OXYTOCIN. THE ACTIVITY OF THIS RECEPTO
MEDIATED BY G PROTEINS WHICH ACTIVATE A PHOSPHATIDYLINOSITOL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mutelcostomi; Mammalla; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oxytocin receptor (OT-R).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-JUL-1998 (Rel.
15-JUL-1998 (Rel.
15-JUL-1998 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical protein; SIGNAL 1 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                EMBL; D86599; BAA18995.1;
                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kubota Y., Kimura T., Hashimoto K.,
Azuma C., Saji F., Murata Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                            -!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=97179034; PubMed=9027321;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10090;
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36, Last sequence update)
36, Last annotation update)
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Pred. No. 7.6e-07
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                                                                                       (See http://www.isb-sib.ch/announce/
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Best Local Similarity
Matches 2; Conserv
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                                                                                                                                                                                    Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: RECEPTOR FOR OXYTOCIN. THE ACTIVITY OF THIS RECEPTOR MEDIATED BY G PROTEINS WHICH ACTIVATE A PHOSPHATIDYLINOSITOL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CARBOHYD
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-Sprague-Dawley; TISSUE-Liver; MEDLINE-95116525; PubMed-7816817; Rozen F., Russo C., Banville D., Zingg H.H.; "Structure, characterization, and expression receptor gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         G-protein coupled receptor; Transmembrane; DOMAIN 1 38 EXTRACELLULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rat
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16-OCT-2001 (Rel. 40, Last seq
16-OCT-2001 (Rel. 40, Last ann
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PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.

PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
                                                                                                                                                                                                                                                                               Zingg H.H.;
                                                                                                                                                                                                                                                                                                                                                                                             receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID-10116;
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                                                                                                                                                                                                                                                                                                           REVISION TO 84.
                                                                                                                                                                                                                                                                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 92:200-204(1995).
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                                                                                                  CALCIUM SECOND MESSENGER SYSTEM.
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7 (POTENTIAL).
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Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G., Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S., Borriss R., Boursier L., Brans A., Braum M., Brignell S.C., Bron S., Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M., Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
                                                                                                                                                                                     MEDLINE-97021444; PubMed-8867804; Yoshida K.-I., Fujinyra M., Yanai N., Fujita "Cloning and sequencing of a 23-kb region of genome between the iol and hut operons."; DNA Res. 2:295-301(1995).
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DISULFID
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PROSITE; PS00237; G_PROTEIN_RECEP_F1_1;

PROSITE; PS50262; G_PROTEIN_RECEP_F1_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                         MEDLINE=98044033; PubMed=9384377;
                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-JUN-2002
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Koring Kr. Lauber J. Lazarevic V.,
Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
Moone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
Parro V. Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
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Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
                 Submitted (MAR-1999) to the EMBL/Ge-i- FUNCTION: SPORE WALL COMPONENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; Z99124; CAB159
SubtiList; BG11887;
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--- STMTLARITY: BELONGS TO THE NTAA/SNAA/SOXA(DSZA) FAMILY
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                                           Bohne W., Ferguson D.J.P., Kohler K., Gross U.;
"Molecular characterisation of a developmentally expressed spor
protein from the human microsportidate Encephalitozoon cuniculi.
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                         SEQUENCE FROM N.A.
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RESULT 9
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01-APR-1993 (Rel. 2
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                                                                     use by non-profit institutions as lon modified and this statement is not removenthities requires a license agreement (S or send an email to license@isb-sib.ch).
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MEDLINE=92342131; PubMed=1353249;

Link R.E., Daunt D.A., Barsh G., Chruscinski A.J., Kobilka B.K.;

Link R.E., Daunt D.A., Barsh G., Chruscinski A.J., Kobilka B.K.;

**Cloning of two mouse genes encoding alpha 2-adrenergic receptor subtypes and identification of a single amino acid in the mouse alpha 2-C10 homolog responsible for an interspecies variation in
  EMBL; M99376;
EMBL; M97516;
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                                                                                                                                                                    the European Bioinformatics Institute.
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                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                    -!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS
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                                                                                                                                                                                                                                                                                                                                                                                                                    adrenoceptor subtype gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-DBA/
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Mol. Pharmacol. 42:16-27(1992)
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Mammalia; Eutheria; Rodentia;
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35, Last annotation update)
ic receptor (Alpha-2C adrenoceptor) (Subtype C4).
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Best Local
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                                                                                                                                                                                                                                                         WEDLINE-91126047; PubMed-1704126; Flordellis C.S., Handy D.E., Bresnahan M.R., Zannis V.I., G "Cloning and expression of a rat brain alpha 2B-adrenergic Proc. Natl. Acad. Sci. U.S.A. 88:1019-1023(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR00237; GPCRRHODOPSN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
MEDIINE-91244823; PubMed-1645350;
Lanier S.M., Downing S., Duzic R., Homey C.J.;
"Isolation of rat genomic clones encoding subtypes of
                                                                                                                               Voigt M.M., McCune S.K., Kanterman R.Y., "The rat alpha 2-C4 adrenergic receptor pharmacological subtype.";
                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Motazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Butheria; Rodentia; Sciurognathi; Muridae; Murinac; Rattus
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Alpha-2C adrenetyic receptor (Alpha-2C adreneeptor) (Subtype C4)
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01-NOV 1997 (Ref. 35, Last annotation updat
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Pfam; PF00001; 7tm_1; 1.
                                                                                                                                                                                           MEDLINE-91130596; PubMed=1704314;
                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                             FMBS Lett. 278:45-50(1991).
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                                                                  SEQUENCE FROM N.A.
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51 EXTRAC
76 1 (PO)
88 CYTOP1
114 2 (PO)
124 EXTRAC
147 3 (PO)
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18.28;
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G -> V (IN REF. 2).
G -> A (IN REF. 2).
L -> V (IN REF. 2).
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Jagels K.,

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RESULT 11

LIP_SERM 1D

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SMART; SM00344; HTH_ASNC; 1.
PROSITE; PS00519; HTH_ASNC_FAMILY; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commen
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01-0CT-1994 (Rel. 30, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
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Pfam; PF01037; ASNC_trans_reg; 1.
SMARR; SM00344; HTH_ASNC; 1.
PROSITE; PS00519; HTH_ASNC_FAMILY; 1.
                                                                                                                                                                                                                                                                                SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR000485; ASNC_trans_reg.
Pfam; PF01037; ASNC_trans_reg; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWIS:-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (SEP-1993) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Calvo J.M.
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InterPro; IPR00048
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SIMILARITY: BELONGS TO THE ASNC FAMILY OF TRANSCRIPTIONAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AFFECTS THE EXPRESSION OF A NUMBER OF DIFFERENT OPERONS; LRP MEDIATES THIS EFFECT FOR AT LEAST SOME OF THESE OPERONS. FOR EXAMPLE IT IS REGULATOR OF THE BRANCHED-CHAIN AMINO ACID TRANSPORT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: MEDIATES A GLOBAL RESPONSE TO LEUCINE. EXOGENOUS LEUCINE
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                                  LSKRVGLS 40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18725 MW;
                                                                                                                                                                                                                                                                                18725 MW;
                                                                                                                                                                                                                                                                                                               49
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85
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87.5%;
                                                                                                                                                                                    71.4%;
87.5%;
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                                                                                                                                                                                    Score 35; DB
Pred. No. 8.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 35; DB Pred. No. 8.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              H-T-H MOTIF (POTENTIAL).
A -> G (IN REF. 1).
                                                                                                                                                                                                                                                                             H-T-H MOTIF (POTENTIAL).
; 0940AC4C7937AE48 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A0193595B8EBDE25 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     163 AA.
                                                                                                                                                                                                                DB 1; Length 163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1;
                                                                                                                                                           0,:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBI, outstation
                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
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                                                                                                                                                       0,
                                                        Rutherford K., Ruther S., Saunders D., Seeger K., Sharp S.,

& Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,

Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitchead S.,

& Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,

& Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,

& Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,

& Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,

& Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,

& Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,

& Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,

& Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,

& Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,

& Lucas M., Rochet M., Galilardin C., Tallada V.A., Garzon A., Thode G.,

& Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,

& Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,

& Cerrutti I., Lowe P. McCombie W. P. Boltsch T. Detsekbin I.
Query Match
                                                                  TIGREAMS: TIGR00131; gal_kin; 1.

PROSITE: PS00106; GALACTOKINASE; 1.

PROSITE: PS00627; GHMP_KINASES_ATP; 1.

PROSITE: PS00627; GHMP_KINASES_BATP; 1.

PROSITE: PS00627; GHMP_KINASES_ATP; 1.

PS00627; GHMP_KINASES_ATP; 1.

PS00627; GHMP_KINASES_ATP; 1.

PS00627; GHMP_KINASES_ATP; 1.

P
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15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Galactokinase (EC 2.7.1.6) (Galactose kinase)
                                                                                                                                                                                                                                       InterPro; IPR001459; mev_gal_kin.
Pfam; PF00288; GHMP_kinases; 1.
PRINTS; PR00473; GALCTOKINASE.
PRINTS; PR00959; MEVGALKINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cerrutti I., Lowe T., McCombie W.R., Paulsen I., Potashkin Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.; The genome sequence of Schizosaccharomyces pombe."; Nature 415:871-880(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S., Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M., Collins M., Connor R., Croolin A., Davis P., Feltwell T., Fraser A., Collins S., Coble A., Hamlin N., Harris D., Hidalgo J., Hodgson G., Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          James K., Jones b., Jones M., Leather S., McDonald S., McLean J., Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C., Oliver K., O'Neil S., Pearson D., Quail M.A., Rabbinowitsch E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Schizosaccharomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAL1_SCHPO
                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AL512522; CAC21415.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            between the Swiss Institute of Bioinformatics and the the European Bioinformatics Institute. There are no reuse by non-profit institutions as long as its contenues by non-profit institutions as long as its contenues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID~4896;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9HDU2;
                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000705; Galactokinase.
InterPro; IPR001745; GHMPknse_ATP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SIMILARITY: BELONGS TO THE CHMP KINASE FAMILY. GALK SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=21848401; PubMed=11859360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- CATALYTIC ACTIVITY: ATP + D-galactose - ADP + D-galactose 1-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PATHWAY: Galactose metabolism; first step
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 phosphate
                                                        519 AA;
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                                                            58385 MW;
   71.48;
   Score 35;
                                                        5EE9C129896F8C40 CRC64;
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There are no restrictions on ong as its content is in no

EMBL outstation

Benito J.,

Usage

by and for

DB 1;

Length 519;

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RESULT 13

YW04_SCHPO

ID 4_W04PO

AC Q9HGM

OC Q9T 16-OC

DT 16-OC

DT 15-JI

OC SChi
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RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Gollins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hillet D., Odell C.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Gylorer S., Saunders D., Seeger K., Sharp S.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Welljens J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Welljens I., Vonstreels E., Rieger M., Schaefer M., Mueller Auer S.,
RA Welljens I., Vanstreels E., Rieger M., Schaefer M., Mueller Auer S.,
RA Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lclaure V., Mottier S.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lclaure V., Mottier S.,
RA Galibert F., Aves S. J., Xiang Z., Hunt C., Moore K., Hurst S. M.,
RA Daga R. R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Henilto J.,
RA Dominguez A., Revuelta J.L., Mocron S., Amstrong J., Forsburg S.L.,
RA Cerrutti L., Lowe T., McCombie W. R., Paulsen I., Potashkin J.,
RA Cerrutti L., Lowe T., McCombie W. R., Paulsen I., Potashkin J.,
                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-OCT-2001 (Rel. 40,
16-OCT-2001 (Rel. 40,
15-JUN-2002 (Rel. 41,
Hypothetical protein C
SPBC543.04.
                                                                                                                                                                                               Pfam; PF03666; UPF0171; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J., Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.; "The genome sequence of Schizosaccharomyces pombe."; Nature 415:871-880(2002).

-1- SIMILARITY: BELONGS TO THE UPF0171 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SCHPO
                                                                                                                                                      Hypothetical SEQUENCE 5
                                                                                                                                                                                                                                                                                                    entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                   use by non-profit institutions as long a modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Schizosaccharomycetales;
Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09нсм7;
                                                                                                                                                                                                                                                   EMBL; AL391604; CAC05246.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wood V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=21848401; PubMed=11859360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=4896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Schizosaccharomyces pombe (Fission yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YW04_SCHPO
                                                                                                                                                                                                                              InterPro; IPR005365; UPF0171.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               352
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       1 LSKRIGLSVSE 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 LSKRIGLSVSE 11
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                                                      Similarity 6; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gwilliam R.,
                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Rel. 40, Created)
(Rel. 40, Last sequence update)
(Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                   B5 AA; 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                        66868 MW;
                                                                           71.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rajandream M.A., Lyne M., Lyne R., Stewart A.
                                                      Score 35; DB
Pred. No. 31;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 28;
2; Mismatches
                                                                                                                                                        92F53DFB5AC1BE59 CRC64;
                                                                                                                                                                                                                                                                                                                                                                     There are no restrictions ong as its content is in
                                                                                                  DB 1; Length 585;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ΑA
                                                                                                                                                                                                                                                                                                                                                     Usage
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                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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                                                      0;
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     RESULT 14
RS4_BACSU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Sequencing and functional annotation of the Bacillus subtilis genes in the 200 kb rrnB-dnaB region."; Microbiology 143:3431-3441(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P21466; Q53282; Q45662;

01-MAY 1991 (Rel. 18, Crealed)

01-AGG-1991 (Rel. 19, Last sequence up

15-JUN-2002 (Rel. 41, Last annotation

305 ribosomal protein $4 (B$4).
                                                                                                                                           the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                      Henkin T.M., Chambliss G.H., Grundy F.;
"Bacillus subtilis mutants with alterations in ribosomal protein S4.";
J. Bacteriol. 172:680-6385(1990).
-!- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 16S RIBOSOMAL RNA.
-!- FUNCTION: PROTEIN S4 IS ALSO A TRANSLATIONAL REPRESSOR PROTEIN, IT
- CONTROLS THE "TRANSLATION OF THE ALDHA-OPERON (WHICH CODUS FOR S13,
S11, S4, RNA POLYMERASE ALPHA SUBUNIT, AND L17) BY BINDING TO 1TS
     EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Higo K.I., Otaka M., Osawa S.; "Purification and characterization of 30S ribosomal proteins from Bacillus subtilis: correlation to Escherichia coli 30S proteins."; Mol. Gen. Genet. 185:239-244(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "The rpsD gene, encoding ribosomal regulated in Bacillus subtilis."; J. Bacteriol. 173:4595-4602(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Grundy F.J., Henkin T.M.; "The rpsD gene, encoding:
                                                                                                  EMBL;
                                                                                                                                                                                                                                                                             between
                                                                                                                                                                                                                                                                                                    This
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-!- SIMILARITY: BELONGS TO THE S4P FAMILY OF RIBOSOMAL PROTEINS.
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, M59358; AAA22717.1; -, AF008220; AAC00397.1; -, S45404; AAB19387.1; -, 599119; CABH4944.1; -, M60889; AAA22716.1; -,
                                                                                                                                                                                                                                                                                                                                                                                                      MRNA
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RESULT 15
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RA Ghim S.Y., Glaser P., Goffeau A., Gollightly E.J., Grandi G.,
RA Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
RA Kobyashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,
Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medique C.,
Redina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Raponott G., Rose M.,
Rater T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
Sak Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
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Matches 6; Conser
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Ogasawara N., Nakai S., Yoshikawa H.;
Ogasawara N., Nakai S., Yoshikawa H.;
"Systematic sequencing of the 180 kilobase region of the Hacillus subtilis chromosome containing the replication origin.";
DNA Res. 1:1-14(1994).
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01-OCT-1994 (Rel. 30, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
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InterPro; IPR002942; S4.
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HSSP; P81288; 1C05.
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RNASGING (IN UNTANI RPSD2).

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                                                                                                                                                                                                                           EMBL;
                                                                                                                                                                                                                                                                modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
Viari A., Wantt K., Wedler E., Wedler H., Weitzenegger T.,
Viari A., Wintt K., Wedler E., Wedler H., Weitzenegger T.,
                                                                                                                                                   Hypothetical protein SEQUENCE 201 AA;
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LSKKIGLTV 45
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non-profit institutions as long as its content
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2012 MW; 77A149C6F0979317 CRC64:
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ALIGNMENTS

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Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                       "The complete genome of hyperthermophile Methanopyrus kandleri AV19 and monophyly of archaeal methanogens.";
Proc. Natl. Acad. Sci. U.S.A. 99:4644-4649(2002).
EMBL; AF311944; AAK60014.1;
EMBL; AF311944; AAK60014.1;
EMBL; AF311944; AAK602649.1;
                                                                                                                                                                                                                                                                                                                                                             Slesarev A.I., Mezhevaya K.V., Makarova K.S., Polushin N.N., Shcherbinina O.V., Shakhova V.V., Belova G.I., Aravind L., Natale D.A., Rogozin I.B., Tatusov R.L., Wolf Y.I., Stetter K.O., Malykh A.G., Koonin E.V., Kozyavkin S.A.,
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STRAIN-AV19 / DSM 6324 / JCM 9639;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           "A type IB topoisomerase with DNA repair activities."; Proc. Natl. Acad. Sci. U.S.A. 98:6015-6020(2001).
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Archaea; Euryarchaeota;
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984 AA; 112207 MW;
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Q9Z4G7;
       01-MAY-1999 (TrEMBLrel. 10, Created) 01-MAY-1999 (TrEMBLrel. 10, Last seq
                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00893; DUF7; 1.
Plasmid; Hypothetical protein; Complete proteome.
SEQUENCE 117 AA; 12444 MW; 1D01801CDB574AF3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-Z1082930; PubMed=11214968; Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto Watanabe A., Idessawa K., Ishikawa A., Kawashima K., Kimura T., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Suqimolo M., Patanaki Y., Nakayama S., Nakazaki N., Shimpo S., Suqimolo M.
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01-OCT-2001
01-MAR-2002
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EMBL; AP003015; BAH54438.1; -.
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SEQUENCE FROM N.A.
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MCMUTTAY A.A.;
MCMUTTAY A.A.;
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NCBI_TaxID=381;
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01-027-2001 (TrEMBLrel, 18, Last sequence update)
01-MAR-2002 (TrEMBLrel, 20, Last annotation updat
Hypothetical protein ml19408.
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InterPro; IPR000168; 7TM_nematode.
Pfam; PF01461; 7tm_4; 1.
SEQUENCE 352 AA; 40920 MW; A51
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EMBL; Z83218; CAB05691
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Similarity 63.6%;
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                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nakayama S., Nakazaki N., Shimpo S.,
                                                                                                                                                                                                                                                                                                                   75.5%;
88.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      40920 MW; A512D50FF03860C9 CRC64;
Last sequence update)
                                                                                                                                                                                                                                                                                        1; Mismatches
                                                                                                                                                                                                                                                                                                                      Pred. No.
                                                                                                                                                                                                                                                                                                                                         Score 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           . No. 26;
                                                                              79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        117
                                                                                                                                                                                                                                                                                                                                  DB 16; Length 117;
                                                                            B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A
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                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 352;
                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sugimoto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sasamoto
                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                 Gaps
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Q8TMU7
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                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                         Q8TMU7;
Q8TMU7;
01-JUN-2002
Galagan J.E., Nusbaum C., Roy A., Endrizzi M.G., Macdonald P., FitzHugh W., Calvo S., Engels R., Smirnov S., Atnoor D., Brown A., Allen N., Maylor J., Stange-Thomann N., DeArcliano K., Johnson R., Linton L., McGwan P., McKernan K., Talamas J., Tirrell A., Ye W., Zimmer A., Barber R.D., Cann I., Graham D.E., Grahame D.A., Guss A.M.,
                                                                                                                                                                                                             01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last seq
01-JUN-2002 (TrEMBLrel. 21, Last ann
                                                                                                                                         Methanosarcina acetivorans.
Archaea; Euryarchaeota; Methanococci;
Methanosarcinaceae; Methanosarcina.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SPECIES-5.typhimurium; PLASMID-INCN R46; Belogurov A.A., Hall R.M., Winans S.C., Woodgate R.; "Complete sequence of R46 and its deletion derivative, I submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases EMBL; U72482; AAD17386.1; -.
                                                                    STRAIN-C2A / ATCC 35395 / DSM 2834;
MEDLINE-21929760; PubMed-11932238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Organization of the leading region of IncN pla
regulation controlled by CUP sequence elements
J. Mol. Biol. 271:13-30(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-2002 (TrEMBLrel.
Hypothetical 8.5 kDa pro
ORF80 OR CCGEIII.
                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                Predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Belogurov A.A., Delver E.P., Rodzevich O.V.; "Plasmid pKM101 encodes two nonhomologous antirestriction proteins (ArdA and ArdB) whose expression is controlled by homologous
                                                                                                                          NCBI_TaxID=2214;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical protein; Plasmid.
SEQUENCE 79 AA; 8482 MW; 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                regulatory sequences.";
J. Bacteriol. 175:4843-4850(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SPECIES=S.typhimurium; PLASMID=I
MEDLINE=93328690; PubMed=8393008;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 66-79 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SPECIES=E.coli; PLASMID=PKM101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Delver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SPECIES-E.coli, and S.typhimurium; PLASMID-PKM101, AND INCN MEDLINE-97445167; PubMed-9300052;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=562,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Salmonella typhimurium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                           69
                                                                                                                                                                                                                                                                                                                                                                    LSKRIGLSVSE 11
                                                                                                                                                                                                                                                                                                                                           LAKKLGITVSE 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AY046276; AAL13409.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E.P., Belogurov A.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pKM101, and Plasmid IncN R46.
a: Proteobacteria; gamma subdivision;
                                                                                                                                                                                                                                                                                                                                                                                                 Similarity

6. Conser
                                                                                                                                                                                                protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (MAR-1999) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               602;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               kDa protein
                                                                                                                                                                                                                                                                                                                                                                                                            73.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PLASMID-INCN R46;
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                                                                                                                                                                                                             Last sequence up
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                                                                                                                                                                                                                                                                                                                                                                                                             Score 36; DB
Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       9EF624EBBD16E297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (CcgEIII).
                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                       243
                                                                                                                                                        Methanosarcinales;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                          Length 79,
                                                                                                                                                                                                                                                                                                                                                                                                indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R46;
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Q8XXI6
ID Q8
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AC Q8
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local
                                                                                                                  Q8XXI6;
01-MAR-2002 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.

STRAIN-ATCC 824 / DSM 792 / VKM B-1787;

STRAIN-ATCC 824 / DSM 792 / VKM B-1787;

MEDLINE=21359325; PubMed=11466286;

Moelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.1., Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.1.,
     Ralstonia solanacearum (Pseudomonas solanacearum)
Bacteria; Proteobacteria; beta subdivision; Ralst
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-2001
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hedderich R., Ingram-Smith C., Kuettner H.C., Krzycki J.A., Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K., Springer T.A., Umayam L.A., White O., White R.H., de Macario E.C., Ferry J.G., Jarrell K.F., Jing H., Macario A.J.L., Paulsen I., Pritchett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E., Maccalf W.W., Birren B.;
                                                     DALR OR RSC2127 OR RS01506.
                                                                                 protein
                                                                                             Putative transcriptional regulator (Repressor) transcription regulator
                                                                                                                                                                                                                          91XX80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR003740; DUF161.
Piam; PF02588; DUF161; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AE007644; AAK79294.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            bacterium Clostridium acetobutylicum.", J. Bacteriol, 183:4823-4838(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J., Bennett G.N., Koonin E.V., Smith D.R.; "Genome sequence and comparative analysis of the solvent-producing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiales; Clostridiaceae; Clostridium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Clostridium acetobutylicum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAC1325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Uncharacterized
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q97JG0;
01-0CT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "The genome of Methanosarcina acetivorans reveals extensive metabolic and physiological diversity.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCB1_TaxID=1488
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AE010950; AAM05936.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genome Res.
                                                                                                                                                                                                                                                                                                                                              144 LDKRIGFSIGE 154
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                                                                                                                                                                                                                                                                                                                                                                                            1 LSKRIGLSVSE 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 LSKRIGLSVSE
                                                                                                                                                                                                                                                                                                                                                                                                                                          l Similarity
7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          285 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      243 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12:532-542(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                          PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   73.5%;
63.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30797 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28216 MW;
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54.5%;
                                                                                                                       20, Created)
20, Last sequence update)
20, Last annotation updat
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9, Last annotation updat
protein, YitT (B.subtil
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score
                                                                                                                                                                                                                       PRT;
  subdivision;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51A2742392A0CB06 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0A84089E7430ED5C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    36;
                                                                                                                                                                                                                       315 AA
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43;
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     Ralstonia
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RESULT 10
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  01-MAR-2001 (
01-MAR-2001 (
01-MAR-2002 (
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EMBL, AL64668, CAD15834.1; -.
                                                                                    Q9I0X3;
                                                                                                               Q910X3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLRel. 20, Last annotation update)
Putative muconate cyclofsomerase I CatB.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00908; MR_MLE_1; UNKNOWN_1.
PROSITE; PS00909; MR_MLE_2; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF01188; MR_MLE; 1.
Pfam; PF02746; MR_MLE_N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (JAN-2001) to the 
EMBL; AY026914; AAK52296.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              originated from the strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pieper D.H.; "Cloning, is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Totevova S., Armengaud J., Cajthaml T., Demnerova K., Brenner V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-P111;
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Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q93SR2
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                                                                                                                                                                                                                                                  118 KRLGLAVSE 126
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les 7; Conserv
                                                                                                                                                                                                                                                                                                    3 KRIGLSVSE 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        315 AA;
(TrEMBLrel. 16, Created)
(TrEMBLrel. 16, Last sequence update)
(TrEMBLrel. 20, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                            PRELIMINARY;
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72.7%;
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  Last annotation update)
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Pred. No.
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Pred. No. 68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E7E791D73B8CC6F4 CRC64;
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RESULT 11
           RA Kawai J. Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., None H., Baldarelli R., Barsh G.,
RA Schriml L.M., Staubi F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming J.,
RA Haysahi Y., Yoshida R., Hasegawa Y., Kawaji H., Kohtsuki S.,
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                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-C57BL/6J; TISSUE-EMBRYONIC LIVER; MEDLINE-21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryola: Metazoa: Chordata: Craniata; Vertebrata; Euteleostomi;
Mammalia: Eutherlu: Rodentia; Sciurognathi: Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chaperonin subunit 8 (Theta) (Fragment).
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLREL. 21, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90806
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Pfam; PF02746; MR_MLE_N; 1.
PROSITE; PS00908; MR_MLE_1; 1.
PROSITE; PS00909; MR_MLE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathogen.";
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                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCHI_Tax1D=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                118 KRLGLAVSE 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity hes 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 KRIGLSVSE 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15692 / PAO1;
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77.8%;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  949BB0FAB3744E76 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   update)
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Hayashizaki Y.;

Thermococcales; Thermococcaceae;

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Q9WVS5
ID Q9WVS
AC Q9WVS
AC Q9WVS
AC Q9WVS
DT 01-NC
DT 01-NC
DT 01-NC
DT 01-U
DE Chape
GN CCTB
OC EUkar
OC Muss n
OC Mamma
OX NCBLI
RN [1]
RP SEQUI
RC STRAI
RX MEDLI
RX MEDLI
RX MEDLI
RX EMUL
RX EMUL
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RX Intel
DR HSSP;
DR HSSP;
DR HSSP;
DR Intel
DR PFOSS;
DR PROSS;
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DR PROSS;
DR PROSS;
DR PROSS;
DR SEQUI
 RESULT 13
Q8U425
ID Q8U42
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Best Local S
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Best Local
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                                                                                                                                                                                                  InterPro; IPR002194; Chaperonin_TCP-1.
InterPro; IPR002423; Cpn60/TCP-1.
Pfam; PF00118; cpn60 (TCP-1); 1.
PRINTS; PR00304; TCOMPLEXTCP1.
PROSITE; PS00750; TCP1_1; 1.
PROSITE; PS00751; TCP1_3; 1.
PROSITE; PS00955; TCP1_3; 1.
  Q8U425
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9WVS5; PRELIMINARY; PRT; 547 AA.
Q9WVS5;
01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. *12, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Chaperonin containing TCP-1 theta subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00750; TCP1_1; 1.
PROSITE; Px.00751; TCP1_2; 1.
PROSITE; Ps-0995; TCP1_3; 1.
ATP-binding; Chaperone.
NON_TER
458
458
                                                                                                                                                                                                                                                                                                                                       Kubota H., Yokota S., Yanagi H., Yura T.; "Structures and co-regulated expression ocytosolic chaperonin CCT subunits"; Eur. J. Biochem. 262:492-500(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR002194; Chaperonin_TCP-1.
InterPro; IPR001844; Chaprnin_Cpn60.
InterPro; IPR001234; Cpn60_TCP-1.
Pfam; PF00118; cpn60_TCP1; 1.
                                                                                                                                                                             ATP-binding; Chaperone
SEQUENCE 547 AA; 59!
                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=129SV;
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PRINTS; PR00304; TCOMPLEXTCP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AK010882; BAE
HSSP; P48424; 1A6D.
                                                                                                                                                                                                                                                                                                  MGD; MGI:107183; Cct8.
                                                                                                                                                                                                                                                                                                               HSSP; P48424; 1A6D
                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-99269022; PubMed-10336634;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Functional annotation of a full-length mouse cDNA collection."; Nature 409\!:\!685\!-\!690(2001).
                                                                     120 RIGLSVSE 127
                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                             4 RIGLSVSE 11
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                                                                                                                      8; Conserv
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                                                                                                                       Conservative
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  PRELIMINARY;
                                                                                                                                                                            AA;
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                                                                                                                                    73.5%;
                                                                                                                                                                            59568 MW;
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                                                                                                                       0;
                                                                                                                                    Score 36; pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 36;
Pred. No.
    PRT;
                                                                                                                                                                            6BC34987F74B94CE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BB053A0F4DDC217C CRC64;
                                                                                                                         Mismatches
  914 AA
                                                                                                                                   DB 11; Length 547; le+02;
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RESULT 15
Q9AHY8
ID Q9AHY
AC Q9AHY
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
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DE LIP (
GN LRP.
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01-JUN-2002
01-JUN-2002
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   086256;
01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Leucine responsive element (Fragment).
                     Q9AHY8;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                        Albrecht C., Kleiner D.;
Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE ASMC FAMILY OF TRANSCRIPTIONAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-VC1 / DSM 3638 / ATCC 4358? / JCM 8422; Weiss R.B., Dunn D.M., Robb F.T., Brown J.R.; "The complete sequence of the Pyrococcus furiosus Submitted (FEB-2002) to the EMBL/GenBank/DDBJ data EMBL; AE010151; AAL80394.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alanyl-tRNA synthetase
            Lrp (Fragment).
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Archaea; Euryarchaeota;
                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                     DNA-binding; Transcription regulation. NON_TER 51 51
                                                                                                                                                                                                                                                                                               InterPro; IPR000485; ASNC_trans_reg,
PRINTS; PR00033; HTHASNC.
                                                                                                                                                                                                                                                                                                                       EMBL; Y16963; CAA76565.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Klebsiella
                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Klebsiella oxytoca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=2261;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pyrococcus.
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                                                                                                                                               34 LSKRVGLS 41
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2 (TrEMBLrel.
2 (TrEMBLrel.
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                                                                               PRELIMINARY;
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                                                                                                                                                                                                                                                        5857 MW;
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87.5%;
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                                                                                                                                                                                                            Score 35;
Pred. No.
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4; Mismatches
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36; No.

DB 17; 1.8e+02;

Length 914; CRC64;

Indels

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51

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Mismatches

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DB 2; 12;

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Search completed: January 15, 2003, 12:36:03 Job time : 32.5714 secs
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Best Local Similarity 87.5%;
Matches 7; Conservative
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InterPro; IPR000485; ASNC_trans_reg.
Pfam; PF01037; ASNC_trans_reg; 1.
PRIN'S; PR00033; HTHASNC; 1.
PRIN'S; PR00034; HTH_ASNC; 1.
PROSTITE; PS00519; HTH_ASNC; 1.
PROSTITE; PS00519; HTH_ASNC_FAMILY; 1.
DNA-Dinding; Transcription regulation.
NON_TER 72
SEQUENCE 72 AA; 8407 MW; 803932BD88EI
                                                                                                                                                                                                                                                                                                                                                                     MEDITINE-21225535; PubMed=11325940;
Ciche T.A., Bintrim S.B., Horswill A.R., Ensign J.C.;
Ciche T.A., Bintrim S.B., Horswill A.R., Ensign J.C.;
"A Phosphopantetheinyl Transferase Homolog Is Essential for Photorhabdus luminescens To Support Growth and Reproduction of the Entomopathogenic Nematode Heterorhabditis bacteriophora.";
J. Bacteriol. 183:3117-3126(2001).
-1- SIMILARITY: BELONGS TO THE ASNC FAMILY OF TRANSCRIPTIONAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Photorhabdus luminescens (Xenorhabdus luminescens).
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Photorhabdus.
MCBI_TaxID=29488;
[1]
SEQUENCE FROM N.A.
STRAIN=NC19;
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34 LSKRYGLS 41
                                                                                                     1 LSKRIGLS 8
                                                                                                                                                                                                    72 AA; 8407 MW; 803932BD88EDB2DB CRC64;
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Pred. No. 18;
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Listing first 45 summaries
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AAY21800
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Arabidopsis thalia
Arabidopsis thalia
Arabidopsis thalia
Drosophila melanog
Breast and ovarian
Arabidopsis thalia
Arabidopsis thalia
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                                                                                                                      Arabidopsis thalia
Arabidopsis thalia
 RESULT 1
AAG10443
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21	22	21	22	21	22	21	21																			22				22	22	22	22	22
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uman IL-1 re	tamicum r	IL-1Rla	سا	interleuki	435.	S	-	phila mela	Tango-77	extracel	radia	1L-1	IL-1 rece	Tango	IL-1	interle	zilla4	211124	zilla4	zilla4 s	onibac	ORFX prot	Tango	-	Human polypeptide	ibacterium		Intestinal mucin d	യ.	cte	a	∄	ರ	Human polypeptide,

ALIGNMENTS

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(first entry)

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25-FEB-1999 05-MAR-1999 09-MAR-1999 23-MAR-1999 25-MAR-1999 29-MAR-1999 01-APR-1999 06-APR-1999 08-APR-1999 25-FEB-2000; 06-SEP-2000. EP1033405-A2 Arabidopsis thaliana. 2000EP-0301439 99US-0123180 99US-0123548 99US-0126264 99US-0126788 99US-0126785 99US-0127462 99US-0128234 99US-012874 99US-0130077. 99US-0121825

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Pred. No. 2.3e
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5. 2.3e+02;
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990S-015865

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05-MAR-1999;
09-MAR-1999;
23-MAR-1999;
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29-OCT-1999;
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Matches 2; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL101840-ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                              The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                        27-MAR-2001
                                                             AAB58817;
                                                                                                    AAB58817 standard; Protein; 324 AA
                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosu :: SEQ ID NO 35388; 21pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
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11-JUL-2000; 2000US-0614150.
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New human breast and ovarian cancer associated gene sequences and the polypeptides encoded by these genes, useful in the prevention, treatment and diagnosis of cancer, immune disorders, cardiovascular
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; breast cancer; ovarian cancer; cytostatic; immunosuppressive; nootropic; neurpprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antinflammatory; antiulcer; vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic; cardiant; immune disorder;
                                                                                disorders and neurological diseases -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                      2000-611515/58.
Page 958-960; 1299pp; English
                                                                                                                                                                                                                                                                                                                                                                                                   Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99US-0124270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             525
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cerebral anoxia and epilepsy; arthritis and ulcerative colitis; cardiovascular disorders such as myocardial ischaemias; wound healing; neurological diseases such as allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoi polynucleotide and protein sequences are used in the diagnosis of cancer, particularly breast and ovarian cancer. The nucleic acid sequences, proteins, agonists and agonists may also be used in the diagnosis, prevention and treatment of immune disorders e.g. Addison's disease, or antagonist sequences exhibit cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antialergic; hepatotropic; antidiabetic; antiniflammatory; antiulcer; vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic and cardiant activity. The Sequences AAF21614 - AAF22031 represent DNA sequences encoding human proteins AAB58711 - AAB59128. The DNA and protein sequences are sequences AAF22032 - AAF22040 and AAB59129 which are used in the associated with breast and ovarian cancer isolation and characterisation of the DNA and protein sequences of the invention. The breast and ovarian cancer associated DNA, protein, agonist and infectious diseases Included in the invention are

Sequence 324 AA;

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Query Match
Best Local S
Matches 2
AAG05407;
                 AAG05407 standard; Protein;
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                                                                                                             Local Similarity
les 2; Conserv
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                                                                                                                    50.0%;
                   375
                                                                                                         Score 9; DB 21; Pred. No. 2.7e+02; Score 9;
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990S-0123180, 990S-0125180, 990S-0125788, 990S-0125788, 990S-0126784, 990S-0126784, 990S-0126784, 990S-0126784, 990S-013047, 990S-013047, 990S-013049, 990S-013248, 990S-013248, 990S-013248, 990S-013248, 990S-013248, 990S-013248, 990S-013421, 990S-013421, 990S-013421, 990S-013421, 990S-013421, 990S-013421, 990S-013421, 990S-013421, 990S-013421, 990S-013426, 990S-013424, 990S-013426, 990S-013424, 990S-013424, 990S-013424, 990S-013424, 990S-013425, 990S-013425, 990S-013425, 990S-013425, 990S-013445, 990S-013445, 990S-013945,	Arabidopsis thaliana protein fragment SEQ ID NO: 1803. Protein identification; signal transduction pathway; metabolic hybridisation assay; genetic mapping; gene expression control; termination sequence. Arabidopsis thaliana. EP1033405-A2.
	ntrol; promoter;
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RESULT 9
AAGO16
ID AAGO2
XX AAGO
XX AAGO
XX AAGO
XX 17-O
XX Arab
XX Prot
KW Prot
KW hybr
KW hybr
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                                                                                                               17-OCT-2000
                                                                                                                                             AAG05406;
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9908-0157117-
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.o. 2.9e+02;
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14-MAY-
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05-MAR-1999;
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18-JUN-1999;
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99US -0134256
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990S-0139461

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99US-0123548.
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S-0128234.
S-0128714.
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5-0131449.
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-0136021
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-0132485
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30-JUN-1999; 01-JUL-1999; 01-JUL-1999;

99US-0141287. 99US-0141842. 99US-0142154. 99US-0142055. 99US-0142030. 99US-0142030. 99US-0142977.

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RESULT 10
AAY21800
ID AY21
XX
AC AAY21
XX
DE Human
XX
Vacuc
KW Vacuc
KW Vacuc
KW Cance
XX
Homo
XX
10593
XX
PD 03-AU
XX
PF 28-OC
XX
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Best I
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06-007-1999
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16-SEP-1999;
20-SEP-1999;
22-SEP-1999;
23-SEP-1999;
24-SEP-1999;
28-SEP-1999;
29-SEP-1999;
                                                                              Vacuolar ATPase subunit AC45; HAC45; vacuolar ATPase; ion transport;
        28-OCT-1997;
                        03-AUG-1999
                                                                        cancer; immune disorder; human.
                                                                                                  Human
                                        US5932444-A
                                                        Homo sapiens
                                                                                                                  20-SEP-1999
                                                                                                                                   AAY21800;
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                                                                                                vacuolar ATPase subunit AC45 (HAC45).
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Similarity 18.2%;
2; Conservative
                                                                                                                                                   standard;
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99US-0154019
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99US-016185
        97US-0959011.
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                                                                                                                                                   Protein;
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Pred. No. 2.9e+02;
0; Mismatches 9;
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99US-0145088.
99US-014708.

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RESULT 11
AAM93671
ID AAM93
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This represents a human vacuolar ATPase subunit AC45 (HAC45). Vacuolar ATPase provides most of the energy required for ion transport processes within the vacuolar system in eukaryotic cells. The polypeptide can be produced recombinantly by culturing host cells transformed with a vector comprising the HAC45 nucleic acid. Compositions comprising the HAC45 polynucleotide sequences are useful in the treatment of cancers and immune disorders. The sequence complementary to the HAC45-encoding sequence is useful for inhibiting expression of naturally occurring
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Fig 1A-F; 32pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Corley NC, Hillman JL,
The invention relates to primers for synthesising full length CDNA
                         Claim 8; SEQ ID NO 3556; 1380pp + sequence listing; English.
                                                         830 Primers useful for synthesizing full length cDNA clones and their
                                                                                     N-PSDB; AAK94606.
                                                                                                                        Wakamatsu A,
                                                                                                                                                                                                               08-JUL-1999;
                                                                                                                                                                                                                                          07-JUL-2000; 2000EP-0114089.
                                                                                                                                                                                                                                                                                             EP1130094-A2
                                                                                                                                                                                                                                                                                                                                            Human; full length cDNA; cDNA synthesis; oligo-capping.
                                                                                                                                                                                                                                                                                                                                                                   Human polypeptide, SEQ ID NO: 3556.
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                                                use in genetic manipulation
                                                                                                    WPI; 2001-524255/58.
                                                                                                                                                                (HELI-) HELIX RES INST.
                                                                                                                                                                                                                                                                                                                    Homo sapiens
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                                                                                                                                                                                                    11-JAN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 LXXXXXXXXXX 11
                                                                                                                                       Nishikawa T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                470 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                       2000JP-0118774.
2000JP-0183765.
                                                                                                                         Sugiyama T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97US-0959011.
                                                                                                                                                                                                               99JP-0194486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         50.0%;
18.2%;
                                                                                                                                     Isogai T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Shah P;
                                                                                                                         Nagai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 9;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                     Hayashi K,
                                                                                                                           Kojima S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 20;
. 3.2e+02;
                                                                                                                                       Ishii S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 470;
                                                                                                                           Otsuki T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                     Kawai Y;
                                                                                                                           Koga H;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   clones. 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA
                                             The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIFO
                                                                                            insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                               useful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of
                                                                                                                                                                                capable of detecting 1000 or more genes from Drosophila.
                                                                                                                                                                                                                                                                             New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for clucidating cell signalling and cell-cell interactions -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-MAR-2000;
11-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster polypeptide SEQ ID NO 24441.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABB65883;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly from EPO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA casily without any special methods. The prosent sequence is a polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by
                              at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                    The invention relates to an isolated nucleic acid detection reagent
                                                                                                                                                                                                                                     Disclosure; SEQ ID NO 24441; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                             N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                Venter JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                (PEKE ) PE CORP NY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pharmaceutical.
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                                                                                                                                                                                                                                                                           interactions
                                                                                (ABB57737-ABB72072)
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803 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          developmental biology; cell signalling; insecticide;
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18.2%;
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Pred. No.
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Matches 2; Conserv
                                                                2558 LSSSTTTSTTE 2568
ABB68812 standard; Protein; 99 AA.
                                                                                                                                                                           Sequence
                                                                                                                                                                                                     at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                               The sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                           sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                      insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
                                                                                                                                                                                                                                                                                                   cell-cell
                                                                                                                                                                                                                                                                                                             capable of detecting 1000 or more genes from Drosophila. The inventuseful in developmental biology and in elucidating cell signalling
                                                                                                                                                                                                                                                                                                                                        The invention relates to an isolated nucleic acid detection reagent
                                                                                                                                                                                                                                                                                                                                                                  Disclosure; SEQ ID NO 31983; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                           New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Venter JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (PEKE ) PE CORP NY.
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11-JUL-2000; 2000US-0614150
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                                                                                                                                                                                                                    specification,
                                                                                                                                                                                                                                            (ABB57737-ABB72072)
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                                                                                                                                                                                                                                                                                                   interactions in higher eukaryotes for the development of
                                                                                                                                                                             2768 AA;
                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             developmental biology; cell signalling; insecticide
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18.2%;
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Pred. No.
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Pred. No. 4.1e+02;
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                                                                                                                                    DB 22;
7e+02;
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                                                                                                                                                Length 2768,
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RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of
                                                                                                                                                                                            AAB79413 standard; Protein; 104 AA.
                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                            The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; SEQ ID NO 33228; 21pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to an isolated nucleic acid detection reagent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated nucleic acid detection reagent for detecting 1000 or more
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pharmaceutical
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2: Conserv
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                                                                                                                                                                                                                                                                                                                                                  18.28;
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SMP protein; sugar metabolism and oxidative phosphorylation protein; fine chemical production; organic acid; proteinogenic amino acid; nonproteinogenic amino acid; purine base; pyrimidine base; nucleoside;

Corynebacterium glutamicum; carbon metabolism and energy production; Corynebacterium glutamicum SMP protein sequence SEQ ID NO:342. 30-APR-2001

(first entry)

0;

nucleotide; lipid; saturated fatty acid; unsaturated fatty acid; diol; carbohydrate; aromatic compound; vitamin; cofactor; polyketide; enzyme;

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cofactor, a polyketide, or an enzyme. The presence of (I) or SMP proteins (III) encoded by them are used for diagnosing the presence or activity of Corynebacterium diphtheriae in a subject. (I), (II), (III) or host cells containing them are used to map genomes of organisms related to C. glutamicum, identify and localise C. glutamicum sequences of interest, in evolutionary studies, in determining SMP protein regions required for function, in modulating SMP protein activity, in modulating the metabolism of sugars, and in modulating high-energy molecule production in a cell (i.e. ATP, NADPH).
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08-JUL-1999
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08-JUL-1999
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09-JUL-1999
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08-JUL-1999;
08-JUL-1999;
08-JUL-1999;
                                                                                                                               AAF71360 to AAF71750 encode the Corynebacterium glutamicum sugar metabolism and oxidative phosphorylation (SMP) proteins given in AAB79243 to AAB 79633 which are involved in carbon metabolism and energy production. The C. glutamicum SMP gene can be used in vectors (II) for expression in host cells and production or modulation of production of fine chemicals, such as, an organic acid, a proteinogenic or nonproteinogenic amino acid (preferred), a purine or pyrimidine base, a nucleoside, a nucleotide, a lipid, a saturated or unsaturated fatty acid, a diol, a carbohydrate, an aromatic compound, a vitamin, a acid, a diol, a carbohydrate, an aromatic compound, a vitamin, a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                03-SEP-1999;
03-SEP-1999;
03-SEP-1999;
                                                                                                                                                                                                                                                                                                                New isolated Corynebacterium glutamicum nucleic acid encoding a sugar metabolism and oxidative phosphorylation protein for production or modulation of production of fine chemicals e.g. amino acids,
                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-061975/07.
N-PSDB; AAF71530.
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27-AUG-
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03-SEP-1999;
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                                 Score 8;
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                                 DB 22;
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Search completed: January 15, 2003, 11:20:12 Job time: 32.2857 secs

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Sequence:

Run on:

Sequence 7, A Sequence 79, Sequence 20, Sequence 20,

Sequence 20, Appl Sequence 24, Appl Sequence 24, Appl Sequence 24, Appl Sequence 5, Appli Sequence 6, Appli Sequence 6, Appli Sequence 21, Appli Sequence 2, Appli Sequence 4, Appli Sequence 4, Appli Sequence 1, Appli Sequence 2, Appli

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US-08-180-524-10
US-08-180-524-10
US-08-975-166-1
US-08-975-166-9
US-08-975-166-10
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US-09-917-121-39
US-09-144-529-4
US-08-58-0548-18
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US-08-481-130-2
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1 5169933-42

2 Patent NO. 5169933

3 PATENT NO. 5169933

4 APPLICANT: ANDERSON, DAVID C., MORGAN, CHARLES JR., FRITZBERG,

APPLICANT: EVERETT J.

APPLICANT ON THE PROPERTY OF THE
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TITLE OF INVENTION: CAVALENTLY-LINKED COMPLEXES AND METHODS FOR ENHANCED CYTOTOXICITY AND IMAGING NUMBER OF SEQUENCES: 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 1, Application US/08959011
; Patent No. 5932444
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APPLICANT: Hillman, Jennifer L.
  ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ FOR Windows Version
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APPLICANT: Shah, Purvi
APPLICANT: Corley, Nei
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APPLICATION NUMBER: 232,337
FILING DATE: 15-AUG-1988
                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
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CURRENT APPLICATION DATA:
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TITLE OF INVENTION: VACUOLAR ATPASE SUBUNIT AC45
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US-09-562 - 737 - 79
US-08-482 - 847 - 20
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US-09-296 - 715 - 24
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US-08-705 - 8758 - 6
US-09-20 - 731 - 21
US-09-220 - 731 - 21
US-09-220 - 731 - 21
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SEQ ID NO 243
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Best Local Similarity 18.2
Matches 2; Conservative
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                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: VIRULENCE-ASSOCIATED NUCLEIC ACID TITLE OF INVENTION: SEQUENCES AND USES THEREOF FILE REFERENCE: 00786/361002
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                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 437
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                        ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                        TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: U. FILING DATE: Herewith
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Mahajan-Miklos, Shalina
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18.2%;
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18.28;
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Pred. No. 17;
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CURRENT FILING DATE: 1998-08-03
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; Sequence 2, Application US/09128155 ; Patent No. 6117654
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Best Local Similarity
Yeiches 2; Conserva
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US-09-128-155-7
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                                                                               ; GENERAL INFORMATION: ; APPLICANT: Pan, Yan
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                                                                                                                                                                         US-09-128-155-2
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Best Local Similarity 18.2
The hes 2; Conservative
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Patent No. 6117654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 7, Application US/09128155 Patent No. 6117654
                  TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY TITLE OF INVENTION: AND USES THEREOF FILE REFERENCE: 09404/052001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/128,155
CURRENT FILING DATE: 1998-08-03
EARLIER APPLICATION NUMBER: US 60/091,650
EARLIER FILING DATE: 1998-07-02
EARLIER APPLICATION NUMBER: US 60/054,646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY TITLE OF INVENTION: AND USES THEREOF FILE REFERENCE: 09404/052001
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CURRENT FILING DATE: 1998-08-03
EARLIER APPLICATION NUMBER: US 60/091,650
EARLIER FILING DATE: 1998-07-02
CURRENT APPLICATION NUMBER: US/09/128,155
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18.28;
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Pred. No.
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89;
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US-09-293-625-2
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CURRENT FILING DATE: 1999-04-16
NUMBER OF SEQ ID NOS: 2 - *
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/08245295 Patent No. 5700658
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Matches 2; Conservative
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APPLICANT: MCDONNell, Peter C
TITLE OF INVENTION: INVERTLEUKIN-1 HOMOLOGUE, IL-1H4
FILE REFERENCE: GP-70607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EARLIER APPLICATION NUMBER: US 60/091,650
EARLIER FILING DATE: 1998-07-02
EARLIER APPLICATION NUMBER: US 60/054,646
EARLIER FILING DATE: 1997-08-04
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FASTSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 218
TYPE: PRT
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                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 233 South Wacker Drive, Suite 6300
                                                                                                                                                                                                                                                                    APPLICANT: Gallatin, W. Michael APPLICANT: Kilgannon, Patrick D. TITLE OF INVENTION: ICAM-4 Materials and Methods
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                                     CURRENT APPLICATION DATA:
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Local imilarity 18.2%;
les 2; Conservative
APPLICATION NUMBER: US/08/245,295 FILING DATE:
                                                                                                                                                                                             CITY: Chicago
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                                                                                                                                                             COUNTRY:
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Pred. No. 1.1e+0
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Pred. No. 1e+02;
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; MOLECULE TYPE: protein US-08-245-295-2
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Best Local Similarity
Matches 2; Conserv
                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/
APPLICATION NUMBER: US 07/
FILING DATE: 27-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
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                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 27
TELECOMMUNICATION INFORMATION: 312-474-6300
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APPLICATION NUMBER: US 07
FILING DATE: 27-JAN-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Gallatin, v
APPLICANT: Kilgannon,
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TELEFAX: 25-3856
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                                                                                                                                         APPLICATION NUMBER: FILING DATE:
                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                  STREET: 233 Sc
CITY: Chicago
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REGISTRATION NUMBER: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
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                  FILING DATE:
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233 South Wacker Drive, 6300 Sears Tower
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                                                                                                                                                                                                                                                                                                    United States of America
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05-AUC-1993
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                                                                                   US 07/827,689
                               US 07/889,724
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Pred. No. 2.1e+02;
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US-08-481-130-2
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                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/656,984A
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                                 PRIOR APPLICATION DATA:
                                                                                       FILING DATE: 26-MAY-1992 PRIOR APPLICATION DATA:
                                                                                                                                            PRIOR APPLICATION DATA:
                                                                                                                                                                                                    CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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                                                   APPLICATION NUMBER: US 07/894,061 FILING DATE: 05-JUN-1992
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FILING DATE:
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                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                              APPLICATION NUMBER: US 0
FILING DATE: 27-JAN-1992
                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: WILLIAMS, JR. JOSEPH A. REGISTRATION NUMBER: 38,659
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WENTION: ICAM-4 Materials and Methods
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22-JAN-1993
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                 us 08/009,266
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Best Local 9
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                                                               PRIOR APPLICATION DATA:
              FILING DATE: 22-JAN-1993 PRIOR APPLICATION DATA:
                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US 07/827,689
                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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REFERENCE/LOCKET NUMBER: 276
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
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ATTORNEY/AGENT INFORMATION:
NAME: WILLIAMS, JR. JOSEPH A.
REGISTRATION NUMBER: 38,659
                                                                                                                   FILING DATE: 26-MAY-1992 PRIOR APPLICATION DATA:
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APPLICANT: Kilgannon, Patrick D.
TITLE OF INVENTION: ICAM-4 Materials and Methods
NUMBER OF SEQUENCES: 32
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APPLICATION NUMBER:
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APPLICATION NUMBER: US 08/102,852
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                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                              CLASSIFICATION: 435
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les 2; Conservative
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APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                  IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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18.2%;
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                                                                                                                                                       US 07/889,724
US 08/102,852
                                                US 08/009,266
                                                                                                  US 07/894,061
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Pred. No. 2.1e+02;
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; MOLECULE TYPE: protein US-08-485-604-2
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Patent No. 5852170
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                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
PRIOR APPLICATION DAYA:
APPLICATION NUMBER: US 07/827,689
FILING DATE: 27-JAN-1992
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ATTORNEY/AGENT INFORMATION:
NAME: WILLIAMS, JR. JOSEPH A.
REGISTRATION NUMBER: 38,659
   FILING DATE: 18-MAY-1994
ATTORNEY/AGENT INFORMATION:
                                                     PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
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                                                                       FILING DATE: 05-AUG-1993
                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                      APPLICATION NUMBER: US 07 FILING DATE: 26-MAY-1992
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TOPOLOGY: linear
                                      APPLICATION NUMBER:
                                                                                                                              FILING DATE:
                                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/487,595
                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.
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Local Similarity 18.28;
es 2; Conservative
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REFERENCE/DOCKET NUMBER: 27866/32715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            233 South Wacker Drive,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    917 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      United States of America
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Marshall, O'Toole, Gerstein, Murray & Borun
                                                                                                                              22-JAN-1993
                                                                                                                                                                                    NUMBER: US 07/894,061
05-JUN-1992
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                                                                                                                                                US 08/009,266
                                    US 08/245,295
                                                                                          US 08/102,852
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Pred. No.
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, 2.1e+02;
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US-08-180-524-1
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SEQ ID NO 4463
LENGTH: 2137
                                                                                                                                                                                                                                                         Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                         Sequence 1,
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                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR FILING DATE: 1997-08-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
                       APPLICANT: Chicoye, Etzer
APPLICANT: Barney, Michael C.
APPLICANT: Bower, Patricia A.
APPLICANT: Cronan, Charles L.
APPLICANT: Cronan Charles L.
TITLE OF INVENTION: METHOD OF EXPRESING ANTIFREEZE PROTEINS
TITLE OF INVENTION: IN YEAST
                                                                                                                                                                                                                                                                                                                                                               1701 LSDSTSTSTSE 1711
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LENGTH: 917 amino acids
TYPE: amino acid
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CORRESPONDENCE ADDRESS
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                   NUMBER OF SEQUENCES:
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REFERENCE/DOCKET NUMBER: 2786
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l Similarity 18.28;
2; Conservation
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. 3e+02;
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Gaps

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Matches

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Search completed: January 16, 2003, 11:04:51 Job time: 1662.14 secs

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Database :
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                                                                                                                                                                                                                                                                           Score
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SIDSZ/gcgdata/geneseq/geneseqp-embl/AA198.DAT: *
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Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1980
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/SIDS2/gcgdata/gencscq/geneseqp-cmb1/AA2002.DAT:*
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690
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  AAR23169
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AAM48268
AAR23174
AAR23173
                                                                                                                                                                                                                                                                        Description
                                                                                                                    Mutant
Mutant
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Native DNA polymer
Mutant thermostabl
Taf DNA polymerase
Human 5' EST relat
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an melanocorti	AAU08750	22	311		32	U
isseria meningi	AAY38896	20	256	65.3	32	4
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D)	AAY38894	20	182		32	2
steria monocyto	ABB49471	23	119	S.	32	J
lus an	AAE11177	22	119	'n	32	0
ORFX	ABP05858	23	91	5	32	· w
dAlod	AA007530	22	37	5	32	80
acid sec	AAY29106	20	1046	7	ω ω	7
protein seq	AAB93299	22	956	7.	3 3	σ
uman lung spe	AAE20268	23	889	7	ယ	U
S. salivarius 1,6-	AAU79551	23	822	7.	33	4
reptococcus	ABP29511	23	549	7.	33	w
	AAW20621	38	165	7.	ω ω	N
an	AAY07970	20	79	7.	ω ω	-
ori c	AAW20505	18	62	7.	ω ω	0
ORFX prot	ABP06956	23	59	7.	33	9
Human secreted pro	AAY94997	21	779	9	34	000
Arabidopsis thalia	AAG43428	21	532	69.4	34	7
Arabidopsis thalia	AAG23937	21	532	69.4	34	o
<	ABB91449	23	502	69.4	34	Ŋ
_+	AAG43429	21	502	69.4	34	4
opsis thali	AAG23938	21	502	69.4	34	ω
	AAY60505	20	408	69.4	34	2
Arabidopsis thalia	AAG43430	21	382	69.4	34	,4
dopsis	1.4	21	382	69.4	34	0
lising and	AAH23653	23	373	69.4	34	9
n secret	AAY12988	20	79	69.4	34	80
el human diagn	ABG08827	22	1043	71.4	35	7
neumoni	584	19	90	71.4	3 5	9
l human	ABG21966	22	584	ω.	36	ر.
l human d	196	22	555	73.5	36	4
l cancer asso	90	20	548	٠	36	ω
e CCT-theta s	58	13	548	w	36	2
Human cancer assoc	AAB43412	21	258		36	1 4

ALIGNMENTS

AAB47796 standard; peptide; 11

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RESULT 1
AAB47796
ID AAB4
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AC AAB4
XX
DT 25-1
DT 25-1
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EVA
C AB
OT 25-1
IVA
KW CTA
KW CTA
XX
FP DO 7
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PP DO 7
XX
PP 11
XX
PR 11
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                                                                                                                                                                                                                                                                                                                                                                         (HOFF ) HOFFMANN LA ROCHE & CO AG F.
                                                                                                                                                                                                                               n CM, Gelfand DH, Wang AM;
                                                                                                                                                                                                                                                                           Higuchi RG,
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Reverse transcribing an $\mathtt{RNA},$ comprises performing a reverse transcriptase polymerase chain reaction amplification of a mixture

using a mutant thermoactive DNA polymerase

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RESULT 2
AAM48268
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The sequences given in AAB47791-97 and AAM48259-AAM48270 represent the native forms of motifs derived from DNA polymerases used in the method of the invention. The method for reverse transcribing an RNA, comprises treating a transverse transcription reaction mixture which comprises the RNA, a primer, a divalent cation, and a mutant thermoactive DNA polymerase. These motifs represent a conserved region which affects the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          to previous high temperature reverse transcription methods, and provide a wider range of usable salt concentrations. The use of the mutant DNA polymerase provides faster reverse transcription extension rates, and consequently less time is needed for the reaction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The sequences given in AAB47791-97 represent the native forms of motifs derived from NA polymerases used in the method of the invention. The method for reverse transcribing an RNA, comprises treating a transverse transcription reaction mixture which comprises the RNA, a primer, a divalent cation, and a mutant thermoactive DNA polymerase. These motifs represent a conserved region which affects the DNA polymerase's ability to incorporate dideoxynucleotides labelled with fluorescein and cyanine
                                                                                                                                                      Reverse transcribing an RNA, comprises performing a reverse transcriptase polymerase chain reaction amplification of a mixture using a mutant thermoactive DNA polymerase
                                                                                                                                                                                                                                                            Schoenbrunner NJ,
                                                                                                                                                                                                                                                                                                               (HOFF ) HOFFMANN LA ROCHE & CO AG F
                                                                                                                                                                                                                                                                                                                                                18-APR-2000; 2000US-198336P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     dye; amplification
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Native DNA polymerase motif #17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAM48268;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAM48268 standard; Peptide; ll AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             transcription/amplification reactions. The method provides improved reverse transcription efficiency at lower enzyme concentrations relative
                                                                                                                                                                                                                                                                                                                                                                                 12-APR-2001; 2001EP-0109341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          transverse transcription reaction; fluorescein; cyanine; thermoactive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 family dyes. The method of the invention is useful in reverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 LSKRIGLSVSE 11
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                                                                                                                                                                                                                                                                               ES,
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                                                                                                                                                                                                                                                                               Elfstrom CM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11 AA;
                                                                                                                      Page 7; 23pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                            Wang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%;
                                                                                                                                                                                                                                                              AM;
                                                                                                                                                                                                                                                                               Gelfand DH,
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Pred. No. 0.0014;
Mismatches 0
                                                                                                                                                                                                                                                                             Higuchi
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                                                                                                                                                                                                                                                                               RG,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
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RESULT 3

AAR23174
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Best Local
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                                                                                                                                                                                                                                                                                                                                                         28-SEP-1990;
28-SEP-1990;
28-SEP-1990;
activity than the native enzyme. Thermostable DNA polymerases are useful in many recombinant DNA techniques, esp. nucleic acid amplification by PCR, self-sustained sequence replication (SSR) and high temp. DNA sequencing. The absence of 5'-3' nuclease activity may facilitate higher sensitivity allelic discrimination in a combined polymerase ligase chain reaction (PLCR) assay. An enhanced amt.pf 5'-3' exonuclease activity may be desirable in enzymes used in 5'-3' exonuclease activity may be desirable in enzymes used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA polymerase's ability to incorporate dideoxynucleotides labelled in fluorescein and cyanine family dyes. The method of the invention is useful in reverse transcription/amplification reactions. The method provides improved reverse transcription efficiency at lower enzyme concentrations relative to previous high temperature reverse transcription methods, and provide a wider range of usable salt concentrations. The use of the mutant DNA polymerase provides faster reverse transcription extension rates, and consequently less time is
                                                                                                The sequence is that of a mutant of Thermosipho africanus polymerase mutant MET-ILE 284 Taf. having a different amt. of 5'-3' exonuclease activity than the native enzyme. Thermostable DNA polymerases
                                                                                                                                                                                                        Thermostable DNA polymerases with altered 5'-3' exo nuclease activity __having conserved regions mutated or deleted, for u
                                                                                                                                                                 Claim 11; Page 59;
                                                                                                                                                                                                                                                          N-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Thermosipho
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5'-3'; exonuclease; PCR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mutant thermostable DNA polymerase enzyme MET-ILE 285 TAF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22-OCT-1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR23174 standard; Protein;
                                                                                                                                                                                          in e.g. PCR, sequencing and detection assays
                                                                                                                                                                                                                                                                                                    Abramson RD,
                                                                                                                                                                                                                                                                                                                               (CETU ) CETUS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-APR-1992
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                                                                                                                                                                                                                                                                                                   Geliand
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900S-0590490.
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                                                                                                                                                              185pp; English.
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                                                                                                                                                                                                                                                                                                    DH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "residues 2-284 deleted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amplification; SSR; sequencing; PLCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0.0014;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the native
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RESULT 4
AAR23173
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                28-SEP-1990;
28-SEP-1990;
28-SEP-1990;
                                        activity than the native enzyme. Thermostable DNA polymerases are useful in many recombinant DNA techniques, esp. nucleic acid amplification by PCR, self-sustained sequence replication (SSR) and high temp. DNA sequencing. The absence of 5'-3' nuclease activity may facilitate higher sensitivity allelic discrimination in a combined polymerase ligase chain reaction (PLCR) assay. An enhanced amt. of 5'-3' exonuclease activity may be desirable in enzymes used in homogeneous assays for the amplification and detection of a target nucleic acid sequence. Mutation of the DNA encoding particular
                                                                                                                                                                                                                                                                   Thermostable DNA polymerases with altered 5'-3' exo nuclease activity - having conserved regions mutated or deleted, for use in e.g. PCR, sequencing and detection assays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nucleic acid sequence. Mutation of the DNA encoding particular regions of the enzymes can be used to prepare a range of recombinant proteins haring 5'-3' exonuclease activity to a complete lack of
                                                                                                                                                                                       The sequence is that of a mutant of Thermosipho africanus polymerase mutant MET-THR 204 Taf. having a different amt. of 5'-3' exonuclease
                                                                                                                                                                                                                                        Claim 11; Page 59; 185pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Thermosipho africanus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5'-3'; exonuclease; PCR; amplification; SSR; sequencing; PLCR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mutant thermostable DNA polymerase enzyme MET-THR 204 TAF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR23173 standard; Protein; 690 AA
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          proteins having 5'-3'
             regions of the enzymes can be used to prepare a range of recombi proteins having 5'-3' exonuclease activity to a complete lack of
                                                                                                                                                                                                                                                                                                                                                                                     Abramson RD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-APR-1992
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                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAQ24333
                                                                                                                                                                                                                                                                                                                                                                                                                    (CETU ) CETUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-SEP-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     activity.
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                                                                                                                                                                                                                                                                                                                                                       1992-150885/18.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     609 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                90US-0590213.
90US-0590466.
90US-0590490.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "residues 2-203 deleted from the native
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. 0.12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 49;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 13; Length 609;
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                               recombinant
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RESULT 5
AAR23172
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Best Local S
Matches 11
                                                                                                     present in the given sequence at position 140 is an Asp.

Thermostable DNA polymerases are useful in many recombinant DNA techniques, esp. nucleic acid amplification by PCR. self-sustained sequence replication (SSR) and high temp. DNA sequencing. The absence of 5.3 nuclease activity may facilitate higher sensitivity allelic discrimination in a combined polymerase ligase chain reaction (PLCR) assay. An enhanced amt. of 5.3 exonuclease activity may be
                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-SEP-1990;
28-SEP-1990;
                                    desirable in enzymes used in homogeneous assays for the amplification and detection of a target nucleic acid sequence. Mutation of the DNA encoding particular regions of the enzymes can be used to prepare a range of recombinant proteins having 5'-3' exonuclease activity to a complete lack of activity.
                                                                                                                                                                                                 The sequence is that of a mutant of Thermosipho africanus polymerase mutant designated MET-GLU 140 Taf. having a different amt. of 5'-3' exonuclease activity than the native enzyme. However the residue
                                                                                                                                                                                                                                                          Claim 11; Page 59; 185pp; English.
                                                                                                                                                                                                                                                                                                 Thermostable DNA polymerases with altered 5: 3' exo nuclease activity - having conserved regions nutated or deleted, for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR23172 standard; Protein; 754 AA
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                                                                                                                                                                                                                                                                                  in e.g. PCR, sequencing and detection assays
                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAQ24332.
                                                                                                                                                                                                                                                                                                                                                           WPI; 1992-150885/18.
                                                                                                                                                                                                                                                                                                                                                                                     Abramson RD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-SEP-1991;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mutant thermostable DNA polymerase enzyme MET-GLU 140 TAF.
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                        See also
                                                                                                                                                                                                                                                                                                                                                                                                            (CETU ) CETUS
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                       AAR23140-79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        690 AA;
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                                                                                                                                                                                                                                                                                                                                                                                     Gelfand
                                                                                                                                                                                                                                                                                                                                                                                                               CORP.
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90US-0590466.
90US-0590490.
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                        and
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                        AAR23722
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Pred. No. 0.13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              from the native
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                                                                                                                                                                                                                                                                                                    use
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-SEP-1990;
28-SEP-1990;
28-SEP-1990;
                                                                                                                      amplification by PCR, self-sustained sequence replication (SSR) and high temp. DNA sequencing. The absence of 5'-3' nuclease activity may facilitate higher sensitivity allelic discrimination in a combined polymerase ligase chain reaction (PLCR) assay. An enhanced ant. of 5'-3' exonuclease activity may be desirable in enzymes used in homogeneous assays for the amplification and detection of a target nucleic acid sequence. Mutation of the DNA encoding particular regions of the enzymes can be used to prepare a range of recombinant proteins having 5'-3' exonuclease activity to a complete lack of
                                                                                                                                                                                                                                                mutant MET-TYR 94 Taf. having a different amt. of 5'-3' exonuclea activity than the native enzyme. Thermostable DNA polymerases are useful in many recombinant DNA techniques, esp. nucleic acid
                                                                     Sequence
                                                                                                                                                                                                                                                                             The sequence is that of a mutant of Thermosipho africanus polymorase mutant MET-TYR 94 Taf. having a different amt. of 5'.3' exonuclease
                                                                                                                                                                                                                                                                                                                   Claim 11; Page 59; 185pp; English.
                                                                                                                                                                                                                                                                                                                                             Thermostable DNA polymerases with altered 5'-3' exo nucl activity - having conserved regions mutated or deleted, in e.g. PCR, sequencing and detection assays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Thermosipho africanus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5'-3'; exonuclease; PCR; amplification; SSR; sequencing; PLCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mutant thermostable DNA polymerase enzyme MET-TYR 94 TAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-OCT-1992 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR23171;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR23171 standard; Protein; 800
                                                                                              See also AAR23140-79 and AAR23722.
                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Abramson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (CETU ) CETUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-SEP-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-APR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                W09206200-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Misc-difference 1..2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  on.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 LSKRIGLSVSE 11
                                                                                                                                                                                                                                                                                                                                                                                                                     1992-150885/18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LSKRIGLSVSE 612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                l Similarity
11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                       AAQ24331.
                                                                                                                                                                                                                                                                                                                                                                                                                                               RD,
              100.0%;
ilarity 100.0%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; ilarity 100.0%; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                               Gelfand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90US-0590213.
90US-0590466.
90US-0590490.
                                                                     AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           91WO-US07035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "residues 2-93 deleted from the native
                                                                                                                                                                                                                                                                                                                                                                                                                                               DH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                           Score 49; DB 1
Pred. No. 0.16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 49; DB 1:
Pred. No. 0.15;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA
                                          DB 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 13; Length 754;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                        Length 800;
                                                                                                                                                                                                                                                                                                                                                                            exo nuclease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                               for use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
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0;

Mismatches

0;

Indels

0;

Gaps

0

В Qγ

704 LSKRIGLSVSE 714

1 LSKRIGLSVSE 11

Query Match Best Local : Matches

Similarity

100.0%; Score 49; DB 1 100.0%; Pred. No. 0.17; tive 0; Mismatches

DB 13; Length 856; 0

0;

Gaps

0;

Conservative

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RESULT 7
AAR23170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           B
 28-SEP-1990;
28-SEP-1990;
28-SEP-1990;
                                        activity than the native enzyme. Thermostable DNA polymerases are useful in many recombinant DNA techniques, esp. nucleic acid amplification by PCK, self-sustained sequence replication (SSK) and high temp. DNA sequencing. The absence of 5'-3' nuclease activity may facilitate higher sensitivity allelic discrimination in a combined polymerase liquse chain reaction (PLR) assay. An enhanced amt. of 5'-3' exonuclease activity may be desirable in enzymes used in homogeneous assays for the amplification and detection of a target nucleic acid sequence. Mutation of the DNA encoding particular regions of the enzymes can be used to prepare a range of recombinant proteins having 5'-3' exonuclease activity to a complete lack of activity.
                                                                                                                                                                                                           The sequence is that of a mutant of Thermosipho africanus polymerase mutant MET-LEU 38 Tail, having a different amt, of 5'-3' exonuclease activity than the native enzyme. Thermostable DNA polymerases
                                                                                                                                                                                                                                                                                                          Thermostable DNA polymerases with altered 5'-3' exo nuclease activity - having conserved regions mutated or deleted, for use in e.g. PCR, sequencing and detection assays
                                                                                                                                                                                                                                                                                                                                                                                         WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR23170 standard; Protein; 856 AA
Sequence
                                                                                                                                                                                                                                                                            Claim 11; Page 59; 185pp; English.
                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAQ24330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-SEP-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers Misc-difference 1..2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Thermosipho africanus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5'-3'; exonuclease; PCR; amplification; SSR; sequencing; PLCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mutant thermostable DNA polymerase enzyme MET-LEU 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-OCT-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR23170;
                                                                                                                                                                                                                                                                                                                                                                                                                       Abramson RD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-APR-1992.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             W09206200-A
                             See also AAR23140-79 and AAR23722.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    (CETU ) CETUS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         648 LSKRIGLSVSE 658
                                                                                                                                                                                                                                                                                                                                                                                        1992-150885/18.
856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                     Gelfand
ΑA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 900S-0590466
900S-0590490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               91WO-US07035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                90US-0590213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "residues 2-27 deleted from the native sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                       DH;
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RESULT 8
AAR23169
ID AAR2
XX AAR2
XX AAR2
XX Muta
XX S(-)
DE HKW S(-)
DE HKW S(-)
FF HKW S
RESULT 9
AAR23122
ID AAR2
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                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                              Matches
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28-SEP-1990;
28-SEP-1990;
AAR23122 standard; Protein; 892 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nucleic acid sequence. Mutation of the DNA encoding particular regions of the enzymes can be used to prepare a range of recombinations having 5'-3' exonuclease activity to a complete lack of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           polymerase ligase chain reaction (PLCR) assay. An enhanced amt. of 5'-3' exonuclease activity may be desirable in enzymes used in homogeneous assays for the amplification and detection of a target
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The sequence is that of a mutant of Thermosipho africanus polymerase nutant ASP37 Taf, having a different amt. of 5'-3' exonuclease activity than the native enzyme. Thermostable DNA polymerases are useful in many recombinant DNA techniques, esp. nucleic acid amplification by PCR, self-sustained sequence replication (SSR) and high temp. DNA sequencing. The absence of 5'-3' nuclease activity may facilitate higher sensitivity allelic discrimination in a combined
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Thermostable DNA polymerases with altered 5'-3' exo nuc. activity - having conserved regions mutated or deleted, in e.g. PCR, sequencing and detection assays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5'-3'; exonuclease; PCR; amplification; SSR; sequencing; PLCR.
                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                  See also AAR23140-79 and AAR23722.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 11; Page 59; 185pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Abramson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (CETU ) CETUS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-SEP-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-APR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Thermosipho atricanus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mutant thermostable DNA polymerase enzyme ASP37 Taf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-OCT-1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      W09206200-A
                                                                                                                                              740 LSKRIGLSVSE 750
                                                                                                                                                                                                     1 LSKRIGLSVSE 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1992-150885/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RD,
                                                                                                                                                                                                                                                                                                                                                                               892 AA;
                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gelfand.DH/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                90US-0590213.
90US-0590466.
90US-0590490.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "Gly in native sequence"
                                                                                                                                                                                                                                                                                       100.0%;
                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                       Score 49; DB 1:
Pred. No. 0.18;
                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                  DB 13;
                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     An enhanced amt. of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    exo nuclease
                                                                                                                                                                                                                                                                                                                  Length 892;
                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           for use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       recombinant
                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                AAY65382
                                                                                                                                                                                                                              RESULT 10
                                                                                                                                                                                                                                                                                                                       Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                              The thermostable polymerase from Thermosipho africanus (Taf) has DNA polymerase activity, reverse transcriptase activity, and opt. 5'-3' and/or 3'-5' exonuclease activity. The Taf enzyme does not become irreversibly denatured for relatively short exposures to temperatures of 90-100 deg.C. The Taf enzyme has an optimum temperature above 45 deg.C and exhibits activity over a broad temperature range of 37-90 deg.C. The Taf polymerase is suitable for use in PCR and in other techniques such as DNA sequencing, nick-translation and reverse transcription.
                                                           Human; 5' EST; expressed sequence tag; secreted protein; diagnosis; gene therapy; chromosome mapping; upstream regulatory sequence; forensi; location; development; protein synthesis; stability;
                                                                                                              Human 5' EST related polypeptide SEQ ID NO:1543.
                                                                                                                                             01-FEB-2000 (first entry)
                                                                                                                                                                                                AAY65382 standard; Protein; 128 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 7; Page 68; 80pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Abramson RD, Gelfand DH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Thermostability; PCR; polymerase chain reaction; reverse transcription; exonuclease; proofreading
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Taf DNA polymerase I.
                        Homo sapiens
                                                                                                                                                                          AAY65382
                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                       See also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Thermostable DNA polymerase from Thermosipho africanus - propd.
by purificn, from cells or by expression of Taf polymerase gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAQ23917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (CETU ) CETUS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-SEP-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-SEP-1991;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  W09206202-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-OCT-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR23122;
                                                   regulation; identification.
                                                                                                                                                                                                                                                                    740 LSKRIGLSVSE 750
                                                                                                                                                                                                                                                                                              1 LSKRIGLSVSE 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1992-150887/18.
                                                                                       5' EST;
                                                                                                                                                                                                                                                                                                                                                                                                     AAQ23918-Q23961.
                                                                                                                                                                                                                                                                                                                                                                             892 AA;
                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90US-0590490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               91WO-US07076
                                                                                                                                                                                                                                                                                                                                    100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   exonuclease; proofreading.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Greenfield L,
                                                                                                                                                                                                                                                                                                                         0
                                                                                                                                                                                                                                                                                                                                   Score 49; DB 1
Pred. No. 0.18;
                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                 DB 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lawyer FC,
                                                                                                                                                                                                                                                                                                                         0,
                                                                                                                                                                                                                                                                                                                                               Length 892;
                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Reichert FL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene
                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                       Gaps
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W09953051-A2

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RESULT 11
AAB43412
ID AAB43
XX AAB43
AC AAB43
AC AAB43
AC AAB43
XX O8-FE
XX Uman
DE Human
DE Human
XX Human
KW Jingan
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                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                immune disorder; haematopoietic cell disorder; autoimmune disorder; allergic reaction; graft versus host disease; organ rejection;
                                                                                               Human; cancer associated gene; cancer antigen; detection; cancer; diagnosis; cytostatic; proliferative; vulnerary; immunomodulator; antidiabetic; antiasthmatic; antiheumatic; antiartritic; antiviral; antiinflammatory; antithyroid; antiallergic; antibacterial; cardiant; antiinflammatory; antithyroid; antiallergic; antibacterial; cardiant; cardiant; neuroprotective; thrombolytic; coagulant; neuroprotective;
                                                                                                                                                                                                      Human cancer associated protein sequence SEQ ID NO:857.
                                                                                                                                                                                                                                            08-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    used for directing extracellular secretion of a polypeptide or the insertion of a polypeptide into a membrane, or importing a polypeptide into a cell. The proteins encoded by the EST sequences may be useful in treating a variety of human conditions. Secreted proteins have
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     diagnostic procedures to identify individuals having genetic diseases resulting from abnormal gene expression. The products may also be used gene therapy protocols. The nucleic acids encoding signal peptides can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        chromosome mapping, and to obtain full length cDNA clones. The ESTs can also be used in forensic procedures to identify individuals, or in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequences, corresponding to human secreted proteins. AAY6451 AAX6458 to AAX6438 represent the EST-related proteins corresponding to AAX4225 to AAX43052. The 5' ESTs can be used for producing secreted human gene products. They can be used to identify and isolate 5' untranslated products. They can be used to identify and isolate 5' untranslated regions (UTRs) and upstream regulatory regions which control the location, development stage, rate, and quantity of protein synthesis, as well as stability of mRNA. The ESTs are also useful as probes for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-APR-1998;
28-APR-1998;
                  neurological disease; drug screening
                                                                                   vasotropic; antipsoriatic; antiangiogenic;
                                                                                                                                                                                                                                                                                                            AAB43412 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     therapeutic value, and the identification of new secreted proteins is valuable. AAZ42249 to AAZ42264 and AAY64644 to AAY64650 represent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 3; Page 815; 837pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               diagnostic, forensic, gene therapy,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel secreted protein 5' expressed sequence tag sequences used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dumas Milne Edwards J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-OCT-1999.
                                    haemostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (GEST ) GENSET
                                                                                                                                                                                                                                                                                                                                                                                                120 RIGLSVSE 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                 4 RIGLSVSE 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000-038446/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   æ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .o AAZ43075 represent novel 5' expressed sequence tag (EST)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      128 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                          (first entry)
                                  thrombolytic; cardiovascular disorder; infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98US-0057719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98US-0069047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99WO-IB00712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  73.5%; Score 36; 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Duclert A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Giordano J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and chromosome mapping procedures
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 21; Length 128; 11;
                                                                                 gene therapy; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Db
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       XX
                                                                                                                                                                                                                                                                                           RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                   3000
03-AUG-1995.
                                                                 Mus musculus
                                                                                                   murine; denaturation; renaturation.
                                                                                                            Chaperonin containing TCP-1; CCT; subunit; protein folding complex;
                                                                                                                                                Mouse CCT-theta subunit sequence, deduced from clone pTthetal.
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antidiabetic; antiasthmatic; antirheumatic; antiarthritic; antiviral; antinflammatory; antithyroid; antiallergic; antibacterial; antiviral; dermatological; neuroprotective; cardiant; thrombolytic; coagulant; nootropic; vasotropic; antipsoriatic and antianglogenic. The polynucleotides and polypeptides can be used for preventing, treating cameliorating medical conditions and diagnosing pathological conditions.
                                                                                                                         inflammation, cancers, cardiovascular disorders, neurological disease and bacterial or viral infections. The peptides, nucleotides, antibodies, agonists and antagonists may be also be used in drug screens. AAC78449 to AAC78457 and AAB44240 represent sequences used in the exemplification of
Sequence
                                                                                                                                                                                                                                                                                                                                                              immune cells, to treat disorders of haematopoietic cells, autoimmune disorders, allergic reactions, graft versus host disease and organ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Polynucleotides, polypeptides, antibodies, agonists and antagonists from the present invention may be used to treat immune disorders by activating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                       the present invention.
                                                                                                                                                                                                                                                                                                                   rejection, modulate haemostatic or thrombolytic activity, modulate
                                                                                                                                                                                                                                                                                                                                                                                                                                                      or inhibiting the proliferation, differentiation or mobilisation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            include: cytostatic; proliferative; vulnerary; immunomodulator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             in AAB43398 to AAB44239. The proteins can have activities based on the tissues and cells the genes are expressed in. Example of activities
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAC77607 to AAC78448 encode the human cancer associated proteins given
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 11; Page 1411-1412; 2352pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel isolated nucleic acids comprising sequences encoding poptides useful for treating or diagnosing e.g. cancer - \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAC77621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                08-MAR-2000; 2000WO-US05882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-SEP-2000.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000-587533/55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ruben SM
258 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99US-0124270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          treating or
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Query Match
148 RIGLSVSE 155
                                            hos 8; Conser
                      4 RIGLSVSE 11
                                              Conservative
                                                         100.0%;
                                                        73.5%; Score 36; 100.0%; Pred. No.
                                            0; Mismatches
                                                        DB 21; Length 258; 23;
                                            indels
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17-JUL-1996 (first entry)
                                                 AAR79585;
                                                                                     AAR79585 standard; Protein; 548 AA
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RESULT 13
AAY07062
ID AAY07
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                                                                                                                                                                                                                                                                                                                                                                                     Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 XX PF
                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
  22-JUN-1998;
17-JUL-1997;
10-OCT-1997;
10-OCT-1997;
                                                                                                                                                                                Cancer associated antigen; diagnosis; research; treatment; human; breast cancer; colon cancer; gastric cancer; renal cancer; lung c
                                                                                                                                                                                                                                                02-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  kidney cDNA library during a screen for ion transport channel genes. TCP-1 and the proteins encoded by the cDNA clones are individual subunits of a heteromeric chaperonin which has been designated "chaperonin, containing TCP-1" (CCT). The chaperonin acts a protein folding complex. The present sequence is that of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 human pr bes recovered by PCR of human HT1080 cell line cDNA using degenerate primers from a conserved region of TCP-1 and TF55. Clone pCBL80 was isolated during a mouse testis CDNA sequencing project and clone pTgamma7 was recovered by hybridisation with a mouse cDNA PCR product which was made with primers derived from the sequence of a TCP-1 related gene fragment recovered accidentally from a human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mouse cDNAs encoding novel TCP-1-related proteins were isolated using a combination of methods. Clones prdelta2 and pTzetal2 were isolated by cross-hybridisation with C-elegans cDNA probes recovered from a 5'-expressed sequence tag collection. The clones pTbeta2, pTepsilon5 and pTthetal were isolated by cross-hybridisation with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09-SEP-1994;
31-JAN-1994;
                                                                                                                  WO9904265-A2
                                                                                                                                         Homo sapiens
                                                                                                                                                                     prostate cancer.
                                                                                                                                                                                                                    Renal cancer associated antigen precursor sequence
                                                                                                                                                                                                                                                                         AAY07062;
                                                                                                                                                                                                                                                                                              AAY07062 standard; Protein; 548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 19; Fig 4; 94pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Folding protein complex sub-unit(s) - with ability to form complex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ashworth A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31-JAN-1995;
                                                                 15-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              in vitro,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (CANC-) INST
                                                                                                                                                                                                                                                                                                                                                             120 RIGLSVSE 127
                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
les 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                     4 RIGLSVSE 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1995-275439/36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              useful in facilitating folding of proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 548
                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CANCER RES ROYAL CANCER HOSPITAL.
                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kubota H,
  98US-0102322.
97US-0896164.
97US-0061599.
97US-0061765.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA;
                                                                                                                                                                              colon cancer; gastric cancer; renal cancer; lung cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94GB-0018234.
94GB-0001791.
                                                                 98WO-US14679
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                                                                                                                                                                                                                                                                                                                                                                                                                          73.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                            Score 36; 
; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                          DB 16;
53;
                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 548;
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N-PSDB; AAS86151
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## ABG21964
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AC ABG2
DY 18-1
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NOVE
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NOVE
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NOVE
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HUMB
KW FOOD
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OS HOME
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PM WO20
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PD 11--
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PF 30-B
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PF 30-B
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PF 23-F
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PR 31-D
R N-PP
XX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          binds to the NAM, an expression product or a fragment of an expression product complexed with an HLA molecule; and (b) determining the interaction between the agent and the NAM or the expression product as a determination of the disorder. The products and methods can be used in the diagnosis, monitoring, research, or treatment of conditions characterised by the expression of various cancer associated antigens. The invention provides nucleic acid sequences and encoded polypeptides which are cancer associated antigen precursors expressed in human breast cancer, renal cancer, colon cancer, gastric cancer, prostate cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a method for diagnosing a disorder characterised by expression of a human cancer associated antigen precursor coded for by a nucleic acid molecule (NAM). The method comprises: (a) contacting a biological sample isolated from a subject with an agent that specifically binds to the NAM, an expression product or a fragment of an expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated cancer associated nucleic acids and polypeptides - isolated using sera from cancer patients, used to develop products for the diagnosis, monitoring or treatment of cancers
                                                        Drmanac RT, Liu C,
                                                                                                                                        31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
                                                                                                                                                                                                                                                                                                                                                                                                                   Novel human diagnostic protein #21955.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           18-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABG21964 standard; Protein; 555 AA
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                    WPI; 2001-639362/73
                                                                                                                                                                                                  30-MAR-2001; 2001WO-US08631
                                                                                                                                                                                                                                          11-OCT-2001
                                                                                                                                                                                                                                                                                  WO200175067-A2
                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                             food supplement;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABG21964;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (LUDW-) LUDWIG INST CANCER RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10-OCT-1997;
11-OCT-1997;
                                                                                                  (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    lung cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
ses 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 RIGLSVSE 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RIGLSVSH 127
                                                                                                                                                                                                                                                                                                                                                         chromosome mapping; gene mapplement; medical imaging;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA;
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97GB-0021697.
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Sahin
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100.0%; Prr
                                                        Tang YT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              O'Hare M, O
Scanlan MJ,
                                                                                                                                                                                                                                                                                                                                                         gene mapping; gene therapy; forension
maging; diagnostic; genetic disorder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 36;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB
53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20;
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                                                                                                                                                                                                                                                                                                                                                                              forensic;
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RESULT 15
ABG21966
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity
New isolated polynucleotide and encoded polypeptides, useful in
                                    N-PSDB; AAS86153
                                                                                        Drmanac RT, Liu C,
                                                                                                                                                               31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
                                                                                                                                                                                                                                                                                                                                                                Human; chromosome mapping; gene mapping; gene therapy; torensic; food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           18-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABG21966 standard; Protein; 584 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The
                                                                                                                              (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                      30-MAR-2001; 2001WO-US08631.
                                                                                                                                                                                                                                                           11-OCT-2001.
                                                                                                                                                                                                                                                                                             WO200175067-A2
                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                        Novel human diagnostic protein #21957.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 20; SEQ ID No 52323; 103pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          polynucleotides are also used in diagnostics as expressed sequence tags
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              127 RIGLSVSE 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 RIGLSVSE 11
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                                                       2001-639362/73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
8; Conserv
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                                                                                        Tang YT;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 22; Length 555; 54;
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                                                                                                                                                                                                                                                                                                                          polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics. forensics, gene mapping. identification of mutations
                                                                                                                                       diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention. Note: The sequence data for this pattent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 20; SEQ ID No 52325; 103pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity -
     Local Similarity
hes 8; Conserv
                                                                                                 584 AA;
     Conservative
                         73.5%;
  0;
                         Score 36; DB 22;
Pred. No. 57;
  Mismatches
  0
                                              Length 584;
  Indels
0;
Gaps
0;
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Search completed: January 15, 2003, 11:20:21 Job time: 32.2857 secs

DЬ γQ

108 RIGLSVSE 115

4 RIGLSVSE 11

Sequence Sequence Sequence Sequence Sequence Sequence

4 Appli
5073 Appl
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29, Appl 27, Appl 29, Appl 27, Appl 27, Appl 29, Appl

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Title:
Perfect score:
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Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Scoring table:
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              2005443
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
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/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/Dackfiles1.pep:*
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     US-07-977-434-12
US-08-458-8195-12
POT-US91-07035-12
US-08-687-590-31
US-08-96-875-13
US-09-199-637A-13
US-09-199-637A-13
US-08-706-281A-16
US-09-797-231-16
US-08-706-711-8
US-08-706-711-8
US-08-70-511-8
US-08-70-511-8
US-08-70-511-9
US-08-70-9
US-09-134-001C-3866
US-08-564-972-8
US-09-516-914-7
US-08-148-058A-29
US-08-148-058A-29
US-08-478-042-27
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(without alignments)
34.855 Million cell updates/sec
Sequence 12, Appl Sequence 12, Appl Sequence 12, Appl Sequence 13, Appl Sequence 13, Appl Sequence 14, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 17, Appl Sequence 27, Appl Sequence 32, Appl Sequence 32, Appl Sequence 32, Appl Sequence 30, Appl Sequence 31, Appl Sequence 32, Appl Sequence 37, Appl Sequence 37,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Description
                                                                                                                                                                                            Patent No
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US-07-977-434-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US
APPLICATION NUMBER: US
FILING DATE: 28 SEP-19
PRIOR APPLICATION NUMBER: US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 8: FILING DATE: 22-AUG-1986 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 7: TITTED AMERICATION NUMBER: US 8: AMERICATION NUMBER: US 8: AMERICATION NUMBER: US 8: AMERICATION NUMBER: US 8: AMERICATION NUMBER: US 7: AMERICATION NUMBE
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Gelfand, David H.
APPLICANT: Abramson, Richard D.
TITLE OF INVENTION: 5' TO 3' EXONUCLEASE MUTATIONS
TITLE OF INVENTION: THERMOSTABLE DNA POLYMERASES
                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: 17-JUN-
FILING DATE: 17-JUN-
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 12-JAN-
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APPLICATION NUMBER: US 5:
FILING DATE: 15-MAY-1990
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PRIOR APPLICATION DATA:
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FILING DATE: 15-AUG-1991 PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: Macintosh
OPERATING SYSTEM: 7
SOFTWARE: WordPerfect 2.1
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STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
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o. 5466591
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07110-1199
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                                                           US 746,121
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                                                                                                                                                                                                                                                                                                                                                                              US 523,394
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                                                                                                                                    US 899,241
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US-08-645-215-27

US-08-645-215-29

US-08-646-604-29

US-08-466-604-29

US-08-37-716-4

US-09-134-001C-5073

US-09-134-001C-5073

US-09-186-27-376-13

US-09-186-27-376-2

US-09-186-27-37-16-2

US-09-186-27-39-56

US-09-186-27-39-56

US-09-186-1988-56

US-09-186-1988-56

US-09-186-1988-56

US-09-186-1988-56

US-09-171-969-9

US-09-250-131-2
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US-08-216-971-2
US-08-812-979-2
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Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 11; Conservative
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APPLICANT: Gelfand, David H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 12:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: Ca:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 814-2972
                                                                                              PRIOR APPLICATION DATA:
                                                                                                                                                                                    CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                      SOFTWARE: WordPerfect 2.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Gelfand, David H.
APPLICANT: Abramson, Richard D.
TITLE OF INVENTION: 5' TO 3' EXONUCLEASE MUTATIONS OF
TITLE OF INVENTION: THERMOSTABLE DNA POLYMERASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
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LENGTH: 892 amino acid
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                                             PRIOR APPLICATION DATA:
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                                                             APPLICATION NUMBER: US 590,466 FILING DATE: 28-SEP-1990
                                                                                                               APPLICATION NUMBER: US 59 FILING DATE: 28-SEP-1990
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                                                                                                                                                                                                                                                                                                                                                                                                                  340 Kingsland Street
                                                                                                                                                                                                                                                                                                                                                                                                                                 Hoffmann-La Roche Inc.
   UMBER: US 590,213
28-SEP-1990
                                                                                                                                                   23-FEB-1993
                                                                                                                                                                                                                       02-JUN-1995
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24-JUL-1990
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                                                                                                                                                                  07/977,434
                                                                                                                                 US 590,490
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Pred. No. 0.022;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.0%; Score 49; DB 1; Best Local Similarity 100.0%; Pred. No. 0.022;
                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
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                                                                                                                                                                                        APPLICANT: Gelfand, David H.
APPLICANT: Abramson, Richard D.
TITLE OF INVENTION: 5'TO 3' EXONUCLEASE MUTATIONS OF
TITLE OF INVENTION: THERMOSTABLE DNA POLYMERASES
NUMBER OF SEQUENCES: 38
                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
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APPLICATION NUMBER: 1
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                                                                              STATE: CL. 94608
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APPLICATION NUMBER: US 523,394
                                                                                                                                                                                                                                                                                                                                                                                         740 LSKRIGLSVSE 750
COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOPTWARE: WordPerfect 5.0
                                                                                                                               CITY:
                                                                                                                                              STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: WO PCT/US90/07641
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                                                                                                                           r: 1400 Fifty-third Street
Emeryville
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                                                                                                       California
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                                                                                                                                                              Cetus Corporation
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02-NOV-1990
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740 LSKRIGLSVSE 750

US-07-977-434-12

TOPOLOGY: TYPE:

amino acid

FILING DATE:

APPLICATION NUMBER:

FILING DATE: APPLICATION NUMBER:

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FILING DATE:

APPLICATION NUMBER:

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APPLICATION NUMBER:

US-08-458-819-12

Patent No.

NUMBER OF SEQUENCES:

0;

ADDRESSEE:

STATE:

:: New Jersey 07110-1199 Nutley

SOFTWARE: COMPUTER: Macinto OPERATING SYSTEM:

Macintosh

FILING DATE: APPLICATION NUMBER:

FILING DATE: APPLICATION NUMBER:

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APPLICATION NUMBER:

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RESULT 4
US-08-687-590-31
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                             Sequence 31, Application US/08687590 Patent No. 6255070 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 892 amino acid
APPLICANT: Willison, Keith Robert APPLICANT: Kubota, Hiroshi
                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
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ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: PC
                                                                                                                                            740 LSKRIGLSVSE 750
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                                                                                                                                                                          1 LSKRIGLSVSE 11
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                                                                                                                                                                                                                                                                                                                    AMINO ACID
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                                                                                                                                                                                                                                                                                                                                      892 amino acids
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                                                                                                                                                                                                                         100.0%; Score 49; DB 5; 100.0%; Pred. No. 0.022;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               us 557,517
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                                                                                                                                                                                                                                                                                                                                                                                                                  Case No.
                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                        DB 5; Length 892;
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; MOLECULE TYPE: US-08-687-590-31
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US-08-905-223-272
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                                                                                                                                                                                                                                                                                                                                                                         Sequence 272, Application US/08905223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION: Edward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
SUPTIMARE. FOR CURRENT APPLICATION DATA:
CURRENT APPLICATION NUMBER: US/08/905,223
                                                                                                                                                                                                                                                   APPLICANT: Lacroix, Bruno
TITLE OF INVENTION: 5' ESTS FOR SECRETED PROTEINS
NUMBER OF SEQUENCES: 503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9401791.0
FILING DATE: 31-JAN-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: United States of America COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                     APPLICANT: Duelert,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              120 RIGLSVSH 127
                                         SOFTWARE:
                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: Win95
                                                                                                                              COUNTRY: USA
ZIP: 92101-3505
                                                                                                                                                                  CITY: San Diego
STATE: Californ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
les 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: FILING DATE: 31-JUI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 RIGLSVSE 11
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                                                                                                                                                                  California
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                                                                                                                                                                                           501 West Broadway
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                                                                                                                                                                                                                                                                                                                       Edwards,
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                                                                                                                                                                                                                  Knobbe, Martens, Olson & Bear
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                                                                                             Floppy Disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Floppy disk
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N: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             73.5%; Score 36; DB 4; 100.0%; Pred. No. 8.6;
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                                                                                                                                                                                                                                                                                                                     Jean-Baptiste D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GB 9418234.2
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US-09-199-637A-13
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US-09-586-875-1
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              Sequence 13, Application US/09199637A
Patent No. 6355411
                                                                                                                                                                                                                Query Match 69.4%;
Best Local Similarity 77.8%;
Matches 7; Conservative
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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APPLICANT: G. dman, Adrian
APPLICANT: Helin, Sari
TITLE OF INVENTION: STABILIZING AND DESTABILIZING PROTEINS
FILE REFERENCE: 08036-018002
CURRENT APPLICATION NUMBER: US/09/586,875
CURRENT FILING DATE: 2000-06-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 08/971,004
PRIOR FILING DATE: 1997-11-14
PRIOR APPLICATION NUMBER: 60/030,926
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NUMBER OF SEQ ID NOS: 2
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
TELEPAX: (619) 235-0176
TELEPAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 272:
                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                        ENGTH: 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: PROTEIN ORIGINAL SOURCE: ORGANISM: Homo Sapiens
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                                                                                                                                       118 KRLGLPVSE 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69.4%; Score 34; DB 4; Length 79; Local Similarity 63.6%; Pred. No. 2.4; hes 7; Conservative 7. William
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IDENTIFICATION METHOD: Von Heijne matrix OTHER INFORMATION: score 10.8 OTHER INFORMATION: seq VLLFFVLLGMSQA/GS
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER:
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AMINO ACID
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                                                                                                                                                                                                                  Score 34; DB 4; Length 373; Pred. No. 15; 1; Mismatches 1; Indels
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE:
SEQ ID NO 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/08662560
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               INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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TITLE OF INVENTION: VINULENCE-ASSOCIATED NUCLEI
TITLE OF INVENTION: SEQUENCES AND USES THEREOF
FILE REFERENCE: 00786/361002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS:
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TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
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                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-8864
                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Huszar, Dennis
APPLICANT: Wei, Gu
TITLE OF INVENTION: SCREENING METHODS FOR COMPOUNDS
TITLE OF INVENTION: USEFUL IN THE REGULATION OF BODY WEIGHT
                                                                                                                                                                 ATTORNEY/AGENT INFORMATION: NAME: Coruzzi, Laura A
                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             656 LAKREGLSV 664
                                                                                                                        NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-060
                                                                                                                                                                                                                                                   FILING DATE: 10-JUN-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/662,560 FILING DATE: 10-JUN-1996
                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM:
SOFTWARE: FastSE(
                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: New York
STATE: NY
                                                       TELEX:
                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                  COMPUTER:
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                                                     66141 PENNIE
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Rahme, Laurence G.
Mahajan-Miklos, Shalina
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332 amino acids
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1155 Avenue of the Americas
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; TOPOLOGY: lir; MOLECULE TYPE: FRAGMENT TYPE: US-08-662-560-2
     US-08-706-281A-16
: Sequence 16, Application US/08706281A
; Patent No. 6100048
                                                                                                                                                                                                          US-08-780-749A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-780-749A-6
                                                                                                                                                 Matches
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Matches 5; Conserva
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APPLICANT: Gu, Wei
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US-08/780,749A
FILING DATE: 08-0AN-1997
CLASSIFICATION: 800
                                                                                                                                                                                                                    TOPOLOGY: unknown MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Laura A. Coruzzi
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 78
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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                                                                                         164 KRVGISIS 171
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                                                                                                                                                Local Similarity
les 5; Conserv
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                                                                                                                                                                                                                                                               TYPE: amino acid
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                                                                                                                     3 KRIGLSVS 10
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(212) 869-8864/9741
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internal
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62.5%;
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Pred. No. 36;
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US-09-097-231-16
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Matches 5; Conserv
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                                                                                                                                                                                                                                                                                                                                 164 KRVGISIS 171
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ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                     CITY: Chicago
STATE: Illinois
COUNTRY: USA
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Sequence 16, Application US/09097231
Patent No. 6278038
GENERAL INFORMATION:
APPLICANT: Cone, Roger D
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: No. 6100048nan, Kevin
REGISTRATION NUMBER: 35,303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/OFFILING DATE: 04-SEP-1996
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CORRESPONDENCE ADDRESS:
ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
                                                  Low, Malcolm J
TITLE OF INVENTION: Mammalian Melanocortin Receptor and Uses
NUMBER OF SEQUENCES: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          332 amino acids
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                                                                                                               Chen, Wenbiao
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62.5%;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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APPLICANT: Lee, Frank
APPLICANT: Huszar, Jennis
APPLICANT: Gu, Wei
ITILE OF INVENTION: SCREENING METHODS FOR COMPOUNDS USEFUL IN THE
TITLE OF INVENTION: REGULATION OF BODY WEIGHT
FILE REFERENCE: 7853-083
CURRENT APPLICATION UMBER: US/08/870,511
CURRENT APPLICATION UMBER: US/08/870,511
CURRENT APPLICATION UMBER: 1997-06-06
NUMBER OF SEQ ID NOS: 45
NUMBER OF SEQ ID NOS: 45
                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                          Sequence 8, Application US/08870511 Patent No. 6287763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 6
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Best Local Similarity
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      APPLICANT: Lee, Frank
APPLICANT: Huszar, Dennis
APPLICANT: Gu, Wei
TITLE OF INVENTION: SCREENING METHODS FOR COMPOUNDS USEFUL IN THE
TITLE OF INVENTION: REGULATION OF BODY WEIGHT
FILE REFERENCE: 7853-083
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CURRENT APPLICATION NUMBER: US/08/870,511
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                                                                                                                                                                                                                                                                                164 KRVGISIS 171
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NAME: NO. 6278038nan, Kevin E
REGISTRATION UNMBER: 35,303
REFERENCE/DOCKET NUMBER: 96,886-C
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LENGTH: 332 amino acids
TYPE: amino acid
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Pred. No.
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Pred. No. 36;
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                                                                      ; ORGANISM: Homo sapiens US-08-870-511-12
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; Patent No. 6287763
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                                                                                                                     SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 12
LENGTH: 332
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NUMBER OF SEQ ID NOS: 45
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 8
LENGTH: 332
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SEQ ID NO 10
LENGTH: 332
 Query Match 65.3%;
Best Local Similarity 62.5%;
Matches 5; Conservative
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                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/08/870,511
CURRENT FILING DATE: 1997-06-06
NUMBER OF SEQ ID NOS: 45
                                                                                                                                                                                                                                                                                        APPLICANT: Lee, Frank
APPLICANT: Huszar, Dennis
                                                                                                                                                                                                                             FILE REFERENCE: 7853-083
                                                                                                                                                                                                                                    TITLE OF INVENTION: SCREENING METHODS FOR COMPOUNDS USEFUL IN THE TITLE OF INVENTION: REGULATION OF BODY WEIGHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/08/870,511 CURRENT FILLING DATE: 1997-06-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: GU, Wei TITLE OF INVENTION: SCREENING METHODS FOR COMPOUNDS USEFUL IN THE TITLE OF INVENTION: REGULATION OF BODY WEIGHT FILE REFERENCE: 7853-083
                                                                                                                                                                                                                                                                             APPLICANT: Gu, wei
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Search completed: January 15, 2003, 12:38:25 Job time : 10.2857 secs

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10 US-09-823-649A-17
10 US-09-825-301-857
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11 US-09-981-900B-9
11 US-09-815-242-10980
10 US-09-815-242-10980
10 US-09-815-242-1087
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Sequence 44, Appl
Sequence 44, Appl
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Sequence 6454, Ap
Sequence 5520, Ap
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Sequence 17, Appl
Sequence 857, App
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US-09-823-649A-6
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TYPE: PRT
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ALIGNMENTS

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US-09-83-649A-17
US-09-823-649A-17
; Sequence 17, Application US/09823649A
; Patent No. US20020012970A1
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Smith, Edward
APPLICANT: Elistrom, Cari
APPLICANT: Gelfand, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 21
SOFTWARK: Patentin version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/823,649A CURRENT FILING DATE: 2001-03-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE: RPA1006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: HIGH TEMPERATURE REVERSE TRANSCRIPTION USING MUTANT DNA POLYME
                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                        Similarity
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US-09-925-301-857; Sequence 857, Application.; Patent No. US20020052308A1
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                                                    GENERAL INFORMATION:
APPLICANT: Inouye,
APPLICANT: Hsu, Mei-
APPLICANT: Eagle, S
APPLICANT: Inouye,
                                                                                                                                                 Sequence 2, Application US/08808031A Patent No. US20020048802A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Patent No. US2002005
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 857
                                                                                                                                                                                                                                                                                                                                                 Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/925,301
CURRENT FILING DATE: 2001-08-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 1694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies FILE REFERENCE: \mathtt{PA106}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/823,649A CURRENT FILING DATE: 2001-03-30 PRIOR APPLICATION NUMBER: US 60/198,336 PRIOR FILING DATE: 2000-04-18 NUMBER OF SEQ ID NOS: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Rosen et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentln version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: HIGH TEMPERATURE REVERSE TRANSCRIPTION USING MUTANT DNA POLYMERAS FILE REFERENCE: RPA1006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
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            APPLICANT: Inouye, Masayori
TITLE OF INVENTION: PROKARYOTIC REVERSE TRANSCRIPTASE
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ENGTH:
                                                                                                                                                                                                                                                                       148 RIGLSVSE 155
                                                                                                                                                                                                                                                                                             4 RIGLSVSE 11
                                                                                                                                                                                                                                                                                                                                                 Local Similarity es 8; Conserv
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Elfstrom, Carita
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wang, Alice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Myers, Thomas
Schoenbrunner, Nancy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gelfand, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Application. US/09925301
                                                                                           Inouye, Sumiko
Hsu, Mei-Yin
                                                                        Eagle, Susan
                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                  73.5%; Score 36; DB 10; Length 258; 100.0%; Pred. No. 5.5;
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                                                                                                                                                                                                                                                                                                                                                 Mismatches
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Query Match
Best Local Similarity
"hehes 7; Conserva"
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                                                                                                                              ; TYPE: PRT; ORGANISM: Streptococcus salivarius US-09-981-900B-9
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                                                                                                                                                                         SOFTWARE: PatentIn version 3.1
SEQ. 1D NO 9
LENGTH: 822
                                                                                  Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 9, Application US/09981900B Patent No. US20020138878A1
                                                                 Matches
                                                                                                                                                                                                                             PRIOR FILING DATE: 2000-10-20
NUMBER OF SEQ ID NOS: 22
                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/981,900B CURRENT FILING DATE: 2002-03-18 PRIOR APPLICATION NUMBER: 60/242,408
                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: TRANSGENIC PLANTS CONTAINING LIGHTNASE AND CELLULASE WHICH DEG
TITLE OF INVENTION: AND CELLULOSE TO FERMENTABLE SUGARS
FILE REFERENCE: MSU 4.1-539
                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Sticklen, Masomeh B
APPLICANT: Magbool, Shahina B
APPLICANT: Dale, Bruce E
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 37.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-875-8383
TELEFAX: 215-875-8394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              155 LAKALGLSVSK 165
 63
                                                                              Local
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REGISTRATION NUMBER: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: FILING DATE: 03-MAI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 230 South I CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: WEISER & ASSOCIATES STREET: 230 South Fifteenth Street, Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE:
                              2 SKRIGLSVSE 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 LSKRIGLSVSE 11
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SKRAGLSVED 72
                                                               Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PA
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03-MAR-1997
V. "Г"
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                                                                             67.3%;
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                                                           1; Mismatches
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                                                                             Score 33; DB 10;
Pred. No. 78;
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Pred. No. 28;
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                                                                                            Length 822;
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RESULT 6 US-09-214-474A-6

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Query Match
Best Local Similarity
"herhes 6; Conserve
US-09-815-242-10980
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; ORGANISM: Streptococcus pneumoniae
US-09-214-474A-6
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                                                                          NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10980
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SEQ ID NO 6
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APPLICANT:
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CURRENT FILING DATE: 1999-01-21
PRIOR APPLICATION NUMBER: US 60/057,520
PRIOR FILING DATE: 1997-09-04
PRIOR APPLICATION NUMBER: PCI/US98/18291
PRIOR PILING DATE: 1988-09-03
NUMBER OF SEQ ID NOS: 7
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APPLICANT: Chappell, Amy M.
TITLE OF INVENTION: No. US20020049311A1el Rnase P
                                                                                                                                                                                                                                                                                     PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
                                                                                                                                                                                                                                                                                                                                                                                           CURRENT FILING DATE: 2001-03-21 PRIOR APPLICATION NUMBER: 60/191,078 PRIOR FILING DATE: 2000-03-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: EL'TRA.011A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Haselbeck, Robert
                                                                                                                                           PRIOR FILING DATE:
                                                                                                                                                           PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
                                                                                                                                                                                                    PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
                                                                                                                                                                                                                     PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/815,242
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               ORGANISM: Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 60/206,848
                                                      LENGTH: 146
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Hegg, Lisa A.
Li, Hu
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Zyskind, Judith W.
Wall, Daniel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yamamoto, Robert T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Trawick, John D.
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                                                                                                                                           2001-02-16
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US-09-815-242-5030
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US-09-888-911-4
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Best Local Similarity 45.5%;
Matches 5; Conservative
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                                                                                                                                                  CURRENT FILLING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Haseibeck, Robert APPLICANT: Ohlsen, Kari L.
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TITLE OF INVENTION: 46508, A NOVEL HUMAN PEPTIDYL-TRNA
TITLE OF INVENTION: HYDROLASE FAMILY MEMBER AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/888,911 CURRENT FILING DATE: 2001-06-25
                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/815,242
                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes
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                                   PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
                                                                                                                                                                                                                                                                                               FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
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PRIOR APPLICATION NUMBER: 60/269,308
                    PRIOR FILING DATE:
                                                       PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
                                                                                               PRIOR APPLICATION NUMBER: 60/242,578 PRIOR FILING DATE: 2000-10-23
                                                                                                                                      PRIOR FILING DATE: 2000-05-26
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Xu, H. Howard
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Pred. No.
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RESULT 11
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                    Sequence 44, Application US/10027806 Patent No. US20020160476A1 GENERAL INFORMATION:
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NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FASKSEQ for Windows Version 4.0
SEQ ID NO 5030
LENGTH: 201
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        APPLICANT: Swanson, Ronald V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Identification of Essential Genes
TITLE OF INVENTION: Drokafyotes
FILE REFERENCE: ELITA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
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PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
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                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS:
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PRIOR FILING DATE: 2000-05-26
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FILING DATE: 2000-11-27
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Yamamoto, Robert T.
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Pred. No.
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US-08-808-031A-42
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; Patent No. US20020048802A1
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                                                                                               APPLICANT:
APPLICANT:
                                                 NUMBER OF SEQUENCES: 5
                                                                                  APPLICANT: inouye, Masayori
TITLE OF INVENTION: PROKARYOTIC REVERSE TRANSCRIPTASE
                                                                                                                                                 APPLICANT:
                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                  ADDRESSEE: WEISER & ASSOCIATES
STREET: 230 South Fifteenth Street, Suite 500
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                               3 KRIGLSVSE 11
                                                                                                             Eagle, Susan
                                                                                                                                  Hsu, Mei-Yin
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Publication No. US20020198365Al
                                                                      Sequence 44, Application US/10034623
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Matches 6; Conserv
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APPLICANT: Schleper, Christa
APPLICANT: Schleper, Christa
TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM CENARCHAEUM SYMBIOSUM
FILE REFERENCE: DCORP.002A
CURRENT APPLICATION NUMBER: US/10/027,806
CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: FARLIER APPLICATION NUMBER: 09/408,020
PRIOR APPLICATION NUMBER: FARLIER FILING DATE: MARLIER FILI
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; ORGANISM: Cenarchaeum symbiosum US-10-034-623-44 Query Match Best Local Similarity GENERAL INFORMATION: TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM CENARCHAEUM SYMBIOSUM FILE REFERENCE: DCOR-DCA CURRENT APPLICATION NUMBER: US/10/034,623
CURRENT FILING DATE: 2001-12-21 PRIOR APPLICATION NUMBER: 60/102,294 PRIOR FILING DATE: 1998-09-29 PRIOR APPLICATION NUMBER: 09/408,020 PRIOR FILING DATE: 1999-09-29 APPLICANT: Weldman, Robert A. APPLICANT: Schleper, Christa APPLICANT: Swanson, Ronald V. SOFTWARE: FastSEQ for Windows Version NUMBER OF SEQ ID NOS: 6; Conservative 66.7%; ۲. Score 41; DB Pred. No. 67; Mismatches 9 Length 310 Indels 0; Gaps

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Query Match
Best Local Similarity
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                                                                                ; ORGANISM: Corynebacterium glutamicum US-09-738-626-6454
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                                                                                                                                                  SOFTWARE: PatentIn ver. 3.0 SEQ ID NO 6454
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Best Local :
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PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: NAKAGAWA, SATOSHI APPLICANT: MIZOGUCHI, HIROSH
                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: JP 99/377484 PRIOR FILING DATE: 1999-12-16
                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
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                                                                                                                                                                                                                                                                                                                                     APPLICANT: OZAKI, AKIO
IITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
ILE REFERENCE: 249-125
                                                                                                                    TYPE: PRT
                                                                                                                                   LENGTH: 526
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LENGTH: 480 amino acid
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-875-8383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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                 Conservative
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                                             Query Match
Best Local Similarity 70.0
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 4, Application US/09999248 Patent No. US20020176852A1
                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 60/289,172
PRIOR FILING DATE: 2001-05-07
PRIOR APPLICATION NUMBER: US 60/289,537
                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/999,248
CURRENT FILING DATE: 2001-11-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Lambeth, APPLICANT: Cheng,
                                                                                                                                                                                                                                                                                                                                                        PRIOR FILING DATE: 2000-11-16
PRIOR APPLICATION NUMBER: US 60/251,364
PRIOR FILING DATE: 2000-12-05
                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 60/249,305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: mitogenic Oxygenase Regulators FILE REFERENCE: 05501-0180 43150-266489
                                                                                                                                                                                                                                                                                PRIOR FILING DATE: 2001-05-07
                                                                                                                                                                                        TYPE: PRT
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232 LEKAIGLAVS 241
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                                   1 LSKRIGLSVS 10
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    Mismatches

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Search completed: January 15, 2003, 12:39:52 Job time: 11.8571 secs

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45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	
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67.3	67.3	67.3	67.3	67.3	67.3	67.3	67.3	67.3	67.3	67.3	69.4	69.4	69.4	69.4	69.4	
302	263	175	162	160	151	129	112	87	79	-77	637	530	502	501	500	
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		hypothetical prote	shikimate kinase I	hypothetical prote	conserved hypothet	_	hypothetical prote		hypothetical prote	hypothetical prote	acetylcholinestera	sigma-54 dependent	RNA polymerase sig	probable ABC subst	transcription init	

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ALIGNMENTS

magnesium and cobalt transport protein homolog - Methanococcus jannaschii C;Species: Methanococcus jannaschii C;Species: Methanococcus jannaschii C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999 C;Accession: H64428

RESULT H64428

rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A. Science 273, 1058-1073, 1996
A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese A;Title: Complete genome sequence of the methanogenic archaeon, Mcthanococcus jannasc A;Reference number: A64300; MUID:96337999; PMID:8688087

R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blak; Reich, C.I.; Overboek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek,

A;Map position: FOR965089-966042 C;Superfamily: magnesium and cobalt transport protein

A;Cross-references: GB:U67546; GB:L77117; NID:g1591687; PIDN:AAB99037.1; PID:g1499876 C;Genetics:

A; Molecule type: DNA A; Residues: 1-317 <BUL>

A; Accession: H64428

A; Status: preliminary; nucleic acid sequence not shown; translation

not shown

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Query Match	A; Accession: T19599 A; Accession: T19599 A; Status: preliminary; translated from GB/EMBL/DDBJ A; Molecule type: DNA A; Residues: 1-352 <wil> A; Cross-references: EMBL: Z83218; PIDN: CAB05691.1; GSPDB: GN00023; CESP: C31A11.9 A; Experimental source: clone C31A11 C; Genetics: A; Gene: CESP: C31A11.9 A; Map position: 5 A; Introns: 64/3; 94/1; 214/3</wil>	RHSULE 2 T19599 T19599 hypothetical protein C31A11.9 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999 C;Accession: T1959 R;McMurray, A. R;McMurray, A. Submitted to the EMBL Data Library, December 1996	Query Match Best Local Similarity 72.7 Matches 8; Conservative Qy 1 LSKRIGLSVSE 11
77.6%;	:ranslatec ::283218; :lone C31/	IN11.9 - (is elegans yuence_rev	83.7%; 72.7%; ative
Score 38;	4 from GB/EN PIDN:CAB056	Cy, December	83.7%; Score 41; DB 1; 72.7%; Pred. NO. 1.8; stive 3; Mismatches
DB 2;	MBL/DDB:	cis elec ct-1999	,
Length 352;	J SSPDB;GNC0023;	gans #text_change	Length 317; 0; Indels
	CESD:C31A11	15-Oct-1999	0; Gaps
	Q		0;

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A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; A;Title: The complete genome sequence of the gastric pathogen Helicobacter pyl A;Reference number: A64520; MUID:97394467; PMID:9252185
A;Accession: E64539
                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:AE001437; PIDN:AAK79294.1; A;Experimental source: Clostridium acetobutylicum C;Genetics: A;Gene: CAC1325 A;Gene: CAC1325 C;Superfamily: conserved hypothetical protein yitT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          uncharacterized conserved protein, YitT (B. subtilis) family CAC1325 [imported] - C.Species: Clostridium acerobutylicum c.Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 30-Sep-2001 C.Accession: C97063 R.Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D. Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenne son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L. Nature 388, 539-547, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: GB:AE000536;
C;Superfamily: shikimate kinase;
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muconate cycloisomerase I PA2509 [imported] - Pseudomonas aeruginosa (strain PAO1) C;Species: Pseudomonas aeruginosa C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
                                                                   D83331
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A; Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clc
A; Reference number: A96900; MUID:21359325; PMID:21359325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, ; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R. J. Bacteriol. 183, 4823-4838, 2001
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C;Date: 09-Aug-1997 *sequence_revision 09-Aug-1997 *text_change 18-Jun-1999
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A; Residues: 1-285 <KUR>
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A; Status: preliminary
                                                                                           RESULT 5
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4; Mismatches
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Pred. No.
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17;
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                                                                        A; Reference number: A85480; A; Accession: C86120
                                                                                                                                      G; Paces, 1.7. (C; Accession: C86120 C; Accession: C86120 R; Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, R; Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, R; Perna, N.T.; Dlunkett III, G.; Burland, V.; Mau, B.; Glasner, R; Perna, N.T.; Dlunkett III, Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.;
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C;Superfamily:
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A; Residues: 1-373 <STO>
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                                                                                                                                                                                                                               probable growth inhibitor [similarity] - Escherichia coli (strain 0157:H7, substrain C;Species: Escherichia coli (C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 02-Nov-2001
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       A; Molecule type: DNA
A; Residues: 1-116 <S'
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                                                  A; Status: preliminary
                                                                                             A; Title: Genome sequence of enterohemorrhagic Escherichia A; Reference number: A85480; MUID:21074935; PMID:11206551
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C; Accession: D83331
R; Stover, C.K.; Pham, X.O.; adman, S.; Yuan, Y.; Brody,
                                                                                              C:Superfamily: molecular chaperone t-complex-type C:Keywords: cytosol; molecular chaperone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1995 #sequence_revision 14-Jul-1995 #text_change 20-Aug-1999
C;Accession: JC4073; PC4022; S52867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: GB:AE004678; GB:AE004091; NID:g9948560; PIDN:AAG05897.1; GSPDB:GN
A;Experimental source: strain PAO1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa
A;Reference number: A82950; MUID:20437337; PMID:10984043
                                                                                                                                                                                                                                                                                                                                                                                           A; Title: The eighth Cct gene, Cctq, encoding the theta subunit A; Reference number: JC4073; MUID:95197008; PMID:7890169
                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Kubota, H.; Hynes, G.; Willison, K. Gene 154, 231-236, 1995
                                                                                                                                                                                              C; Comment: This protein is involved in folding, transport
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                                                                                                                                                                                                                                                                                          EMBI.: 237164; NID: g695624; PIDN: CAA85521.1; PID: g695625
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 36;
Pred. No.
                                                  Score 36;
                            Pred. No.
  Mismatches
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22;
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33;
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coli 0157:H7

Potamousis, J.D.;

Apoda

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R;Hayashi,
                                                           C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001
C;Accession: C91279
                                                                                                 probable growth inhibitor [imported] - Escherichia coli (strain 0157:H7, substrain C;Species: Escherichia coli
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                                                                                                                                                                                                                                                               δÃ
                                                                                                                                                                                                                                                                                                                                                                                          A;Gene: chpi
C;Keywords:
                                                                                                                                                                                                                                                                                                                                                                                                                                A;Experimental source: strain
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Title: The complete genome sequence of Escherichia coli K-12 A;Reference number: A64720; MUID:97426617; PMID:9278503 A;Accession: D65234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: EMBL:U14003; NID:g1263172; PIDN:AAA97122.1; PID:g537067
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1994
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cd.
A.; Rose, D.J.; Mau, B.; Shao, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Reference number: S56314; MUID:95334362; PMID:7610040
A;Accession: S56451
A;Status: preliminary; nucleic acid sequence not shown; translation not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Burland, V.; Plunkett III. G.; Sofia, H.J.; Daniels, D.L.; Blatt Nucleic Acids Res. 23, 2105-2119, 1955
A;Title: Analysis of the Esodetichia coli genome VI: DNA sequence A;Reference number: S56314; MUID:95334362; PMID:7610040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Masuda, Y.; Miyakawa, K.; Nishimura, Y.; Ohtsubo, J. Bacteriol. 775, 6850-6856, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Escherichia coli
C;Date: 07-Apr-1994 *sequence_revision 07-Apr-1994 #text_change
C;Accession: D49339; S56451; D65234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:AE000494; GB:U00096; NID:g1790670: A;Experimental source: strain K-12, substrain MG1655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-116 <BLAT>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cell growth regulatory protein ChpBK - Escherichia coli (strain K-12) N;Alternate names: pemk-like protein 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Science 277, 1453-1462, 1997
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A; Residues: 1-116 <BUR>
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A; Residues: 1-116 <MAS>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Status: preliminary; nucleic acid sequence not shown; translation not shown
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N.; Yasunaga, T.; Kuhara,
8, 11-22, 2001
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                                      T.; Makino, K.; Ohnishi,
                                                                                                                                                                                                                                                                                                                                                                                        DNA binding
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7; Conserv
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63.6%;
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Pred. No.
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Pred. No.
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                     Shiba, T.; Hattori, M.; Shinagawa,
                                          Kurokawa, K.; Ishii, K.;
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11;
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                                        Yokoyama,
                                                                                                                                                                                                                                                                                                         0
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RESULT 11
RGECLR
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C;Superfamily:
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Nature 390, 249-256, 1997

A; Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galizci, G.; Rocha, E.; Rocha, B.; Galizci, A.; Canda, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scand, A.; Galizci, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosalo, V.; Gchiya, G.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamamoto, K.; Yasumoto, K.; Yata, K.; Yoshida, A.; Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtili A; Reference number: A69580; MUID:98044033; PMID:9384377

A; Accession: F69592
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C;Species: Bacillus subtilis
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Belitsky, B.R.; Gustatsson, M.C.U.; Somenshein, A.L.; von Wachenfeldt, J. Bacteriol. 179, 5448 5457, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Kunst, F.; Ogasawara, N.; Moszer, J.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Be:
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.;
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Title: An Irp-like grave of Bacillus subrills involved in branched-chain amino acid A;Reference number: Z22437; MUID:974:11495; PMID:9287000
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A; Residues: 1-157 < KUN>
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A;Experimental source: strain 0157:H7, substrain RIMD 0509952
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A; Residues: 1-116 <HAY>
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A; Residues: 1-157 <BEL>
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                                                               1 LSKRIGLSVS 10
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LSKKIGLSPS 36
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8; Conser
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80.08;
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Pred. No.
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                                                                                                                           Mismatches
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15;
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C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 01-Mar-2002 C;Accession: JH0412; I59240; H64827 R;Willins, D.A.; Ryan, C.W.: Platko, J.V.; Calvo, J.M. J. Biol. Chem. 266, 10768-1074, 1991 A;Title: Characterization of Lrp, an Escherichia coli regulatory protein that mediates A;Reference number: JH0412; MUID:91250369; PMID:2040596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Superfamily: regulatory protein asnC
C;Keywords: DNA binding; homodimer; transcription regulation
F;2-164/Product: lacine-responsive regulatory protein #statu
F;30-56/Region: hewix-turn-helix motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: GB:M35869; NID:g146664; PIDN:AAA24089.1; PID:g146665 R;Ito, K.; Kawakami, K.; Nakamura, Y. Proc. Natl. Acad. Sci. U.S.A. 90, 302-306, 1993 A;Title: Multiple control of Escherichia coli lysyl-tRNA synthetase expressions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: H64827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: GB:D11105; NID:g216585; PIDN:BAA01880.1; PID:g216586 R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; A.; Rose, D.J.; Mau, B.; Shao, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Reference number: I59240; MUID:93126364; PMID:7678344
A;Accession: I59240
A;Accession: I59240
                   F;30-56/Region:
                                       C; Superfamily: regulatory protein asnC C; Keywords: DNA binding; transcription
                                                                                        A; Description:
                                                                                                                 C; Function
                                                                                                                                                                C; Genetics:
                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-164 < CAL>
                                                                                                                                                                                                                                                                                                             A; Description:
                                                                                                                                                                                                                                                                                                                                 submitted to the EMBL Data Library, September 1993
                                                                                                                                                                                                                                                                                                                                                         R;Calvo,
                                                                                                                                                                                                                                                                                                                                                                                  C; Accession: S59991
                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Serratia marcescens
C;Date: 15-Feb-1996 #sequence_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                     transcription regulator lrp, leucine-responsive - Serratia marcescens
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A;Experimental source: strain K-12, substrain MG1655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Status: nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: DNA
A;Residues: 1-164 <RES>
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A; Residues: 1-164 <WIL>
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                                                                                                                                          A; Gene:
                                                                                                                                                                                                                                                            A; Accession:
                                                                                                                                                                                                                                                                                    A; Reference number: S59991
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                        helix-turn-helix motif
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R;Calvo, J.M. submitted to the EMBL Data Library, September
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                                                                                                                                           A;Description: activates a number of or C;Superfamily: regulatory protein assoc C;Keywords: DNA binding; transcription F;30-56/Region: helix-turn-helix motif
                                                                                                                                                                                                                                                                         A;Cross-references: EMBL:U02274;
A:Note: the source is designated
                                                                                                                                                                                                                                                                                                                                                                                       A; Description: The amino acid sequence of Erp
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F; 30-56/Region:
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A; Residues: 1-164 < CAL>
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C;Date: 15-reb-1996 *sequence_revision 01-Mar-1996 *text_change 26-Aug-1999
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34 LSKRVGLS
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Mismatches
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B82142
leucine:responsive regulatory protein VC1904 [imported] - Vibrio cholerae (strain N1696] c.Spacies: Vibrio cholerae
C.Spacies: Vibrio cholerae
C.Cate: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C.Accession: B82142
R.Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, H. R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A.Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A.Reference number: A62035; MUID:20406833; PMID:10952301
A.Accession: B82142
A.Status: preliminary
A.Residues: 1-164 (HEI)
A.Residues: 1-164 (
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Title: Perfect score:

US-09-823-649A-6 1 LSKRIGLSVSE 11

Run on:

protein

protein search, using sw model

January 15, 2003, 09:04:22

Scoring table: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5

112892 seqs, 41476328 residues

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Copyright (c) 1993 - 2003 Compugen Ltd
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                                                      AROK_HELPY
ID AROK, H
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Query Match
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MEDLINE=97394467; PubMed=9252185;

Tomb J.-F., White O., Kerlawage A.R., Clayton R.A., Sutton G.G., Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A., Nelson K., Quackenbush J., Zhou L., Kixkness E.F., Peterson S., Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A., McKenney K., FitzGerald L.M., Lee N., Adams M.D., Hickey E.K., McKenney K., FitzGerald L.M., Lee N., Adams M.D., Hickey E.K., Berg D.E., GOcayne J.D., Utterback T.R., Peterson J.D., Kelley J.M., Cotton M.D., Weldman J.M., Fujii C., Bowman C., Watthey L., Wallin E., Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
                                                                                                                                                                                                                                                                                                                                                                           the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-UUN-2002 (Rel. 41, Last annotation update)
Shikimate kinase (EC 2.7.1.71) (SK)
AROK OR HP0157
                                                                            Complete proteome.
                                                                                                                                                            InterPro; IPR000623; Shik_kinase.
pfam; pr01202; SKI; 1.
pRINTS; pr01100; SHIKIMTKNASE.
pROSITE; PS01128; SHIKIMATE_KINASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 388:539-547(1997).
-I- CATALYTIC ACTIVITY: ATP + shikimate = ADP + shikimate 3-phosphate
-I- PATHWAX: Aromatic amino acids biosynthesis; shikimate pathway;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Helicobacter pylori (Campylobacter pylori).
Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
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TIGR; HP0157; -.
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SIMILARITY: BELONGS TO THE SHIKIMATE KINASE FAMILY.
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                                                        162 AA;
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SUMMARIES

NU5M_ALBCO DEXT_STRSL SYA_PYRHO

CAPP_SYNY3

CTB1_ACILW YG2M_YEAST HMA2_CUCSA

AROK_HELPJ PTH_THETN Y625_METJA YA76_METJA

CATB_PSEPU XKDK_BACSU

YYAS_BACSU

LRP_SERMA
GAL1_SCHPO
YW04_SCHPO
RS4_BACSU

PUTR_AGRTU AZLB_BACSU

CHPB_ECOLI

LRP_KLEPN LRP_SALTY

TCPQ_MOUSE SYA_PYRFU

TCPQ_HUMAN AROK_HELPY

RT16_MYXXA

ACES_ANOST
PURL_THEAC
CDBC_HUMAN

Database

SwissProt_40:*

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Minimum DB Maximum DB

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RA Park H.-S., Toyoda A., Ishik K., Totoki Y., Choi D.-K., Soeda E.,
RA Ohki M., Takaji T., Sakaki Y., Taudien S., Blechschmidt K., Polley A.,
RA Ohki M., Takaji T., Sakaki Y., Taudien S., Blechschmidt K., Polley A.,
RA Menzel U., Delabar J., Kumpf K., Lehmann R., Patterson D.,
RA Menzel U., Delabar J., Kumpf K., Lehmann R., Patterson D.,
RA ROSenthal A., Kudoh J., Shibuya K., Kawasaki K., Asakawa S.,
RA Rosenthal A., Kudoh J., Shibuya K., Kawasaki K., Asakawa S.,
RA Minoshima S., Shinizu N., Nordsiek G., Hornischer K., Brandt P.,
RA Minoshima S., Shinizu N., Nordsiek G., Hornischer K., Brandt P.,
RA Minoshima S., Shinizu N., Desario A., Reichelt J., Kauer G., Bloecker H.,
RA Ramser J., Bock A., Klages S., Hennig S., Riesselmann L., Dagand E.,
RA Ramser J., Bock A., Klages S., Hennig S., Riesselmann L., Dagand E.,
RA Wehrmeyer S., Borzym K., Gardiner K., Nizetic D., Francis F.,
Lehrach H., Reinhardt R., Yaspo M.-L.;
The DNA sequence of human chromosome 21.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity Matches 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-0CT-1996 (Rel. 34, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
T-complex protein 1, theta subunit (TCP-1-theta) (CCT-theta).
CCT8 OR CCT9 OR KIAA0002.
                                                                                                                                                                                                      cytosolic chaperonin containing TCP-1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Taudien S., Dagand E., Delabar J., Nordsiek G., Drescher B., Weber J., Schattevoy R., Menzel U., Yaspo M.-L., Rosenthal A.; Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human)
                                                                                                                                                                                Gene 154:231-236(1995)
                                                                                                                                                                                                                                              "The eighth Cct gene, Cctq, encoding the theta subunit of the
                                                                                                                                                                                                                                                                                      Kubota H.,
                                                                                                                                                                                                                                                                                                                    MEDLINE~95197008;
                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 33-65 FROM N.A.
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"Nucleotide sequence surrounding the locus marker D218246 on human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FISSUE-Bone marrow;
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                                 ATP HYDROLYSIS. KNOWN TO PLAY A ROLE, IN VITRO, IN THE FOLDING ACTIN AND TUBULIN.
SUBUNIT: HETERO-OLIGOMERIC COMPLEX OF ABOUT 850 TO 900 kDa THAT
                                                                                                                                       FUNCTION: MOLECULAR CHAPERONE; ASSIST THE FOLDING OF PROTEINS UPON
       FORMS TWO STACKED RINGS, 12 TO 16 NM IN DIAMETER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ISERVGLSVRE 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              line KG-1
                                                                                                                                                                                                                                                                               Hynes G., Willison K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                PubMed=7890169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PubMed=8590283; A., Watanabe K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 u
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 548 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              <u>-</u>-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EWBL outstation
                                                                                                                                                         Gene 154:231-236(1995).
-i- FUNCTION: MOLECULAR CHAPERONE: ASSIST THE FOLDING OF PROTEINS UPON
                                                                                                                                                                                             "The eighth Cct gene, Cctq, encoding the theta subunit of the cytosolic chaperonin containing TCP-1.";
                                                                                                                                                                                                                                  Kubota H.,
                                                                                                                                                                                                                                               MEDLINE=95197008; PubMed=7890169;
                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                         T-complex protein 1, theta subunit (TCP-1-theta) (CCT-theta). CCT8 OR (CCTQ.
                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1995 (Rel. 01-NOV-1995 (Rel. 01-FEB-1996 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chaperone; ATP-binding; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00750; TCP1_1; 1.
PROSITE; PS00751; TCP1_2; 1.
PROSITE; PS00995; TCP1_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PR00298; CHAPERONIN60. PRINTS; PR00304; TCOMPLEXTCP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00118; cpn60_TCP1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    modified and this statement is not removed.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                             NCBI_TaxID-10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                        P42932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genew; HGNC:1623; CCT8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSSP; P48424; 1A6D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  - (- SIMILARITY: BELONGS TO THE TCP-1 CHAPERONIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SUBCELLULAR LOCATION: Cytoplasmic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ICPO_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   120 RIGLSVSE 127
                                                                     I- SIMILARITY: BELONGS TO THE TCP-1 CHAPERONIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
les 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 RIGLSVSE 11
                                                                                SUBUNIT: HETERO-OLIGOMERIC COMPLEX OF ABOUT 850 TO 900 kDa THAT FORMS TWO STACKED RINGS, 12 TO 16 NM IN DIAMETER.
SUBCELLULAR LOCATION: Cytoplasmic.
                                                                                                                                     ATP HYDROLYSIS. KNOWN TO PLAY A ROLE, IN VITRO, IN THE FOLDING ACTIN AND TUBULIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AF129075; -; NOT_ANNOTATED_CDS
AL163249; CAB90433.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            D13627; BAA02792.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IPR002194; Chaperonin_TCP-1.
IPR001844; Chaprnin_Cpn60.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         548 AA;
                                                                                                                                                                                                                                Hynes G., Willison K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                 32. Created)
32. Last sequence update)
33. Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N -> K (IN REF. 1 AND 2).
A -> V (IN REF. 1).
566A6622BC2D15E9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 36;
Pred. No.
                                                                                                                                                                                                                                                                                                          Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                       Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   548 AA
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the European Bioinformatics Institute. use by non-profit institutions as k

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                                                                                                                                            Best
                                                                                                                                                                 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-VC1 / DSM 3638 / ATCC 43587 / JCM 8422;
Weiss R.B., Dunn D.M., Robb F.T., Brown J.R.;
"The complete sequence of the Pyrococcus furiosus genome.";
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
-- CATALYTIC ACTIVITY. ATP + L-alanine + tRNA(Ala) = AMP + diphosphate + L-alanyl-tRNA(Ala).
-- SUBCELLULAR LOCATION: Cytoplasmic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                            entities requires a license agreement (See http://www.isb-slb.ch/announce/or send an email to license@isb-slb.ch).
                                                                                                                                                                                                                                                                                                                                               modified and this statement is not removed entities requires a license agreement (See )
                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROF entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Alanyl-tRNA_synthetase (BC 6.1.1.7) (Alanine--tRNA ligase) (Alans).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00750; TCP1_1; PROSITE; PS00751; TCP1_2; PROSITE; PS00995; TCP1_3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR002423; Cpn60/TCP-1.
Pfam; PF00118; cpn60_TCP1; 1.
PRINTS; PR00304; TCOMPLEXTCP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MGD; MGI:107183; Cct8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pyrococcus furiosus.
Archaea; Euryarchaeota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALAS OR PF0270
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                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                           PROSITE: PS50860; AA_TRNA_LIGASE_II_ALA; 1
Aminoacy1-tRNA synthetase; Protein biosyntl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SYA_PYRFU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chaperone;
                                                                                                                                                                                                                        Complete proteome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=2261;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q8U425;
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                                          317 VAKRYGISVEE 327

    -!- SIMILARITY: BELONGS TO CLASS-II AMINOACYL-TRNA SYNTHETASE FAMILY.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         120 RIGLSVSE 127
                                                                                                                                            Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
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                                                                                1 LSKRIGLSVSE 11
                                                                                                                                                                                                                                                                                        AE010151; AAL80394.1; -
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                                                                                                                        Similarity 6; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
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548 AA; 59555 MW; 485
                                                                                                                                                                                                       914 AA;
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                                                                                                                           Conservative
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                                                                                                                                                                                                       104906 MW; 467F593731BD8BC1 CRC64;
                                                                                                                                            73.5%;
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                                                                                                                                                                                                                                               Protein biosynthesis; Ligase; ATP-binding;
                                                                                                                           Pred. No. 31;
4; Mismatches
                                                                                                                                                                 Score 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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                                                                                                                                                                 DB 1; Length 914;
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    RESULT 5
CHPB_ECOLI
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EcoGene; EG12096; chpB.
InterPro; IPR003477; PemK
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use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for common entitles requires a linear statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                           "Mapping and disruption of the chiph locus in Escherichia coli.",
J. Bacteriol. 176:5861-5863(1994).
J. FUNCTION: MAY HE INVOLVED IN THE REGULATION OF CELL GROWTH.
AS A GROWTH INLIBITOR. BOTH CHES AND CHEB BIND TO THE PROMOTI
REGION OF THE CHESS OPERON TO AUTOREGULATE THEIR SYNTHESIS.
-!- SIMILARITY: BELONGS TO THE PEMK FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-FEB-1994 (Rel. 28, Creatcd)
01-FEB-1994 (Rel. 28, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
PemK-like protein 2.
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                                                                                                                                                                                                                                    entities requires a license agreement (See http://www.isb-sib.ch/announce/
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J. Bacteriol. 170:5901-5907(1988).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Cloning and characterization of the gene encoding inorganic pyrophosphatase of Escherichia coli K-12.";
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ĀZĪĒ_BACSU STANDARD; PRT; 157 AA
007920;
15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
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30-MAY-2000 (Rel. 39, Last annotation update)
Proline dehydrogenase transcriptional activator.
PUTR OR PF
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"Identification of Agrobacterium tumefaciens genes that direct the complete catabolism of octopine.";
J. Bacteriol. 178:1872-1880(1995).
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DNA-binding; Complete proteome.
SEQUENCE 116 AA; 12492 MW;
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Transcription regulation; DNA-binding; Activator; Plasmid DNA_BIND 29 48 H-T-H_MOTIF (POTENTIAL).
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Pfam; PF01037; ASNC_trans_reg; 1.
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SM00344; HTH_ASNC; 1.
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RA Kunst F., Ogasawara N., Moszer J., Albertini A.M., Alloni G.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Boriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Denizot F., Devine K.M., Dusterboft F., Cummings N.J., Daniel R.A.,
RA Denizot F., Devine K.M., Dusterboft A., Ehrlich S.D., Emmerson P.T.,
RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Funa S., Galizzi A., Galleron N.,
RA Ghim S.Y., Glaser P., Goifeau A., Golightly E.J., Grandi G.,
RA Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA Hibert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Guiseppi G., Kasahara Y., Klaerr-Hlanchard M., Klein C.,
RA Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,
RA Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,
RA Kobayashi Y., Medine A., Latdinols S., Lauber J., Lazarevic V.,
RA Kurita K., Lapidus A., Latdinols S., Lauber J., Lazarevic V.,
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Parro V., Pohl Y. M., Portetelle D., Horwollik S., Prescott A.M.,
Parro V., Pohl Y. M., Portetelle D., Horwollik S., Prescott A.M.,
Parro V., Pohl Y. M., Portetelle D., Horwollik S., Prescott A.M.,
Parro V., Pohl Y. M., Portetelle D., Horwollik S., Prescott A.M.,
Parro V., Pohl Y. M., Portetelle D., Horwollik S., Prescott A.M.,
Parro V., Pohl Y. M., Portetelle D., Horwollik S., Prescott A.M.,
Parro V., Pohl Y. M., Portetelle D., Horwollik S., Prescott A.M.,
Parro V., Pohl Y. M., Portetelle D., Horwollik S., Prescott A.M.,
Parro V., Pohl Y. M., Portetelle D., Horwollik S., Prescott A.M.,
Parro V., Pohl Y. M., Porter M., Parro V., Pohl Y. M., Portetelle D., Horwoll R., Parro V.,
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[3]
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Sorokin A., Tacconi E., Takagi T., Takahashi H., Takamaru K.,
Takeuchi M., Tanakoshi A., Tanaka T., Terpstra P., Tognoni A.,
Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M., Prescott A.M., Prescott B., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S., Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y., Sato T., Scanlan E., Schleich S., Schröeler R., Scottone F., Cohine B., Scottone F., Schleich S., Schröeler R., Scottone F., Schleich S., Schleich S., Schröeler R., Scottone F., Schleich S., S
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Belitsky B.R., Gustafsson M.C.U.,
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Like gene of Bacillus subtillis involved in branched-chain
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     Yano M., Horiuchi T.;
"A 718-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 12.7-28.0 min region on the linkage map.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P1949;
01-FBB-1991 (Rel. 17, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Leucine-responsive regulatory protein.
Leucine-responsive Resultation protein.
The area or LIVE OR THB OR OPPI OR B0889 OR Z1234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIINE-91250369; PubMed-2040596; Willins D.A., Ryan C., Platko J.V., Calvo J.M.; "Characterization of Irp, and Escherichia coli regulatory protein that mediates a global response to leucine."; J. Biol. Chem. 266:10768-10774(1991).
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SMART; SM00344; HTH_ASNC, 1.
PROSITE; PS00519; HTH_ASNC_FAMILY; 1.
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InterPro; IPR000485; ASNC_trans_reg.
Pfam; PF01037; ASNC_trans_reg; 1.
                                                                                                                                                                                                                                          "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                               SPECIES=E.coli; STRAIN=K12 / MG1655; MEDLINE-97426617; PubMed-9278503;
                                                                                                                                                                                                                                                                                                                                                                                                                Ito K., Kawakami K., Submitted (MAY-1992)
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Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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                                                                                                                                                                          MEDLINE=97061202; PubMed=8905232;
                                                                                                                                                                                              SPECIES=E.coli;
                                                                                                                                                                                                            SEQUENCE FROM N.A.
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   SPECIES-E.coli;
MEDLINE-92104949; PubMed-1729203;
Haney S.A., Platko J.V., Oxender D.L., Calvo J.M.;
"Lrp, a leucine-responsive protein, regulates branched-chain acid transport genes in Escherichia coli.";
J. Bacteriol. 174:108-115(1992).
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                 EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Platko J.V., Willins D.A., Calvo J.M.;
"The ilvIH operon of Escherichia coli is positively regulated.
J. Bacteriol. 172:4563-4570(1990).
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                                                                                  entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                      use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entrepean Bioinformatics Institute. There are no restitute European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                             "The leucine-responsive regulatory protein: more than a regulator?"; Trends Biochem. Sci. 18:260-263(1993).
                                                                                                                                                                                                                                                                                                                                                                                                 D'Ari R., Lin R.T., Newman E.B.;
                                                                                                                                                                                                                                                                                                                                                                                                                 MEDITINE-94025042; FubMed-8212136;
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MEDLINE-90330567;
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MEDLINE-21156231;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     SPECIES-E.coli;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       REVIEW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PARTIAL SEQUENCE OF N-TERMINUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SPECIES=E.aerogenes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteriol.
                                                                                                                                                                                                                         GENES.
SUBUNIT: HOMODIMER.
SIMILARITY: BELONGS TO THE ASNC FAMILY OF TRANSCRIPTIONAL
                                                                                                                                                                                                                                                                                           FUNCTION: MEDIATES A GLOBAL RESPONSE TO LEUCINE. EXOGENOUS LEUCINE AFFECTS THE EXPRESSION OF A NUMBER OF DIFFERENCY OPERONS; LRP MEDIATES THIS EFFECT FOR AT LEAST SOME OF THESE OPERONS. FOR EXAMPLE IT IS REGULATOR OF THE BRANCHED-CHAIN AMINO ACID TRANSPORT
M35869; AAA24089.1; -. D11105; BAA01880.1; -. AE000191; AAC73975.1; -. гол726 наА35614.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R.A., Blattner F.R.; me sequence of enterchaemorrhagic Escherichia coli 0157:H7.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             177:1624-1626(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=0157:H7 / EDL933 / ATCC 700927;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=0157:H7 / RIMD 0509952;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PubMed-11258796;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PubMed-2115869;
                                                                                                                                 There are no rest
                                                                                                                      Usage
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                                                                                                                      γď
                                                                                                                                                        restrictions on
                                                                                                                        and
                                                                                                                                                                        EMBL outstation
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a collaboration

for

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ALD DESCRIPTION OF COLOR COLOR
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Best Local S
Matches 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LRP_KLEPN
P37424;
01-OCT-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; D90727; BAA35621.1; -. EMBL; AE005278; AA355376.1; -. EMBL; AP005253; BAB34397.1; -. EMBL; U02272; AAA75439.1; -. PIR; JH0412; RGECLR.
DNA-BIND 30 49 H-T-H MOTIF (POTENTIAL).
                                                                                                                           InterPro; IPR000485; ASNC_trans_reg.
Pfam; PF01037; ASNC_trans_reg; 1.
PRINTS; PR00033; HTHASNC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                microorganisms.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIINE-95189743; PubMed-7883720; Friedberg D., Platko J.V., Tyler B., Calvo J.M.; The amino acid sequence of Lrp is highly conserved in four enteric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ECO2DBASE; I015.1; 6TH EDITION EcoGene; EG10547; lrp.
                                                                        SMART; SM00344; HTH_ASNC; 1.
PROSITE; PS00519; HTH_ASNC_FAMILY; 1.
                                                                                                                                                                                                                                                                                                              modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                         the European Bioinformatics Institute. Thuse by non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     <del>-</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        J. Bacteriol. 177:1624-1626(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00519; HTH_ASNC_FAMILY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam;
                                                                                                                                                                                                           EMBL; U02274; AAA75465.1; -.
                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                      entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=573;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Klebsiella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Klebsiella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Leucine-responsive regulatory protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-DEC-1998
15-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBUNIT: HOMODIMER. SIMILARITY: BELONGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AFFECTS THE EXPRESSION OF A NUMBER OF DIFFERENT OPERONS; LRP MEDIATES THIS EFFECT FOR AT LEAST SOME OF THESE OPERONS. FOR EXAMPLE IT IS REGULATOR OF THE BRANCHED-CHAIN AMINO ACID TRANSPORT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION: MEDIATES A GLOBAL RESPONSE TO LEUCINE. EXOGENOUS LEUCINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGULATORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pro; IPR000485; ASNC_trans_reg.
PF01037; ASNC_trans_reg; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SM00344; HTH_ASNC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          . Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PR00033;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   163 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Rel. 37, Last*sequence up
(Rel. 37, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (Rel. 30, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HTHASNC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18755 MW;
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87.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TO THE ASNC FAMILY OF TRANSCRIPTIONAL
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Pred. No. 8.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                H-T-H MOTIF (POTENTIAL).
D -> E (IN LRP-1 MUTANT).
1, B0083495B8F7B255 CRC64;
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                                                                                                                                                                                                                                                                                                                                         There are no restrictions on ng as its content is in no
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                                                                                                                                                                                                                                                                                                           Usage
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Best Local Similarity
Matches 7; Conserv
 EMBL;
EMBL;
                                                                                                                                                                                                                                                    Janes B.K., Bender K.A.;

"Two roles for the leucine-responsive regulatory protein in expression of the alanine catabolic operon (dadAB) in Klebsiella aerogenes.";

J. Bacteriol. 181:1054-1058(1999).

-i- FUNCTION: MEDIATES A GLOBAL RESPONSE TO LEUCINE. EXOGENOUS LEUCINE AFFECTS THE EXPRESSION OF A NUMBER OF DIFFERENT OPERONS; LRP MEDIATES THIS EXPRESSION OF A NUMBER OF THESE OPERONS; LRP MEDIATES THIS EXPRESSION OF THE BRANCHED-CHAIN AMINO ACID TRANSPORTED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Dur., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Kyan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           p37403; 087635;
01-0CT-1994 (Rel. 30, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SPECIES=S.typhimurium;
MEDLINE=95189743; PubMed=7883720;
                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPECIES-S.typhimurium; STRA
MEDLINE-21534948; PubMed-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        J. Bacteriol. 177:1624-1626(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Friedberg D., Platko J.V., Tyler B.
"The amino acid sequence of Lrp is
microorganisms.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Leucine-responsive regulatory protein. LRP OR STM0959.
                                                             use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                   SPECIES-K.aerogenes; STRAIN-W70; MEDLINE-99121052; PubMed-9922277;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Complete genome sequence of LT2.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 413:852-856(2001).
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                                                                                                                                                                                                      SUBUNIT: HOMODIMER.
SIMILARITY: BELONGS
                                                                                                                                                                                          REGULATORS.
                                                                                                                                                                                                                                          GENES
U02273; AAA75467.1; -. AE008741; AAL19894.1; -. AF090144; AAD12584.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-LT2 / SGSC1412 / ATCC 700720;
ed-11677609;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and
                                                                                                                                                                                                           TO THE

    Mismatches

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Pred. No. 8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Salmonella enterica serovar Typhimurium
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                                                                                                                                                                                                           ASNC
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                                                                                                                                                                                                           FAMILY OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  163
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                                                                                                                                                                                                           TRANSCRIPTIONAL
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RESULT 15
YGJ3 YEAST
ID YGJ3 YEAST
AC P53148;
DT 01-CCT-1996
DT 01-CCT-1996
DT 01-NOV-1997
DE HYDOCHETICAL
GN YGL093W.
OS SACCHAROMYCE
OC EUKARYOTA;
IOC SACCHAROMYCE
OC SACCHAROMYCE
OC SACCHAROMYCE
OX NCBI_TAXID=4
RN [1]
RP SEQUENCE FR
RC STRAIN=2744
RA Rieger M., 11
RAT Chromosome N
RL Yeast 13:10-
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Search completed: January 15, 2003, 11:21:36 Job time: 9.28572 secs
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announcc/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P53148;
01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-NOY-1997 (Rel. 35, Last annotation update)
Hypothetical 104.8 kDa protein in PAN2-NUP145
YGL093W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TIGREAMS; TIGR01177; TIGR01177; 1.

PROSITE; PS01261; UPF0020; 1.

Hypothetical protein; Complete proteome.

SEQUENCE 320 AA; 36673 MW; A879F320AA8CD637 CRC64;
                                                                                                                                                                                                                                                                                                                                                                    Hypothetical protein. SEQUENCE 917 AA; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=97435481; pubMed=9290212; Rieger M., Brueckner M., Schaefer M., Mueller-Auer S.; "Sequence analysis of 203 kilobases from Saccharomyces cerevisiae chromosome VII."; Yeast 13:1077-1090(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Pungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                  SGD; S0003061; SPC105.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; Z72615; CAA96799.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=4932;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                           594 LAENLNTLKRE 604
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                                                                                                                                                                                                                                            Similarity 6; Conserv
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IPR000051; SAM_bind.
IPR0004114; THUMP_dom.
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                                                                                                                                                                                                                                                                                                                                                                           104825 MW;
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54.5%;
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Pred. No. 40;
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SUMMARIES

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Database :
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-Q=/cgn2_1/USPTO_Spot/US09823649/runat_14012003_151001_29119/app_query.fasta_1.1393
-DB-_UGenceseq_101002 -QFMT=fastap -SUFFIX=rng -MINNATCH=0.1 -LOOPCL=0
-DOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE-pct -THR_MIX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEARSIZE=500 -MINLEN=0 -MAXILEN=2000000000
-USER=US09823649_@CGN_1_1_0_@runat_14012003_151001_29119 -NCPU=6 -ICPU=3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -MAIT -LONGLOG -DEV_TIMEOUT=120
-WARM_TIMEOUT=30 -THERADS=1 -XOADD=10 -XGAPEXT=0.5 -FGAPEXT=7
-YGAPPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Run on:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Command line parameters:
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49
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1: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:*
2: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Xgapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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                                                                                                                                       /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT:*
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/SIDS2/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

RES AAQ AC AC AC AC AC XX DE XX XX XX XX XX XX XX XX XX XX XX XX XX	0 0	0 0000000000000000	Res
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24334 24334 2CT-1 ant t ant t armosi	ധ ധ ധ ധ ധ ധ ധ ധ ധ ധ ധ ത ത ത ത ത ത ത ത ത ത		Score
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d A A T	20 21 21 21 20 20 20	113 113 113 113 113 113 113 113 113 113	DB
BP. merase pTAFI285. lification; SSR; seque	AAV86138 AAZ42996 AAS65454 AAC77621 AAV65278 AAV65278 AAV65288 AAS6151 AAX39656 AAS9656 AAS9656 AAS967801 AAZ00464	AAQ2433 AAQ24333 AAQ24333 AAQ24333 AAQ24339 AAQ24339 AAQ24339 AAQ28936 AAQ23917 AAQ23917 AAQ23917 AAA235616 AAA23666 AAA3666 AA	ID
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                                                                                                                                                                                                                                                                                                                             Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                   Alignment Scores:
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28-SEP-1990;
28-SEP-1990;
                                                                                                                                                                                                                     1369 CTTTCAAAGAGAATTGGTCTTAGTGTTTCAGAG 1401
                                                                                                                                                                                                                                                                                                                                                                                                                                                 polymerases are useful in many recombinant DNA techniques, esp. nucleic acid amplification by PCR, self-sustained sequence replication (SSR) and high temp. DNA sequencing. The absence of 5'-3' nuclease activity may facilitate higher sensitivity allelic discrimination in a combined polymerase ligase chain reaction (PLCR) assay. An enhanced amt. of 5'-3' exonuclease activity may be desirable in enzymes used in homogeneous assays for the amplification and detection of a target nucleic acid sequence. Mutation of the DNA encoding particular regions of the enzymes can be used to prepare a range of recombinant proteins having 5'-3' exonuclease activity to a complete lack of activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Thermostable DNA polymerases with altered 5'-3' exo nuc activity - having conserved regions mutated or deleted, in e.g. PCR, sequencing and detection assays
Key
                                                                                Mutant thermostable DNA polymerase pTAFd2-203.
                                                                                                                                      AAQ24333;
                                                                                                                                                                AAQ24333 standard; DNA; 2073 BP
                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The sequence is that of Thermosipho africanus polymerase DNA which has been mutated. The mutation designated pTAFIZ85 causes the polymerase enzyme produced to exhibit a different ant. of 5'-3' exonuclease activity than the native enzyme. Thermostable DNA
                           Thermosipho africanus
                                                                                                            22-OCT-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 11; Page 59; 185pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Abramson RD,
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                                                      5'-3'; exonuclease; PCR;
                                                                                                                                                                                                                                                                                                                                                                       No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9206200-A
                                                                                                                                                                                                                                 1 LeuSerLysArgIleGlyLeuSerValSerGlu 11
                                                                                                                                                                                                                                                                                                                                                                                                                                        also AAQ23993-Q24013, AAQ24320-36 and AAQ24343-60.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1992-150885/18.
                                                                                                         (first entry)
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90US-0590466.
90US-0590490.
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  Location/Qualifiers
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100.00%
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                                                                                                                                                                                                                                                                                                                                                                                                               206
                                                      amplification; SSR; sequencing; PLCR;
                                                                                                                                                                                                                                                                                                                                                                                                             C; 352 G;
                                                                                                                                                                                                                                                                                                                                                       Length:
Matches:
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                                                                                                                                                                                                                                                                                                                            Conservative: Mismatches:
                                                                                                                                                                                                                                                                                                                  Indels:
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                                                      SS
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  XXXXXXXXX
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                                                                                                                                                 RESULT 3
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                                                                                                                                      AAQ24332
                                                                                                                                                                                                                                                                       Query Match:
                                                                                                                                                                                                                                                                                                                             Pred. No.:
                                                                                                                                                                                                                                                                                                                  Score:
                                                                                                                                                                             1612
          5'-3'; exonuclease; PCR; amplification; SSR; sequencing; PLCR; ss.
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US-09-823-649A-6 (1-11) x AAQ24333 (1-2073)
                                                                                                                                                                                                                                                                                       Best Local Similarity:
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                                                                                                                                                                                                                                                                                                       Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-SEP-1990;
28-SEP-1990;
28-SEP-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                         nucleic acid amplification by PCR, self-sustained sequence replication (SSR) and high temp. DNA sequencing. The absence of 5'-3' nuclease activity may facilitate higher sensitivity allelic discrimination in a combined polymerase ligase chain reaction (PLCR) assay. An enhanced amt. of 5'-3' exonuclease activity may be desirable in enzymes used in homogeneous assays for the amplification and detection of a target nucleic acid sequence. Mutation of the DNA encoding particular regions of the enzymes can be used to prepare a range of recombinant proteins having 5'-3' exonuclease activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The sequence is that of Thermosipho africanus polymerase DNA which has been mutated. The mutation designated pTARG2-203 causes the polymerase enzyme produced to exhibit a different amt. of 5'-3' exonuclease activity than the native enzyme. Thermostable DNA polymerases are useful in many recombinant DNA techniques, esp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Thermostable DNA polymerases with altered 5'-3' exo nuclease activity - having conserved regions mutated or deleted, for use in e.g. PCR, sequencing and detection assays
                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2073 BP; 820 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 11; Page 59; 185pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       old_sequence
Mutant thermostable DNA polymerase pTAF11.
                                 22-OCT-1992
                                                                                              AAQ24332 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                  to a complete lack of activity.
See also AAQ23993-Q24013, AAQ24320-36 and AAQ24343-60.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P-PSDB; AAR23173.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-SEP-1991;
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                                                                                                                                                                           1 LeuSerLysArgIleGlyLeuSerValSerGlu 11
                                                                                                                                                            CTTTCAAAGAGAATTGGTCTTAGTGTTTCAGAG 1644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1992-150885/18.
                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gelfand DH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              900S-0590466
900S-0590490
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                                                                                                                                                                                                                                                                                                                                                                                  226 C; 399 G;
                                                                                                ВP
                                                                                                                                                                                                                                                     Gaps:
                                                                                                                                                                                                                                                                                       Mismatches:
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old_sequence

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US-09-823-649A-6 (1-11) x AAQ24332 (1-2265)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nucleic acid amplification by PCR, self-sustained sequence replication (SSR) and high temp. DNA sequencing. The absence of feplication (SSR) and high temp. DNA sequencing. The absence of 5'-3' nuclease activity may facilitate higher sensitivity allelic discrimination in a combined polymerase ligase chain reaction (PLCR) assay. An enhanced and: of 5'-3' exonuclease activity may be desirable in enzymes used in homogeneous assays for the amplification and detection of a target nucleic acid sequence. Mutation of the DNA encoding particular regions of the enzymes can be used to prepare a range of recombinant proteins having 5'-3' exonuclease activity to a complete lack of activity.
Mutant thermostable DNA polymerase pTAF09
                                                                                                                AAQ24331 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       exonuclease activity than the native enzyme. polymerases are useful in many recombinant DI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The sequence is that of Thermosipho africanus polymerase DNA which has been mutated. The mutation designated pTAF11 causes the polymerase enzyme produced to exhibit a different amt. of 5'-3'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 11; Page 59; 185pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         See also AAQ23993-Q24013, AAQ24320-36 and AAQ24343-60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              in e.g. PCR, sequencing and detection assays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     activity - having conserved regions mutated or deleted, for use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Thermostable DNA polymerases with altered 5'-3' exo nuclease
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                                                                                                                                                                                                                1 LeuSerLysArgIleGlyLeuSerValSerGlu 11
                                                                                                                                                                                           CTTTCAAAGAGAATTGGTCTTAGTGTTTCAGAG 1836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1992-150885/18.
                                  (first entry)
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90US-0590466.
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sequence."
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Indels:
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AAQ28937
ID AAQ2
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                                                                                                                                                                                                       US-09-823-649A-6 (1-11) x AAQ24331 (1-2403)
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28-SEP-1990;
28-SEP-1990;
                AAQ28937;
                                                                                                                                1942 CTTTCAAAGAGAATTGGTCTTAGTGTTTCAGAG 1974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               detection of a target nucleic acid sequence. Mutation of the DNA encoding particular regions of the enzymes can be used to prepare a range of recombinant proteins having 5'-3' exonuclease activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   polymerases are useful in many recombinant DNA techniques, esp. nucleic acid amplification by PCR, self-sustained sequence replication (SSR) and high temp. DNA sequencing. The absence of 5'-3' nuclease activity may facilitate higher sensitivity allelic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Thermostable DNA polymerases with altered 5'-3' exo nuclease activity - having conserved regions mutated or deleted, for in e.g. PCR, sequencing and detection assays
                                                   AAQ28937 standard; DNA; 2568
                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2403 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            discrimination in a combined polymerase ligase chain reaction (PLCR) assay. An enhanced amt. of 5'-3' exonuclease activity may be desirable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The sequence is that of Thermosipho africanus polymerase DNA which has been mutated. The mutation designated praprograms the polymerase enzyme produced to exhibit a different amt. of 5′-3′ exonuclease activity than the native enzyme. Thermostable DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 11; Page 59; 185pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P-PSDB; AAR23171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                to a complete lack of activity.
See also MAQ2:993 Q24013, AAQ24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            in enzymes used in homogeneous assays for the amplification and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Abramson RD,
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90US-0590466.
90US-0590490.
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                                                                                                                                                                                                                                                                                                                                                                                                                                              AAQ24320-36 and AAQ24343-60
                                                                                                                                                                                                                                                Gaps:
                                                                                                                                                                                                                                                                                         Mismatches:
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P-PSDB; AAR23172.

Abramson RD,

28-SEP-1990; 28-SEP-1990; 28-SEP-1990;

30-SEP-1991;

WO9206200-A

RESULT 4
AAQ24331
ID AAQ2
XX
AC AAQ2
XC AAQ2
XX
DT 22-0
XX
DE Muta

22-OCT-1992

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Db

1804

Best Local Similarity: Query Match:

Percent Similarity:

Alignment Scores:

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Sequence 2265 BP;

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Alignment
Pred. No.:
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Best Local Similarity:
                                                                                                                                                                                                                                                                 2107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The sequence coding for a thermostable DNA polymerase was isolated from chromosomal DNA of Thermosipho afficanus (Taf). The polymerase (see AAR23122) has 5'.3' Exonuclease activity. Deletion of codon 1-37 results in a DNA polymerase which lacks the 5'-3' exonuclease activity. See AAQ23917 for the wild-type Taf Pol I gene and AAQ28936 for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-SEP-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-APR-1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Encodes Taf DNA polymerase I lacking 5'-3' exonuclease activity.
                                                 old_sequence
                                                                                                              5'-3';
                                                                                                                                   Mutant thermostable DNA polymerase pTAFd2-37
                                                                                                                                                                                                                                                                                                                                                                                                        No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2568 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 21; Page 70; 80pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Thermostable DNA polymerase from Thermosipho africanus - prepd. by purificm. from cells or by expression of Taf polymerase gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P-PSDB; AAR23122.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   thermophilic bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Thermostability; PCR; polymerase chain reaction;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27-OCT-1992
                                                                                     Thermosipho africanus
                                                                                                                                                               22-0CT-1992
                                                                                                                                                                                       AAQ24330;
                                                                                                                                                                                                               AAQ24330 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   another preferred mutant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   in
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                                                                                                                                                                                                                                                                 CTTTCAAAGAGAATTGGTCTTAGTGTTTCAGAG 2139
                                                                                                                                                                                                                                                                                                                                                                                                                    Scores:
                                                                                                            exonuclease; PCR; amplification; SSR; sequencing;
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                                                           Location/Qualifiers
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                          "nucleotides 4-111
                                                                                                                                                                                                                2571 BP
           sequence."
                                                                                                                                                                                                                                                                                                                                                                                                                                             278
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                                                                                                                                                                                                                                                                                                                  (1-2568)
                                                                                                                                                                                                                                                                                                                                                                                                                                           C; 494 G;
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                          deleted from the native
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                                                                                                                                                                                       AAQ24329
                                                                                                                                                                                                    RESULT 7
                                                                                                                                                                                                                                                                                                                 Query Match:
             old_sequence
                          Key
                                                                          5'-3';
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-SEP-1990;
28-SEP-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-SEP-1991;
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                                                                                                                          22-OCT-1992
                                                                                                                                                  AAQ24329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (CETU ) CETUS
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Best Local Similarity:
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                                                                                                                                                                                                                                                           2110 CTTTCAAAGAGAATTGGTCTTAGTGTTTCAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          in enzymes used in homogeneous assays for the amplification and detection of a target nucleic acid sequence. Mutation of the DNA encoding particular regions of the enzymes can be used to prepare a range of recombinant proteins having 5'-3' exonuclease activity to a complete lack of activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       replication (SSR) and high temp. DNA sequencing. The absence of 5'-3' nuclease activity may facilitate higher sensitivity alleic discrimination in a combined polymerase ligase chain reaction (PICR) assay. An enhanced amt. of 5'-3' exonuclease activity may be desirable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           activity - having conserved regions mutated or deleted, for use in e.g. PCR, sequencing and detection assays {\sf PCR}
                                                                                                                                                                                                  AAQ24329 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nucleic acid amplification by PCR, self-sustained sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  exonuclease activity than the native enzyme. polymerases are useful in many recombinant D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The sequence is that of Thermosipho africanus polymerase DNA which has been mutated. The mutation designated pTAFd2-37 causes the polymerase enzyme produced to exhibit a different amt. of 5'-3'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 11; Page 59; 185pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W09206200-A.
                                                                                                   Mutant thermostable DNA polymerase from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2571 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Thermostable DNA polymerases with altered 5'-3' exo nuclease
                                            Thermus thermophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             See also AAQ23993-Q24013, AAQ24320~36 and AAQ24343-60.
                                                                                                                                                                                                                                                                                          1 LeuSerLysArgIleGlyLeuSerValSerGlu 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1992-150885/18
                                                                       exonuclease;
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                                                                                                                                    (first entry)
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90US-0590466.
90US-0590490.
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Location/Qualifiers
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                                                                                                                                                                                                  2679
                                                                       amplification;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               494 G;
                                                                                                                                                                                                                                                                                                                                                                     Mismatches:
Indels:
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                                                                                                                                                                                                                                                             2142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 785
                                                                       SSR; sequencing; PLCR;
                                                                                                      Thermosipho africanus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  e. Thermostable DNA DNA techniques, esp.
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Query Match:
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Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity:
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                                                                                                                                                                                                                        native enzyme. Thermostable DNA polymerases are useful in many recombinant DNA techniques, esp. nucleic acid amplification by PCR, self-sustained sequence replication (SSR) and high temp. DNA sequencing. The absence of 5'-3' nuclease activity may facilitate higher sensitivity allelic discrimination in a combined polymerase ligase chain reaction (PLCR) assay. An enhanced amt. of 5'-3' exonuclease activity may be desirable in enzymes used in homogeneous assays for the amplification and detection of a target nucleic acid sequence. Mutation of the DNA encoding particular regions of the enzymes can be used to prepare a range of recombinant proteins having 5'-3' exonuclease activity to a complete lack of activity.
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28-SEP-1990;
28-SEP-1990;
               Thermostability; PCR; polymerase chain reaction; thermophilic bacteria; Taf Pol I; mutant; ss.
                                                                                               27-OCT-1992
                                                                                                                              AAQ28936;
                                                             Encodes Asp37 Taf DNA polymerase I lacking 5'-3' exonuclease activity
                                                                                                                                                           AAQ28936 standard; DNA; 2679 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2679 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The sequence is that of Thermosipho africanus polymerase DNA which been mutated. The mutation causes the polymerase enzyme produced to exhibit a different amt. of 5'-3' exonuclease activity than the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The sequence is that of Thermosipho
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 11; Page 59; 185pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      activity - having conserved regions mutated or deleted, for use in e.g. PCR, sequencing and detection assays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Thermostable DNA polymerases with altered 5'-3' exo nuclease
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                                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 1045 A; 295 C; 515 G; 824 T; 0 other;
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Indels:
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RESULT 9
AAQ23917
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
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W09206202-A
                                                             CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The sequence coding for a thermostable DNA polymerase was isolated from chromosomal DNA of Thermosipho africanus (Taf). The polymerase (see AAR23122) has 5'-3' exonuclease activity. Mutation of the codon specifying Gly at position 37 (i.e. GGA) to an Asp codon results in a DNA polymerase which lacks the 5'-3' exonuclease activity. See AAQ23917 for the wild-type Taf Pol I gene and AAQ28937 for another
                                                                                                          Thermosipho africanus
                                                                                                                                   Thermostability; PCR; polymerase chain reaction; thermophilic bacteria; Taf Pol I; ss.
                                                                                                                                                                                  Taf DNA polymerase I coding sequence
                                                                                                                                                                                                                   27-OCT-1992 (first entry)
                                                                                                                                                                                                                                                     AAQ23917;
                                                                                                                                                                                                                                                                                    AAQ23917 standard; DNA; 4286
                                                                                                                                                                                                                                                                                                                                             2218 CTTTCAAAGAGAATTGGTCTTAGTGTTTCAGAG 2250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2679 BP; 1045 A; 295 C;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Thermostable DNA polymerase from Thermosipho africanus - prepd
by purificn. from cells or by expression of Taf polymerase gen
in host cells
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           preferred mutant.
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                                                                                                                                                                                                                                                                                                                                                                1 LeuSerlysArg[|eGlyLeuSerValSerClu 11
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                         /product= Polymerase_I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         chromosomal DNA from Thermosipho africanus (Taf) was PCR-amplified with degenerate primers corresponding to the amino acid sequences of conserved regions of known thermostable polymerases. When specific PCR products of a similar size to the product generated using Tag chromosomal DNA were produced, the PCR fragments were cloned and sequenced. Fragments with sequences which encoded regions of amino acid homology to known thermostable polymerases were identified. The cloned PCR products were used as probes to screen a genomic Southern blot. The full-length Taf coding sequence was then compiled from various clones. See also AAQ23918-Q23961.
                                                                                                                                                                                                                          Mycoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2515
                                                                                                                                                                                                                                                            megabase shotgun sequencing method; open reading frame; ORF;
                                                                                                                                                                                                                                                                                                                  Mycoplasma
                                                                                                                                                                                                                                                                                                                                                        27-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                          AAT58840
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Thermostable DNA polymerase by purificn. from cells or h in host cells
                                                                                                                                                                                                                                                                                                                                                                                                                             AAT58840 standard;
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                                                                                                                                                                                                                                                                             genitalium; DNAA; DNA gyrase; origin of replication;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTTTCAAAGAGAATTGGTCTTAGTGTTTCAGAG 2547
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8; Page 6; 80pp; English
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                                                                                                                                                                                                                          genitalium.
                                                                                                                                                                                                                                                                                                                genitalium genome
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                                                       "Previously identified as MORF-20076, the encoded protein shows 27.59 percentage identity to thymidylate kinase (CDC8) from Saccharomyces cerevisiae"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 rase from Thermosipho africanus - pı
or by expression of Taf polymerase
       MG009
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                                                                                                                                  MG006
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Conservative:
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                            from B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Previously identified as MORF-19826 and MORF-20093, the encoded protein shows 46.84 percentage identity to GTP-binding protein from E. coli"
                                                                    "Previously identified as MORF-20101, the encoded protein shows 48.13 percentage identity to thymidylate kinase (tdk) from B. subtilis"
                                                                                                                                                                                                                                                                                                                             "Previously identified as MORF-20099, the encoded protein shows 26.82 percentage identity to ATP-dependent nuclease (addA) from B. subtilis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Previously identified as MORF-20080, the encoded protein shows 31.50 percentage identity to the ribosomal protein S6 modification protein (rimK) from Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                *Previously identified as MORF-19823, MORF-20080 and MORF-20081, the encoded protein shows 33.04 percentage identity to 5,10-methylene-tetra-
"Previously identified as MORF-20102, the
                                                                                                                                                                                                                                   "Previously identified as MORF-20100, the encoded protein shows 35.90 percentage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Previously identified as MORF-20092, the encoded protein shows 45.96 percentage identity to fructose-bisphosphate aldolase (tsr) from B. subtilis"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Previously identified
                     MG035
                                                                                                                                                 MG034
                                                                                                                                                                                     identity to glycerol uptake facilitator (glpF) from B. subtilis nt (39871 when to the control of the control of
                                                                                                                                                                                                                                                                           MG033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 encoded protein shows 32.23 percentage identity to transport ATP-binding protein (msbA) from E. coli"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MG010
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coli*

	CDS	CDS		CDS		CDS		CDS	CDS	CES		CDS	CDS	CDS
/label= MG050 /note= "Previously identified as MORF-20117, the encoded protein shows 83.03 percentage	L71 ⇒	" ;n	/note= "Previously identified as MORF-19834, MORF-20114 and MORF-20115, the encoded protein shows 43.02 percentage identity to signal recognition particle protein (ffh) from B.	from Pasteurella haemolytica" complement (5697058310) /*tag= t /*tag= t //aha = MG048	/label MG046 /label MG046 /note- "Previously identified as MORF-20112, the encoded protein shows 36.60 percentage identity to sialogiveoprotesse (GCD)	system permease protein C (potC) from E. coli ⁿ 54658.55605	/ Tubel MG044 //abel MG044 //abel MG044 /note= "Previously identified as MORF-20111, the encoded protein shows 29,45 percentage	.53220	(potA) from E. coli" 51525_5282 /*tag= q /label= MG043 /note= "Previously identified as MORP-20110, the encoded protein shows 26.51 percentage identity to spermidine/putrescine transport everter permanent promises and transport everter permanent permanent permanent.	/*tag- p /*tag- p /label= MG042 /note= "previously identified as MORF-19832 and /note= "previously identified as MORF-19832 and /MORF-20108, the encoded protein shows 41.92 percentage identity to spermidine/ putrescine transport ATP-binding protein	<pre>/*tag= 0 /*label= MG041 /note= "The encoded protein shows 48.86 percentage identity to phosphohistidinoprotein-hexose phosphotransferase (ptsH) from Mycoplasma capricolum"</pre>	/ Label MG039 /label MG039 /note= "Previously identified as MORF-19831 and MORF-20106, the encoded protein shows 43.20 percentage identity to glycerol-3-phosphate dehydrogenase (GUT2) from S. cerevisiae" 4937749643	₹ ."	<pre>encoded protein shows 30.71 percentage identity to histidy1-tRNA synthetase (hisS) from Mycobacterium leprae" complement (4475146277)</pre>
(UYCH-) UNIV CHI	18-MAR-1999; 01-APR-1999; 18-MAY-1999; 13-SEP-1999; 17-SEP-1999;	PD 21-SEP-2000. XX XX PF 17-MAR-2000; 2000WO-US07392.	thaliana.	Arabidopsis thali	AAF22306; 20-MAR-2001 (first entry)	RESULT 11 AAF22306/c ID AAF23306 Standard: DNA: 163319 BP	Qy 1 LeuSerLysArg1leGlyLeuSerValSer 10 	US-09-823-649A-6 (1-11) x AAT58840 (1-580073)	Alignment Scores: Pred. No.: Score: 42.00 Percent Similarity: 100.008 Pest Local Similarity: Query Match: 85.718 DB: Local Similarity: 65.718 Caps: Ca	FT /label= MG070 FT /label= MG070 FT /note= "Previously identified as MORF-20136, the encoded protein shows 34.8 percentage identity to ribosomal protein S2 (rpS2) FT from Spirulina plantensis"	. #	/note= /n	FT /note= "Previously identified as MORF-20122, the encoded protein shows 30.25 percent remains to the protein disclosed in identity to the protein disclosed in GB:026185_99 from B. subtilis" FT CDS complement (6571366249) FT /tag= x /*tag= x	FT identity to deoxyribose-phosphate aldolase FT (deoC) from Mycoplasma pneumoniae" FT CDS complement (6489865731) FT /*tag= w

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Pred. No.:
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26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
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                                                                                                                                                                                         Penn
            The invention
                                                 Claim 1; SEQ ID NO 72; 639pp + sequence listing; English
                                                                                      analyzing
                                                                                                               Human
                                                                                                                                                    WPI;
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04-OCT-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Recombinant DNA construct comprising a plant centromere, useful for producing stably inherited michrosomes which can serve as vectors \mathbf{f} the construction of transgenic plant and animal cells -
                                                                                                                                                                                                                                                                                                           21-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                               30-JAN-2001; 2001WO-US00669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABA51767 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-587529/55
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                                                                                                                                                                                         SG,
                                                                                      genome-derived single exon nucleic acid probes useful for zing gene expression in human fetal liver -
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                                                                                                                                                                                                                               MOLECULAR DYNAMICS INC
                                                                                                                                                                                       Hanzel DK,
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2000US-0207456.
2000US-0608408.
2000US-0632366.
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2000US-0236359.
2000US-0236359.
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            relates
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          to a single exon nucleic acid probe for
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                                                                                                                                                                                         Rank DR;
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                                                                                                                                                                                                                                                                                                                                                                                                    03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
measuring human gene expression in a sample derived from human heart. The present sequence is one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular system
                                                                                                                       The present
                                                                                                                                                              Claim 1;
                                                                                                                                                                                                                                                                                                       Penn
                                                                                                                                                                                                                                                                                                                                                                                 04-OCT-2000;
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30-JUN-2000;
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                                                                                                                                                                                                                        exon
                                                                                                                                                              SEQ
                                                                                                                       invention relates to single exon nucleic acid probes for
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a single exon nucleic acid
                                                                                  WPI; 2001-488899/53
                                                                                                                                                                                                                                                                                                       30-JAN-2001; 2001WO-US00666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABA21596 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Note: The sequence data for this patent did not form printed specification, but was obtained in electronic from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         probe of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 TTAACAAAACGGGTAGGCTCTTCAGTTTCAGAG 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 LeuSerLysArgIleGlyLeuSerValSerGlu 11
                                                                                                                                             MOLECULAR DYNAMICS
                                                                                                              Hanzel DK,
                                                  nucleic
                                                                                                                                                                                         2000US-0632366.
2000US-0234687.
2000US-0236359.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (1-11)
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                                                                                                                                                                                                                                       2000US-0207456
2000US-0608408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                          2000GB-0024263.
                                                                                                                                                                                                                                                                        2000US-0180312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene expression analysis in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            117 A;
    62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA; 471 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 x ABA51767 (1-471)
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72.73%
79.59%
                                             acid probes
                                                                                                              Chen W, Rank DR;
530pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             104
                                             for analyzing gene expression
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Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length: Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          156 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       did not form part of
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Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
                                                                                                                                                 probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Single
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       Sequence 471 BP; 117 A; 94 C; 104 G; 156 T; 0 other;
                                                                                                                   epilepsy and
                                                                                                                                                                                                                                                                                          The present invention provides a number of single exon nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    04-OCT-2000;
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27-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      epilepsy; cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human brain expressed single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 471
                                                                                                                                                                                                                                                                                                                                                             Example 4; SEQ ID NO: 66; 650pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (MOLE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-JAN-2001; 2001WO-US00667
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LeuSerLysArgIleGlyLeuSerValSerGlu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     exon nucleic acid probes for analyzing gene expression in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; 2000US-0207456.
; 2000US-0608408.
; 2000US-0632366.
; 2000US-0234687.
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                                                                                                                   cancers.
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                                                                                                                   The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ВP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches:
Indels:
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                                                                                                               is one of the probes of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          471
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                                                                                                                                                                                                                                                                                              acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             human
                                                                                                                                  Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                  \begin{array}{l} \textbf{S} \times \textbf{C} \times \textbf
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Best Local Similarity:
US-09-823-649A-6 (1-11) x AAK25512 (1-471)
                                                                                                               Query Match:
                                                                                                                                                                                                                   Score:
                                                                                                                                                                                                                                                                                      Alignment Scores:
                                                                                                                                                                                                                                                            Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred.
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21-SEP-2000;
27-SEP-2000;
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26-MAY-2000;
30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is one of
                                                                                                                                                                                                                                                            No.:
                                                                                                                                                                                                                                                                                                                                                             Sequence 471
                                                                                                                                                                                                                                                                                                                                                                                                                                    the probes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             probes which are derived from genomic sequences expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention provides a number of single exon nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 4; SEQ ID NO: 69; 658pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        analyzing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       microarray; cancer; leukaemia; lymphoma; myeloma; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; bone marrow expressed exon; gene expression analysis; probe;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-NOV-2001
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; 2000US-0207456.
; 2000US-0608408.
; 2000US-0632366.
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Search completed: January 15, 2003, 12:56:51 Job time: 202.143 secs

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US-09-199-637A-26/c
; Sequence 26, Application US/09199637A
; Ratent No. 6355411
; GENERAL INFORMATION:
                                                                                                                                                                                                                            Query Match:
DB:
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                                                                                                                                                                                      US-09-823-649A-6 (1-11) x US-09-453-702B-3 (1-635)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (608) 251-5000
TELEPAX: (608) 251-916
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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                                                                                                              485 AGTAAAAGGATTGGGTTAAGCCGTTCT 459
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                                                                                                                                                 2 SerLysArgIleGlyLeuSerValSer 10
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FILING DATE: 04-DEC-1998
ATTORNEY/AGENT INFORMATION:
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MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27386
REFERENCE/DOCKET NUMBER: 960296.95017
TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Diskette, 3.50 inch. 1.44Mb storage
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Blattner, Frederick R.
Burland, Valerie
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CITY: Madison
STATE: WI
COUNTRY: US
LIP: 53701-2113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
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Best Local Similarity:
Query Match:
Search completed: January 15, 2003, 12:58:54 Job time : 31 secs
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                                                                                                                                                                                                                                                                  Pred. No.:
                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 26
LENGTH: 642
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
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APPLICANT:
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Tsongalis, John
TITLE OF INVENTION: VIRULENCE-ASSOCIATED NUCLEIC ACID
TITLE OF INVENTION: SEQUENCES AND USES THEREOF
FILE REFERENCE: 00786/361002
                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE:
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                                                                       371 TTAGCCAAGCGGTTTGGCCTCTCGGTC 345
                                                                                         1 LeuSerLysArgIleGlyLeuSerVal 9
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Cao, Hui
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Goodman, Howard M.
Rahme, Laurence G.
Mahajan-Miklos, Shalina
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Crossland, Lyle

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US-09-823-649A-6 (1-11) x US-09-575-602-11 (1-6596)
                                                              Best Local Similarity:
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INFORMATION FOR SEQ ID NO: 11:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                             No . :
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APPLICATION NUMBER:
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TITLE OF INVENTION:
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LOCATION:
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LOCATION:
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REFERENCE/DOCKET NUMBER: CGC 1915/Reg
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/evidence= EXPERIMENTAL
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                                                                                                                                                                           /function= "translation stop"
                                                                                                                                                                                                                                                                                                                                                                                                                                      /function= "5' Regulatory Region of
B200i4-2"
                                                                                                                                                                                                                                           /function=
                                                                                                                                                                                                                                                                                                                                                                                                                       /evidence= EXPERIMENTAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      experimental
                                                                                                                                                                                                                                           "ATG translation start"
                                                                                            Matches:
                                               Mismatches:
Indels:
                                                                           Conservative:
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RESULT 13
US-09-221-017B-720/c
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                 Percent Similarity:
Best Local Similarity:
                                                               Pred. No.:
                                                                             Alignment Scores:
                                                                                                             US-09-221-017B-720
   Query Match:
                                                Score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
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                                                                                                                                                         FEATURE:
                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION: TELEPHONE: 650-813-5600
                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Monroy, Gladys H
REGISTRATION NUMBER: 32,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: ROSS, Bruce C.
TITLE OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF NUMBER OF SEQUENCES: 1120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1175 CTTTCGAAACGTAAGGGATTGCATTTGTCCGAG 1207
                                                                                                                                                                                         ORIGINAL SOURCE:
                                                                                                                                                                                                      HYPOTHETICAL:
ANTI-SENSE: 1
                                                                                                                                                                                                                                  MOLECULE TYPE:
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APPLICATION NUMBER: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: PCT/
FILING DATE: 10-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 755 PAGE CITY: Palo Alto
                                                                                                                          LOCATION:
                                                                                                                                       NAME/KEY: misc_feature
                                                                                                                                                                        ORGANISM:
                                                                                                                                                                                                                                                                 STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                              TELEX:
                                                                                                                                                                                                                                                                                                                                                             TELEFAX:
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                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                               LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
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                                                                                                                                                                      PORYPHYROMONAS GINGIVALIS
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                Conservative: Mismatches:
 Indels:
                                             Matches:
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Gaps:

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RESULT 10
US-08-961-527-181
; Sequence 181, Application US/08961527
"~+ent No. 6420135
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Best Local Similarity:
Query Match:
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                            US-09-823-649A-6 (1-11) x US-08-961-527-181 (1-8651)
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                                                                      Best Local Similarity:
Query Match:
                                                                                                                                                                              TOPOLOGY: US-08-961-527-181
                                                                                                     Percent Similarity:
                                                                                                                                             Alignment Scores:
                                                                                                                      score:
                                                                                                                                                                                                                                   TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 8651 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: ASCII Text CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences NUMBER OF SEQUENCES: 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Charles Kunsch
                                                                                                                                  No . :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB340P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER:
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                                                                                                                                                                                                                                                                                              TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: MSDOS version 6.2
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1 LeuSerLysArgIleGlyLeuSerValSerGlu 11
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                                                                                                                                                                                                                      nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NE: Human Genome Sciences, Inc.
9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5406 base pairs
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                                                                                                                                                                                                                                                                                               (301) 309-8504
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Indels:
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RESULT 12
US-09-575-602-11
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                                                                                                                                                                                                            Query Match:
                                                                                                                                                                                                                               Best Local Similarity:
                                                                                                                                                                                                                                                                Score:
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                                                                                                                                                                                                                                             Percent Similarity:
Sequence 11, Application US/09575602 Patent No. 6392123 GENERAL INFORMATION:
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: LACTOIX, Bruno
TITLE OF INVENTION: 5' ESTS FOR SECRETED PROTEINS
NUMBER OF SEQUENCES: 503
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                              NO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: CDNA ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 427 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
                                                                                            332 TTGGCAAAGACCCTGGGACTCGAGGTGAGTGAG 364
                                                                                                                                                                                                                                                                                                                                          IDENTIFICATION METHOD: Von Heijne matrix OTHER INFORMATION: Score 10.8 OTHER INFORMATION: Seq VLLFFVLLGMSQA/GS
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CLASSIFICATION: 536
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                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: sig_peptide
LOCATION: 191..268
                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE TYPE: Brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo Sapiens
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                                                                                                                           1 LeuSerLysArgIleGlyLeuSerValSerGlu 11
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US-09-823-649A-6 (1-11) x US-08-987-151-3 (1-1785)
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
Keith Robert
APPLICANT: Willison, Keith Robert
APPLICANT: Kubota, Hiroshi
APPLICANT: Asiworth, Alan
APPLICANT: Asiworth, Alan
TOTAL OF T
                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 61, Appli
Patent No. 6255070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 1785 base pairs
                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: 317-276-3334
                                                                                        CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1065 UCCAGAAGACUUGGCCUAUCUAUUAACGAA 1094
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
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                                                     APPLICATION NUMBER: US/08/687,590 FILING DATE: 31-JUL-1996
                                                                                                                                                                                                                                      STREET: Two Emparcau
CITY: San Francisco
                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Webster, Thomas D. REGISTRATION NUMBER: 39,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/987,151 FILING DATE:
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COMPUTER: IBM PC COMPUTED:
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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                                   CLASSIFICATION:
                                                                                                            SOFTWARE:
                                                                                                                                                                                                          COUNTRY: United States of America
                                                                                                                                                                                                                          STATE: California
                                                                                                                                                                                                                                                                                   ADDRESSEE:
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Lilly Corporate Center
                                                                                                                                                                                                                                                             E: Townsend and Townsend and Crew LLP Two Embarcadero Center, Eighth Floor
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                                                                                                            PatentIn Release #1.0, Version #1.25 (EPO)
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Best Local Similarity:
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                        TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 160
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REFERENCE/DOCKET NUMBER:
INFORMATION FOR SEQ ID NO:
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                                                                                     REFERENCE/DOCKET NUMBER: PB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
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SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                      NAME: Brookes, A. Anders REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 424
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; Sequence 1, Application US/08987151
; Patent No. 6162617
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                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 1602 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION: TELEPHONE: 317-276-3334
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SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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APPLICANT: Rosteck Jr., Paul R.
TITLE OF INVENTION: Strepttococcus Pneumoniae Gene Sequence
TITLE OF INVENTION: dnaG
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STATE: Indiana
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STRANDEDNESS: single
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                                                                                                                   2 SerLysArgIleGlyLeuSerValSerGlu 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/987,151
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Matches:
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Indels:
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US-08-987-151-3
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                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; LOCATION:
US-08-987-151-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No.:
                                                                                                                                                                   Sequence 3, Application US/08987151 Patent No. 6162617
                                                                                                                                                     GENERAL INFORMATION:
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APPLICANT: Jaskun
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                                                                               APPLICANT:
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APPLICANT:
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                                                                                                                                                                                                                                                        1065 TCCAGAAGACTTGGCCTATCTAFTAACGAA 1094
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
                              APPLICANT: Burgett, Stanley G.
APPLICANT: Rosteck Jr., Paul R.
TITLE OF INVENTION: Streptococcus Pneumoniae Gene Sequence
TITLE OF INVENTION: dnaG
                                                                                                                                 APPLICANT:
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FEATURE:
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LENGTH: 1785 base pair
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                  NUMBER OF SEQUENCES:
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CITY: Indianapolis
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                                                                                                                                                                                                                                                                                        2 SerLysArgIleGlyLeuSerValSerGlu 11
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REFERENCE/DOCKET NUMBER: X-11748
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                                                                                                                   Zhao, Genshi
                                                                                                                                 Jaskunas Jr.,
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                                                                                                 Peery, Robert
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                                                                                                                                   Stanley R.
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Best Local Similarity:
Query Match:
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PCT-US91-07035-11
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APPLICANT: Abramson, Richard D.
TITLE OF INVENTION: 5' TO 3' EXONUCLEASE MUTATIONS OF
TITLE OF INVENTION: THERMOSTABLE DNA POLYMERASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2218 CTTTCAAAGAGAATTGGTCTTAGTGTTTTCAGAG 2250
                                                                            PRIOR APPLICATION DATA:
                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 7
FILING DATE: 15-AUG-1991
                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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                                                                                                                                                                                     PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                        FILING DATE: 12-JAN-1988 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                          FILING DATE: 15-MAY-1990
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US 59
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                      FILING DATE: 17-JUN-1987
                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 59 FILING DATE: 28-SEP-1990
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                                           FILING DATE:
                                                                                                                                                  APPLICATION NUMBER: US 89 FILING DATE: 22-AUG-1986
                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 28-SEP-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 590,466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
       APPLICATION NUMBER:
                                                             APPLICATION NUMBER:
                                                                                                                                                                                                                           APPLICATION NUMBER: US 063,509
                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 143,441
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                                         MBER: WO PCT/US90/07641
21-DEC-1990
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       US 585,471
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                                                                                                                US 746,121
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Indels:
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Percent Similarity:
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Percent Similarity:
Best Local Similarity:
Query Match:
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                                                                                                          ; ORGANISM: Staphylococcus epidermidis US-09-134-001C-2379
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                                                                                                                                                                          PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ 1D NOS: 5674
SEQ 1D NO 2379
                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                          Patent No. 6380379
                                                                                                                                                                                                                                                           APPLICANT: Lynn Doucelle-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
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                                                                                                                                               TYPE: DNA
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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LOCATION:
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TYPE: NUCLEIC ACID
STRANDEDNESS: single
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Matches:
              Conservative:
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Mismatches:

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Best Local Similarity:
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                                                                                                                  US-08-458-819-11
Sequence II, Application US/08458819
Patent No. 5795762
GENERRAL INFORMATION:
APPLICANT: Gelfand, David H.
APPLICANT: Abramson, Richard D.
APPLICANT: Abramson, Richard D.
TITLE OF INVENTION: 5' TO 3' EXONUCLEASE MUTATIONS OF
TITLE OF INVENTION: THERMOSTABLE DNA POLYMERASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (510) 814-2972
INFORMATION FOR SEQ ID NO: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: LINCAL MOLECULE YPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HYPOTHETICAL: NO ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                 2218 CTTTCAAAGAGAATTGGTCTTAGTGTTTTCAGAG 2250
                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: WO PCT/US90/07641 FILING DATE: 21-DEC-1990 PRIOR APPLICATION DATA:
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LENGTH: 2679 base pair
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APPLICATION NUMBER: US 609,157
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APPLICATION NUMBER:
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TELEPHONE: (510) 814-2972 INFORMATION FOR SEQ ID NO: 11:
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APPLICATION NUMBER: US 58
FILING DATE: 20-SEP-1990
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PRIOR APPLICATION NUMBER: US 063,509
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                REFERENCE/DOCKET NUMBER: Ca
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                               APPLICATION NUMBER: US 557,517 FILING DATE: 24-JUL-1990 ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: 1
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ORIGINAL SOURCE:
            HYPOTHETICAL: 1
                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 2679 base pair
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PRIOR APPLICATION DATA:
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                                             MOLECULE TYPE:
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FILING DATE: 17-JUN-1987
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                                                               TOPOLOGY: linear
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21-DEC-1990
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                                             DNA (genomic)
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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length: 2000000000
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Delop 6.0,
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
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/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
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US-09-134-001C-2379
US-08-987-151-4
US-08-987-151-3
US-08-987-151-3
US-08-987-151-3
US-08-961-527-166
US-08-961-527-181
US-08-961-527-181
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181, Appl
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; Patent No. 5466591
; CENERAL TARROWS
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US-07-977-434-11
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SOFTWARE: WordPerfect 2.1
CURRENT APPLICATION DATA:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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APPLICANT: Abramson, Richard D.
TITLE OF INVENTION: 5' TO 3' EXONUCLEASE MUTATIONS
TITLE OF INVENTION: THERMOSTABLE DNA POLYMERASES
NUMBER OF SEQUENCES: 38
 PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                 PRIOR APPLICATION DATA:
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                                 APPLICATION NUMBER: FILING DATE: 28-SEE
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                                                                                                                                                                                         CLASSIFICATION: 435
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US-09-199-637A-22
US-08-557-128-2
US-08-557-128-2
US-08-557-128-2
US-09-199-637A-12
US-09-199-637A-12
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US-09-364-543-98
US-09-365-76
US-09-352-616A-76
US-09-352-616A-55
US-09-352-616A-76
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Sequence 26, Appl
Sequence 27, Appl
Sequence 28, Appl
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Sequence 71, Appli
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Sequence 76, Appli
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Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

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TITLE
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           Mycoplasma genitalium section 36 of 039714 L43967
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Abramson,R.D. and Gelfand,D.H.
5' to 3' exonuclease mutations of thermostable DNA polymerases
Patent: US 5795762-A 11 18-AUG-1998;
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Sequence 11 from patent US 5795762.
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                                                           BCT 05-NOV-1998
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AUTHORS
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JOURNAL
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JOURNAL
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AUTHORS
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                                                                                                                                                                                            CDS
                                                                                                                                                                                                                                gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fraser.C.M., Gocayne, J.D., White, O., Adams, M.D., Clayton, R.A., Fleischmann, R.D., Bult, C.J., Kerlawage, A.R., Sutton, G.G., Kelley, J.M., Fritchman, J.L., Weidman, J.F., Small, K.V., Sandusky, M., Fuhrmann, J.L., Nguyen, D.T., Utterback, T., Saudek, D.M., Phillips, C.A., Merrick, J.M., Tomb, J.-F., Dougherty, B.A., Bott, K.F., Hu, P.C., Lucier, T.S., Peterson, S.N., Smith, H.O. and Venter, J.C. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (29-OCT-1995) The Institute for Genomic Research, Medical Center Drive, Rockville, MD 20850, USA (bases 1 to 12486)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fraser.C.M., Gocayne,J.D., White,O., Adams,M.D., Clayton,R.A., Fleischmann,R.D., Bult,C.J., Kerlavage,A.R., Sutton,G., Kelley,J.M., Fritschman,J.L., Weidman,J.F., Small,K.V., Sandusky,M., Fuhrmann,J.L., Nguyen,D.T., Utterback,T.R., Saudek,D.M., Phillips,C.A., Merrick,J.M., Tomb,J.-F., Dougherty,B.A., Bott,K.F., Hu,P.-C., Lucier,T.S., Peterson,S.N., Smith,H.O., Hutchinson,C.A. III and Venter,J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Medical Center Dr, Rockville, MD 20850, USA
On Nov 5, 1998 this sequence version replaced gi:1046022.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma. 1 (bases 1 to 12486)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mycoplasma genitalium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    identity:
                                                                                                             identity: 66.17; identified putative "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(14. .901)
/gene="MG326"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(14. .901)
/gene="MG326"
                                                                                                                                                                                        complement(914. .1720)
                                                                                                                                                                                                                                                                  FGFVKTKFGDNYKIKRIGFCYSFCKNYANEIKKIITDF1EHNKINFQNEIENAF1TSV
                                                                                                                                                                                                                                                                                     QLAKELSEQNKDKEFLVFETSDIAISLKWLVEDIKALVDKGCDNQTIKAKVESHKQNI
LSAVTLKNLVQMRKGGRISGLKKFITTLLRVKPIILFDKGVNTLGAKVFSFSQAVEKI
                                                                                                                                                                                                                                                                                                                       /translation="MKKTAIITDSTASIKPGEINGYYILPLQVIVDGEKSFRDGIEID
/translation="MKKTAIITDSTASIKPGEINTKYDRFIFLPLSKGLSGTYDMLV
                                                                                                                                                                                                                                                                                                                                                             /product="conserved hypothetical protein"
/protein_id="AAC71550.1"
/db_xref="GI:3844906"
                                                                                                                                                                                                                                                                                                                                                                                                                                                            putative'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="similar to GB:U00089
identity: 68.94; identified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Mycoplasma
/isolate="G37"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 to 12486)
translation="MLTSNKNTLFNSIFAFKPKKRKNVFIFLHGFGSEYASFSRIFSL/
                 /transl_table=4
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/protein_id="AAC71551.1"
/db_xref="GI:3844907"
                                                                                             /codon_start=1
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identity: 66.17; identified by sequence similarity;
                                                                                                                                                                      /gene="MG327"
                                                                                                                                                                                                            /gene="MG327"
                                                                                                                                                                                                                                complement(914.
                                                                                                                                                                                                                                                  IIVHTGIDAFSISLLIDNK"
                                                                                                                                                                                                                                                                                                                                                                                                                    /codon_start-1
/transl_table=4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:2097"
                                                                                                                                                                                                                                .1720)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 genitalium"
                                                     putative'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SP:P75312 PID:1674048 percent by sequence similarity;
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gene

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identity:
putative"
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complement(17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NELKKLHDNTSNDENEKYDDLLNQYELLFDENETKFDKLQYKQQALNLDYGKTISALK
HENDYLLDE LEWTASKDNDFNNYKNSFEEQKKALDEKINGLT IQNQQLQDKIAELSEK
NENKYLLDE LEWTASKDNDFNYKNSFEEQKKALDEKINGLT IQNQQLQDKIAELSEK
NENKYLLDKLODGUTEKLORGYGKLKTDFEKLKKNKLNDANEQYQDLLSAFEETNSELEK
AKQSLSASDSENNQLKQQINSLENAKKELQFTPYTSDEHLDELETLKIEKGQLGFLENQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="conserved hypothetical protein"
/protein_id="AAC71552.1"
/db_xref="GI:3844908"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FKKKKWPEFTTNFPGHGDNESTDTDQLKLNHFVDLVCDFTVQKKLNNVILIGHSMGGA
VAVLVNKVIPLKIKALILVAPMNQTSESVNKKRILDTFFKRNNSNHKDFVEHEEKRKS
LLKIAINAFKKRTTFKTLYSDMVQNAKYGNDSLERAYEMIGNKPTLVILGANDIVTPT
                        /note="similar to GB:U00089 SP:P75307 PID:1674042 percent
identity: 39.34; identified by sequence similarity;
putative"
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QVNELNIDLFLKIINQIWWFFEKDAYYINNADITFYITTQSYANIASKIAYDPNIRKI
AVIKQGKLAENKNIYMOGADIGTYVLKINAQLKFELDAKVEIRAQRELQDWGISLSNEK
KLKELIQELKQRDQIDSSRTADPLKKAQDAIYLDTSELSFDAVVKQTLKEAKKVFKL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(5366. .6019)
/gene="MG330"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VPLKVNGEKFLLIDTAGIKRKGKINMGIETASYIKIKLAIARSNVILLMVDGSKPISE
QDEVIGGLAQAALIPVIILVNKWDLVLKNNNTTNAYKKMLKLHFKHLDFAPVLFISVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EWLKRK IAF I DTGGLI AKQTPLQQLI ALQVQAALSQAKA I I FLVSLQEQLNSDDFYVA
KVLKKNKDKPV LLVVNKAENFNPKTAEETLKDYY SLGFGRPVV I SAAHG I G I GDLMDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="conserved hypothetical GTP-binding protein"
/protein_id="AAC71553.1"
/db_xref="GI:3844909"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KRRLSEEKSKHLHTKKLQDDLLQENRDLYEQLQNKPVAINPLSDEVNEELENLKQEKA
LLSDQLDALKNKSSNVQQQLALLPVLNNQINELQNQLLTAREANQRLDLVEQENDFLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VVKRILKEQHPIKKVDELDDYNNKELLLENADLKKQIDDLKENNNDQIFDLEQEIDDL
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QPSEEINETKKPEVQIFSTDKVKEPEQFDDFYSIENLUKAINPVHKTIQYDQNDDQPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(1707. .3977)
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                                                                                                                                            complement(6028. .6666)
                                                                                                                                                                                                       complement(6028. .6666)
                                                                                                                                                                                                                                                                                                                                          /product="cytidylate kinase (cmk)"
/protein_id="AAC71554.1"
/db_xref="G1:3844910"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(5366. .6019)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SQIPHEVLECNDPKYLHESYARFLENKIRENFGFNSVP1SLYFKSKNARIRTKPEV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KNQRLNTIFEQLKIIQSQLETKVATPLLNDVIQQAQUYNQPPLFKGKRLQITYAVQTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /transl_table=4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="similar to GB:U00021 PID:467147 percent identity:
32.18; identified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(4016. .5362)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="MG329"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPTEMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RIQAYAERLAKINANE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALQNQLQYFNDISANQTEEIKEASDEDKPVEIKKPRIKKRDFVIQNKDDKLAKLSKKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          <u>ERNILEKTFFGTVDEAEKEKSIVSFFNWMIDLKVLDKKWDKNVLNHYANQLKTREEEQ</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  translation="MAVDKELEISDFDNELDEKTLLKELVQRTNNILFSPSKITAIPF/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /transl_table=4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="MG328"
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identity: 65.42; identified by sequence similarity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="MG330"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LVKQNQLLPNENNDDLAKIRFCVIGKPNVGKSSLINQLVKQNRVLVSNESGTTRDAID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               translation="MFTVAIIGRTNVGKSTLFNRLIQKPMAIVSDTPNTTRDRIFGIG/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /codon_start=1
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                                                                                                                                               RESULT 4
AC124922/c
LOCUS
   VERSION
KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity:
                                                          ACCESSION
                                                                                                                 DEFINITION
                                                                                                                                                                                                                                                                                                                                                                            US-09-823-649A-6 (1-11) x U39714 (1-12486)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            No.:
                                                                                                                                                                                                                                                                                               1 LeuSerLysArgIleGlyLeuSerValSer 10
                                                                                                                                                                                                                                                              CTGAGTAAACGGTTAGGATTATCAGTTAGT 7086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Scores:
AC124922.2 GI:21671429
HTC; HTGS_PHASE1.
                                                       AC124922
                                                                                                              Rattus norvegicus clone CH230-397L24,
                                                                                                                                               AC124922
                                                                                  28 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="similar to GB:U00089 SP:P75306 PID:1674041 percent identity: 75.64; identified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   identity:
putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PPNLTGTLHIGHAPEVSITDOLMREKKMOGFSINMIPGFDHAGIAYOTKKEKIALKEN
QKYFDADDDKKSEMIMMALNOSEIIKNQLKSIGVCLNWSETKFTLSBQAKIIVNCF
KNILENGFTYQAYTLVNMOTKLNTAISNIEVINKEPVNOHLHYVVYKLANDSKQELIVA
TTRPETIFADVCLLVNPKDKRYTNEWNKLVVNPLTGKQIPVVTDSYVDIKFGTGILKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /codon_start=1
/trans1_table=4
/product="valy1-tRNA synthetase (vals)"
/protein_id="AAC71557.1"
/db_xref="G1:3844913"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(8011. .10524)
/gene="MG334"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  is not the result of a sequencing artifact; similar to GB:000089 SP:P75305 PID:1674040 percent identity: 74.75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(7380. .7974)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="MPKKHLIANQTN"KQQTSAKQLQKLAKRIASAVKKGGTNIQSNP
HLKVAVDLALAKGLSMDSIKRNIHGSEKDTIKISEFCYEIFGPNGVGIIVFGLIDNPN
RLLSSLNGYLAKLKGQLAKPNSVKINE;;5.5GIIFVNKNNYLKDDLIELLILDNINLID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /trans1_table=4
/product="conserved hypothetical protein"
/protein_id="AAC71556.1"
/db_xref="G1:3844912"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(6654. .7373)
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complement(6654..7373)
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/thanslation="mgrvEKFRFYRQSFDNNKIVKKALINAQKNTESWKKQLNKINQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TPAHDFNDYH INTKYKFUFLSCIDSNG LLNQNASKFQGLSVI QARNK IVKWLEKNKLL
VKS IPLTSNVGFSERSCTVVEPMLSKQWFVDLPKLKUHLYLKKYPDFIPKRFNKQVSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(8011.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="MG333"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="similar to GB:U00089 SP:P75304 PID:1674039 percent identity: 63.96; identified by sequence similarity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="This region contains an authentic frame shift and
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*** SEQUENCING IN PROGRESS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oragunye, M., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L., Peters, L., Pickens, R., Primus, E., Pu, L. L., Quiles, M., Ren, Y., Rives, M., Rojubokan, I., Rolfe, M., Ruiz, S., Savery, G., Scherer, S., Scott, G., Shen, H., Shooshtari, N., Sisson, I., Sodergren, E., Sonaike, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H., Tansey, J., Taylor, C., Taylor, T., Telfrod, B., Thomas, N., Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wang, O., Warren, R., Washington, C., Watlington, S., Williams, G., Williams, G., Williams, A., Wheezyk, R., Wooden, S., Worley, K., Williams, G., Williams, A., Wheezyk, R., Wooden, S., Worley, K., Williams, G., Williams, A., Wheezyk, R., Wooden, S., Worley, K., Williams, G., Willia
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Homsi,F., Howard,S., Huber,J., Hulyk,S., Hume,J., Jackson,L.E.,
Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S.,
Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J., Kovar,C.,
Kratovic,J., Kureshi,A., Landry,N., Leel,B., Lewis,L.C., Lewis,L.C.,
Li,J., Li,Z., Lichtarge,O., Lie,C., Liu,J., Liu,W., Loulseged,H.,
Lozado,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R., Ma,J.,
Lozado,R.J., Lu,X., Lucier,A., Lucier,R., Martindale,A., Martinez,E.,
Massey,E., Marhiney,E., McLeod,M.P., Meador,M., Mei,G., Metzker,M.,
Massey,E., Markiney,E., McLeod,M.P., Meador,M., Morgan,M., Morris,S.,
Moser,M., Neal,D., Newtson,J., Newtson,N., Nguyen,A., Nguyen,N.,
Noser,M., Nickerson,B., Neckenkwo,S., Oguh,M., Okwnon,G.,
Orser,M., Nickerson,B., Neckenkwo,S., Oguh,M., Okwnon,G.,
Orser,M., Nickerson,B., Neckenkwo,S., Oguh,M., Okwnon,G.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bouck, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryan Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, Chen, G., Chen, R., Chowdhry, I., Christopoulos, Chen, R., Chen, R., Chowdhry, I., Christopoulos, Chen, R., Chen, R., Chowdhry, I., Christopoulos, Chen, R., Chen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (20-JUN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 3 (bases 1 to 147168)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Falls, T., Geo, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K., Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rattus norvegicus
Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (24-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                   Baylor Plaza,
On Jul 2, 200:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
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Weinstock,G. and Gibbs,R.
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                                                                                                                                                                                                                                                                                                                                                             Jul 2, 2002 this sequence version replaced gi:21490014.
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Center project name: GYQQ
Center clone name: CH230-397L24
Center clone name: CH230-397L24
Chemistry: Summary Statistics
Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
                                                                                                                                                                                            Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                   Center code: BCM
                                                                                                                                                                                                                                                             Web site: http://www.hgsc.bcm.tmc.edu/
                                                                                                                                                                                                                                                                                                                           Center: Baylor College of Medicine
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                                                                                                   FEATURES
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/organism="Rattus norvegicus"
/db_xref="taxon:10116"
                                                                 Location/Qualifiers
1. .147168
                                                                                                      111895: contig ...
111995: gap of unknown lengt...
129976: contig of 17981 bp in ler
129976: qap of unknown length
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103326:
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1659: gap of
                                                                                                                                                                                                                                                      ); gap of unknown length

); contig of 7537 bp in length

7; gap of unknown length

5; contig of 12599 bp in length

5; gap of unknown length

5; contig of 8569 bp in length
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f unknown
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of 4606
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of 3445
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of 3313
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of 3232
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of 1230
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* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown
* This record will be updated with the finished sequence
                                                                                                                                                                                                                                               (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_daia.html).
NOTE: This is a 'working draft' sequence. It currently
consists of 28 contigs. The true order of the pieces
is not known and their order in this sequence record is
                                                                as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                   NOTE: Estimated insert size may differ from sequence length
Length
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least Q30
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BCT 28-JAN-1998

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                                                                                                   Alignment Scores:
                                                                                                                                                                                                      BASE COUNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mol. Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         \label{eq:condition} Ferkowicz, \texttt{M.J.}. \quad \texttt{Stander}, \texttt{M.C.} \quad \text{and} \quad Raff, \texttt{R.A.}. \\ Phylogenetic relationships and developmental expression of three phylogenetic relationships and developmental expression of the phylogenetic relationships and developmental expression of the phylogenetic relationships and developmental expression of the phylogenetic relationships are phylogenetic relationships and the phylogenetic relationships are phylogenetic relationships an
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Echinoidea; Euechinoidea; Echinacea; Echinoida; Echinometri
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1 29771 c 29664 g 38958 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /function="putative cell signaling molecule" /note="secreted glycoprotein with several concesteine residues"
                                                                                                                                                                                                                                                                                                                                                                     /product="Wnt-4 protein"
/protein_id="AAC69242.1"
/protein_id="AAC69242.1"
/protein_id="AAC69242.1"
/db_xref="Gi:11857936"
/translation="GHYLDNOGTBEAAFVNA!SAAGVANAVTRGCGSSGELEKCGGDRTV
/translation="GHYLDNOGTBEAAFVNA!SAAGVANAVTRGCGSSGELEKCGGDRTV
/translation="GHYLDNOGTBEAAFVNA!SAAGVANAVTRGCSSGELEKCGGDRTV
/translation="GHYLDNOGTBEAAFVNA!SAAGVANAVTRGCSSGELEKCGCDRTV
/translation="GHYLDNGTBEAAFVNA!SAAGVANAVTRGCSSGELEKCGCRTTTED
/GNSAEGFWAAGCSSCEMTCWKSMFTFGDIGHTKEKFTGAATEVOSIKIOSRGOLVPR
NARRECKCHGVSGSCEMTCWKSMFTFGDIGHTKEKFTGAATEVOSIKIOSRGOLVPR
NARRECKCHGVSGSCEMTCWKSMFTFGDIGHTKEKFTGAATEVOSIKIOSRGOLVPR
NADFKPHTSSDLVYLVFSPDFCEEDLKGSLGTHGRRCNKTSKAIDGCELMCCGRGFNT
                                                                                                                                                                                                      /note="encodes potential glycosylation site" 300 c 333 g 282 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="Hewnt-4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="Hewnt-4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:7634"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Heliocidaris erythrogramma"
                                                                                                                                                                                                                                                                         /gene="Hewnt-4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ocation/Qualifiers
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Matches:
Conservative:
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AUTHORS
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MEDLINE
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Bull.C.J., White,O., Olsen,G.J., Zhou,L., Fleischmann,R.D.,

Sutton,G.G., Blake,J.A., FitzGerald,L.M., Clayton,R.A.,

Sutton,G.G., Blake,J.A., FitzGerald,L.M., Clayton,R.A.,

Gocayne,J.D., Kerlavage,A.R., Dougherty,B.A., Tomb,J.-F.,

Adams,M.D., Reich,C.I., Overbeek,R., Kirkness,H.F., Weinstock,K.G.,

Merrick,J.M., Glodek,A., Scott,J.D., Geoghagen,N.S., Weidman,J.F.,

Fuhrmann,J.L., Nguyen,D.T., Utterback,T., Kelley,J.M.,

Peterson,J.D., Sadow,P.W., Hanna,M.C., Cotton,M.D., Hurst,M.A.,

Roberts,K.M., Kaine,B.B., Borodovsky,M., Klenk,H.P., Fraser,C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10573 bp DNA linear BCT 28-JAN-199 Methanococcus jannaschii section 88 of 150 of the complete genome. U67546 L77117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (27-AUG-1996) The Institute for Genomic Research, 9712 Medical Center Dr. Nockville, MD 20850, USA on oct 3, 1996 this sequence version replaced viil564062.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii Science 273 (5278), 1058-1073 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fuhrmann,J.L., Nguyen,D.T., Utterback,T., Kellcy,J.M., Peterson,J.D., Sadow,P.W., Hanna,M.C., Cotton,M.D., Hurst,M.A., Peterson,M., Kaine,B.B., Borodovsky,M., Klenk,H.P., Fraser,C.M., Smith,H.O., Woese,C.R. and Venter,J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sutton, G.G., Blake, J.A., FitzGerald, L.M., Claytton, R.A., Adams, M.D., Gocayne, J.D., Kerlavage, A.R., Dougherty, B.A., Tomb, J., Adams, M.D., Reich, C.I., Overbeek, R., Kirkness, E.F., Weinstock, K.G., Merrick, J.M., Glodek, A., Scott, J.D., Geoghagen, N.S., Weidman, J.F.,
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Bult, C.J., White, O.,
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Archaea: Euryarchae
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                                                            DVGRVFPISASISIFILLIGLIYSLSSINKTSSTLTEFIGEFILHFVDSITLSILLIA
VGRFVDTIINSEKDILELLKKYFFCLICIFISRELIISGGEVILKKISFIMFVECVII
                                                                                                                                                           /translation="mekegyknylvlyvdIdDbIGRkAGLNTPILGREENIKALIKLG
LADPGDSDYNAILGGYKIYDELKASGKDVEIATISGDVDVESEKCALRIKEQIDFLLY
LYNPDFIYLVSDGKEDEMILKYLESKNIFYNKKRVIVKQSETLESTYYLLGEFIKKIM
                               YISIVIILSVILFTKSSKEDKFKKLKNSITKG"
                                                                                                                                      EEYTPL1LTF1GFSLILYATFAD1GWR1VVGTIGLY1LSEGVGVRKLLMEK1KKKEEF
                                                                                                                                                                                                                                                                     /product="conserved hypothetical protein"
/protein_id="AAB99036.1"
/db_xref="GI:1499875"
                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="similar to GB:AE000782 percent identity: 34.62;
identified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Methanocaldococcus jannaschii"
/db_xref-"taxon:2190"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualificis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="MJ1032"
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Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="similar to PID:685181 PID:726050 GB:AE000666 percent identity: 66.43; ide sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="MJ1034"
2154. .2417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DLYYDTLQLIDMSATYREVLTSMMDITLSLENIKMNQIMKILTMYTTIFAVPMWITGI
YGMNESYLPLANNPQGFWLYMALMYVIIMIEVYIFRRSGWI"
2154. 2417
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/note="similar to GB:L42023 SP:P44998 PID:1006270
PID:1205285 PID:1221151 percent identity: 25.33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene=#MJ1035"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SKKIGISVSDLQIGLDEQEIPRVEEDEDFYLIIYKAPLFEEDITTTSLGIYIKNNLLL
TIHSDKIKAIGRLHKLISTKKPRIVFERGIGFLLYHILNEITRSYSRILMNLEDELEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="MJ1036"
3682, .4383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KEAEKYIPIVASAHEMIRYAAKLVDEARELEKAMDAVSRKPHHPEGKRLSKKALMEKP
E"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="MIIWPSYIDKKKSRREGRKVPEELAIEKPSLKDIEKALKKLGLE
PKIYRDKRYPRQHWEICGCVEVDYKGNKLQLLKEICKIIKGKN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="MJ1034"
/note="similar to GB:X12791 SP:P09132 PID:36113 percent
identity: 32.89; identified by sequence similarity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="magnesium and cobalt transport protein (corA)"
/protein_id="AAB99037."
/protein_id="AAB99037."
/db_xref="q1:1499876."
/translation-"MITVIAIAKDGSIVEPKLDEISFEDYRLIWIDCYDPKDEELYKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="MJ1033"
1191. .2144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DEMEQQGLGYIIIKCDPMIGARREFLDPVEMALFNADVIRVLAGTGALRIVQEAÌDKM
IDAVKEGKEIELPKIVITEQKAVEAMEFTNPYAKAKAMAAFTIAEKVGDVDVKGCEMT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(2440. .3273)
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/protein_id="AAB99038.1"
/db_xref="GI:1499877"
                                                                                                                                                                             YILLGYILVGIIALH"
                                                                                                                                                                                                     KF1YP1SFF1HTF1DGL11AVSY1SE1GLPLYLA1LMHKLPAGFVL1SPLKGVYKNPL
YPGVFVSFGTVLGT1VGLV1LKDVSTK1LLAFSGGVFLGAFLMLAPH1YEHKEEKTFL
                                                                                                                                                                                                                                                        /translation="mSNMVEVPIFIAILSFIVMCIGELLAYYSVSLKYKYEFEAISFG
FIFGVATLILIPKSYSNMFVLYVILGMITVYLIEKYLAYCPLSKKYCVECDNLBENRI
                                                                                                                                                                                                                                                                                                      /product="M. jannaschii predicted coding region MJ1036"
/protein_id="AAB99045.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                         putative
                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="MJ1036"
/note="hypothet
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="MJ1035"
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                     note="similar to PID:1054861 SP:P50909 percent identity:
14.12; identified by sequence similarity; putative"
                                                                                                                           /gene="MJ1037"
                                                                                                                                                                                                                                                                                                                                                                                      transl_table=11
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codon_start=1
                                                                     'gene="MJ1037"
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                                                                                                        . 5660
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entified by
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Query Match:
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6866. .710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note-"similar to GB:X73293 PID:505290 SP:P41558 percent identity: 70.99; identified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="MJ1038"
5837. .6691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="similar to GB:M65060 SP:P26920 PID:149750
GB:AE000666 percent identity: 47.77; identified i
sequence similarity; putative"
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LGQALLAKKMGKKRVIAETGAGQHGVATAAACAKLGLECIIYMGAKDVERQKLNVFRW
ELMGAKVIPVFGGSQTLKDAVNEALRDWTTNVRTTYYLLGSALGPHPYPMAVREFQRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation-"MKVTDHILVPKHEIVPKEEVEEILKRYNIKIQQLPKIYEDDPVI
QEIGAKEGDVVRVIRKSPTAGVSIAYRLVIKRII"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             similarity; putative"
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/product="tryptophan synthase alpha subunit (trpA)"
/protein_id="AAB99041.1"
/db_xref="GI:1591691"
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/protein_id="AAB99040.1"
/db_xref="01:1591690"
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                                                                                                                                                                                                   DKDHYAYKRAKLAGDLMEDLFRYAFSQLVKDIKYQLERQTLRNKTPSIQAAVRSDILT
ERIKHAMATGTWVGGKTGVSQLLDRTSYLATNSQLRRIVSPLSRSQPHFEARELHGTH
                                                                                                                                                                                                                                                        VAPGQAKDYRLKRAETVLCNYLLPHLGVTKEDFPKKIRFLGIMARNALELYFCYRGED
                                                                                                                                                                                                                                                                              ITQEDLIPNRILCEKAERSGKIVDVAKVFSTRHGFRALCTVERHPDGLLYATFPGMPG
QIPLVILMKALGAETDKDIIESIDDERFFMEIVLNIQEIREEHNINSPEDALEFIGKR
                                                                                                                                                                                                                                                                                                                                   EDAREGETVEVYIGELPVMLGSKICHLYGKSREELIDLGEDPEDPFGYFIINGTEKVL
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                                                                                                                                                                                                                                                                                                                                                                                 /protein_id="AAB99043.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="MJ1040"
7110. .8606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /transl_table=11
/product="DNA-directed RNA polymerase,
/protein_id="AaB89042.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="similar to GB:X59151 SP:P41559 PID:581387 PID:809732 percent identity: 49.33; identified by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KREHVEEITEIADGAIVGSAIVKIVEKHLDENGQIKDEEKFLKELEEFVKNLKEGTKK
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TPDERLKKILEKCSGFVYVVSVTGITGAREKVAEETKELIKRVKKFSKIPACVGFGIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /codon_start-1
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                                                                                                                                                                           WGKICPSETPEGPNCGLVKNFAIMCKVTREEDDSKVIELLKSFGINVS"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         translation="MEWMIMKLAEKFEELKNKGEKAFVAFYVGGDPNLEISEKALEVI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="MJ1038"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="DNA-directed RNA polymerase, subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /transl_table=11
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41.00
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Matches:
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Db 43645 CTTTCAAAACGAATTGGCGTGTCCGTGTCA 43616
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DEFINITION
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AX059549
          Submitted (30-APR-1999) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, MO 63108, USA 4 (bases 1 to 63292)
                                                                                                                                                                                         Arabhdosis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheop
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (Dases 1 to 63292)
Harmon,G., Wohldmann,P. and Lehnert,L.
The sequence of A. thaliana F14G16
                                                                                                                                                                                                                                                                                                                                                                           F14G16 63292 bp
Arabidopsis thaliana BAC F14G16.
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Location/Qualifiers
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                                                             Direct Submission
                                                                              Waterston, R
                                                                                                                              The A. thaliana Genome
                                                                                                                                          2 (bases 1 to 63292)
Washington University
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 Waterston, R.
                                                                                                            Unpublished
                                                                                                                                                                           Unpublished
                                                                                                                                                                                                                                                                                                            Arabidopsis thaliana.
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/db_xxef="taxon:3702"
8769 c 8265 g 14815 +
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from Patent WO0055325.
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                                                                                                                                                                                                                                                                           Tracheophyta;
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                                                                                                  Submitted by:
                                                                                                                      Submitted (13-AUG-1999) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, MO 6~108,
                                                                                                                                                                                                                                                                                                   Direct Submission
                                                                                                                                                                          Direct Submission
                                                                                                                                                                                                 Waterston, R.
Department of Genetics, Washington University, St. Louis, MO 63108, USA e-mail: rwilson@watson.wustl.edu
                                                                        Genome Sequencing Center
                                                                                                                           USA
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M. Lodhi, Cold Spring Harbor Laboratories, and fingerprinted by M. Marra, WashU, to pick the best candidates for sequencing. MAPPING: Clones were assigned to the YAC map by hybridization by M. Lodhi, Cold Spring Harbor Laboratories, and fingerprinted

This sequence was finished as follows unless otherwise noted: neighboring submissions. NOTICE: This sequence may not be the entire insert of this closed it may be shorter because we only sequence overlapping sections once, or longer because we provide a small overlap between this clone.

all regions were double stranded or sequenced with an alternate chemistry; an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone

NEIGHBORING COSMID INFORMATION:

Coding sequences below are predicted from computer analysis, using the program Genefinder(P. Green and L. Hillier, ms in preparation).

Location/Qualifiers The 3' clone is F28D6, 200 bp overlap. Actual is at base position 1 of F14G16; actual end is start of this clone at 41649 of F28D6

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Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K.,
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Mammalia; Eutheria; Rodentia; Sciurograthi; Muridae; Murinae;
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12735. .13052
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (05-MAR-2002) of Molecular and Human G Baylor Plaza, Houston, T 3 (bases 1 to 120885)
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On Jun 18, 2002 this sequence version replaced gi:19525901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (17-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
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                                                                                                                        NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank.draft_data.html).

NOTE: This is a 'working draft' sequence. It ourrently consists of 55 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.

This record will be updated with the finished sequence.
                                                                                               as soon as it is
be preserved.
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                                                                                                                                                                                                                                                     Chemistry: Dye-terminator Big Dye: 100% of a Assembly program: Phrap; version 0.990329 Consensus quality: 57067 bases at least Q30 Consensus quality: 59738 bases at least Q30 Consensus quality: 62357 bases at least Q20
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Center code: BCM
                                                                                                                                                                                                                                                                                                                              Sequencing vector: Plasmid;
                                                                                                                                                                                                                                                                                                                                                       Center project name: GSDR Center clone name: CH230-2
                                                                                                                                                                                                                                                                                                                                                                                   Contact: hgsc-help@bcm.tmc.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                             AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Scores:
                                   Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H.,
Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J.,
Earnhart, C., Edyar, D., Edwards, C.C., Elhaj, C., Escotto, M.,
Ealls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P.,
Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R.,
Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K.,
Falls, F., France, F., Hale, S., Hamilton, K.,
France, F., France, F., Hale, S., Hamilton, K.,
France, F., 
                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 185133)
Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C., Alsbrooks,S.I., Amaratunge,H.C., Are,J.R., Ayele,M., Banks,T., Alsbrooks,S.I., Amaratunge,H.C., Are,J.R., Ayele,M., Banks,T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HTG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rattus norvegicus clone CH230-8L7, 63 unordered pieces.
                                                                                                                                                                        Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C., Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David, Davila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A.,
                                                                                                                                                                                                                                          Bouck, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavagos, S.R., Chacko, J., Chavez, D.,
                                                                                                                                                                                                                                                                                                         Barbaria, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D.,
                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rattus norvegicus
Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A., Hernandez,J.,
Hernandez,O., Hodgson,A., Hogues,M., Holloway,C., Hollins,B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AC095167.3 GI:21722654
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63935:
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of 5645
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of 4416
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of 3163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (16-SEP-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (11-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, Tx 77030, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                      * NOTE: Estimated insert size may differ from sequence length

* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently

* NOTE: this is a 'morking draft' sequence. It currently

* consists of 63 contigs. The true order of the pieces
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         On Jul 10, 2002 this sequence version replaced gi:17942217
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                                                                                                                                                                                                                                                                                                                       * is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: hgsc-help@bcm.tmc.edu
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  Oliver, J., Peterson, K., Phunkhang, P. Raymond, C., Retta, R., Rieback, M., Ri
                                         Hagos, B., Heaford, A., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K., Landers, T., Lehoczky, J., Levine, R., Liu, G., MacLean, C., MacChand, P., Major, J., Marquis, N., Mathews, C., McClarthy, M., McKernan, K., McPheeters, R., Meldrim, J., McReneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, D., O'Neil, D
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     Riley, R., Rise, C.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (18-NOY-2001) Whitehead Institute/MIT Center Research, 320 Charles Street, Cambridge, MA 02141, USA All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             http://ftp.genome.washington.edu/RM/RepeatMasker.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NOTE: This is a "working draft' sequence. It currently consists of 10 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Insert size: 183000; agarose-fp
Insert size: 188400; sum-of-contigs
Quality coverage: 6.8 in Q20 bases; agarose-fp
Quality coverage: 6.6 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Assembly program: Phrap; version 0.960731
Consensus quality: 186360 bases at least Q40
Consensus quality: 187869 bases at least Q30
Consensus quality: 188281 bases at least Q20
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Center clone name: 415_H_15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Web site: http://www-seq.wi.mit.edu
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                                                                                                                                  clone_end:SP6
                           18506. .20378
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/note="assembly_fragment"
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/clone="RP23-415H15"
                                                                                                                                                                                                                                                                                           organism="Mus musculus"
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                                                                                                                                                                                                                                Information on performance of analysis and a more detailed annotation of this entry and other sequences of chromosomes 3, 4 and 5 can be viewed at: http://www.mips.biochem.mpg.de/proj/thal/this fragment has an overlap with ATCHRIV16 at the 5' end and an overlap with ATCHRIV18 at the 3' end.

Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                              lemoke@nips_blochem.mpg.de,mayer@nips_blochem.mpg.de Project
Coordinator: Mike Bevan, Molecular Genetics Department, Cambi
Laboratory, John Innes Centre, Colney Lane, NR4 7UJ Norwich,
E-mail: michael.bevan@bbsrc.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (10-MAR-2000) MIPS, at the Max-Planck-Institut fuer Biochemie, Am Klopferspitz 18a, D-82152 Martinsried, PRG, E-m
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99922. .116348
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                                                                                                                                                           /variety="Columbia"
                                                                                                                                                                                 organism="Arabidopsis thaliana"
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linear

PLN 16-MAR-2000

Mewes, H.W., Lemcke, K.

Norwich, UK Cambridge E-mail:

FEATURES

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Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A., Hernandez,J.,
Hernandez,O., Hodgson,A., Hogues,M., Holloway,C., Hollins,B.,
Homsi,F., Howard,S., Huber,J., Hulyk,S., Hume,J., Jackson,L.E.,
Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S.,
Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J., Kovar,C.,
Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C., Lewis,L.,
Li,J., Lichtarge,O., Lieu,C., Liu,J., Liu,W., Loulseged,H.,
Lozado,R.J., Lu,X., Lucier,R., Lucler,R., Luna,R., Ma,J.,
Maheshwari,M., Mapua,P., Martin,R., Martindale,A., Martinez,E.,
Massey,E., Mawhiney,E., McLeod,M.P., Meaton,N., Mei,G., Metzker,M.,
Miner,G., Miner,Z., Mitchell,T., Wohabbat,K., Morgan,M., Morris,S.,
Moser,M., Neal,D., Newtson,J., Newtson,N., Nguyen,A., Nguyen,N.,
Nguyen,N., Nickerson,E., Nwokenkwo,S., Oguh,M., Okwuonu,G.,
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Douthwalte, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J.,
Barnhart, C., Edgar, D., Edwards, C., Elhaj, C., Escotto, M.,
Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P.,
Gablsi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R.,
Gorrell, J.H., Guevara, W., Gunarathe, P., Hale, S., Hamilton, K.,
Gorrell, J.H., Guevara, W., Gunarathe, P., Hale, S., Hamilton, K.,
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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31062. .31307,31359. .31484))
/gene="AT4g07320"
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/gene="AT4g07310"
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TITLE
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (17-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Jul 14, 2002 this sequence version replaced gi:19263236.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (08-MAR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,K., Tang,H., Tansey,J., Taylor,C., Taylor,T., Telfrod,B., Thomas,N., Thomas,S., Usmani,K., Vasquez,L., Vera,V., Villalon,D., Vinson,R., Wang,Q., Wang,S., Ward-Moore,S., Warren,R., Washington,C., Watlington,S., Williams,G., Williamson,A., Wleczyk,R., Wooden,S., Worley,K., Wu,C., Wu,Y., Wu,Y.F., Zhou,JJ., Zorrilla,S., Nelson,D., Weinstock,G. and Gibbs,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peters,L., Pickens,R., Primus,E., Pu,L.L., Quiles,M., Ren,Y., Rives,M., Rojas,A., Rojubokan,I., Rolfe,M., Ruiz,S., Savery,G., Scher, S., Scott,G., Shen,H., Shooshtari,N., Sisson,I., Sodergren,E., Sonaike,T., Sparks,A., Stanley,H., Stone,H.,
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Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                            * runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                               * arbitrary. Gaps between the contigs are represented as 
* runs of N, but the exact sizes of the gaps are unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   * (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 38 contigs. The true order of the pieces
* consists of 38 contigs. The true order of the pieces
                                                                                                                                                                                                                                                                                                                                                                                                      st as soon as it is available and the accession number will st be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NOTE: Estimated insert size may differ from sequence length
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Consensus quality: 111894 bases at least Q40
Consensus quality: 116026 bases at least Q30
Consensus quality: 119751 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequencing vector: Plasmid;
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US-09-823-649A-6 (1-11) x AC114382 (1-150018)
                                  Percent Similarity:
Best Local Similarity:
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                          Query Match:
                                                                        Alignment Scores:
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11099: contrig of 7230 bp in length
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Submitted (17-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Jul 13, 2002 this sequence version replaced gi:18701531.
                                                                                                                                                                                                                                                                                                                                                            Submitted (16-JAN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
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Direct Submission
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Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J.,
Danhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M.,
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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 61 contigs. The true order of the pieces
                                                                                                                                                                                                                                                                                                                                                                                                                            arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown This record will be updated with the finished sequence
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Chemistry: Dye-terminator Big Dye: 100% of reads Assembly program: Phrap: version 0.990329
Consensus quality: 111369 bases at least Q40
Consensus quality: 116447 bases at least Q30
Consensus quality: 121122 bases at least Q30
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Center clone name: CH230-155M2
Center clone name: Statistics
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                                                                                                    Baylor
On Jul
                                                                                                                                             Submitted (10-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H., Tansey, J., Taylor, C., Taylor, T., Telfrod, B., Thomas, N., Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wang, Q., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S., Williams, G., Williamson, A., Wleczyk, R., Wooden, S., Worley, K., Wu, C., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D., Weinstock, G. and Gibbs, R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (15-SEP-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                          Direct Submission
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Direct Submission
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Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rattus norvegicus
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                                             Jul 9, 2002 this sequence version replaced gi:17941157
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Center: Baylor College of Medicine
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Sciurognathi; Muridae; Murinae;
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Bryant, N.P.,
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COMMENT

bp in length

TITLE

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arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
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NOTE: This is a 'working draft' sequence. It currently
consists of 65 contigs. The true order of the pieces
is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     as soon as it
be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Assembly program: Phrap; version 0.990329 Consensus quality: 124332 bases at least Q40 Consensus quality: 129469 bases at least Q30 Consensus quality: 134129 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center project name: GAOY
Center clone name: CH230-3012
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Post-processing: Minimum Match 0%
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Listing first 45 summaries
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Bacillus stcarothermophilus DNA polymerase I (kicnow) clones including those with reduced 3'-to-5' exonuclease activity Patent: EP 0875576-A 9 04 NOV-1998;
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Bacillus Stearothermophilus DNA polymerase I (klenow) clones including those with reduced 3'-to-5' exonuclease activity Patent: EP 087576-A 10 04-NOV-1998;
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413 c 492 g 215
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DNA polymerase having ability to reduce inpate selective
discrimination against fluorescent dye-labeled dideoxymucleotides
Pitent: US 6165765-A 1 26-DEC-2000;
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Hong, G.Fan., Huang, W.-h. and Zhai, F. deceased.
Bacillus stearothermophilus DNA polymerase with proof-reading 3'-5'
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Patent: US 5834253-A 1 10-NOV-1998;
Location/Qualifiers
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AR008369
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Sequence
AR008369
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Sequence 3 from patent US 6165765.
AR122766
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Location/Qualifiers
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                       AR008369
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                                                                                                                                                                                                                                                                                                                          exonuclease activity
                                                                                                                                                                                                                                                                                                                                     Bacillus stearothermophilus DNA polymerase with proof-reading 3'-5'
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Hong, G. and Huang, W.-h.
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16 from patent US 5753482
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415 c 487 g
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418 c 485 g
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1 (bases 1 to 1779)
Ishino,Y., Uemori,T., Fujita,Y. and Katou,I.
DNA POLYMERASE GENE
PATENT: JP 193284971-A 1 02-NOV-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Method for cloning of a gene for pol I type DNA polymerase
Patent: US 5753482-A 16 19-MAY-1998;
Location/Qualifiers
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Bacillus caldotenax
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JP 1993284971-A/1.
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JP 1993284971-A/1
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ISHINO YOSHIZUMI, UEMORI TAKASHI, EUJITA YOSHIYO,
                                                                                                                                                                                                           *source: strain=YT-G(DSM406);
*source: clone=pUI205;
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/product='a DNA polymerase'

Location/Qualifiers
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425 c 529 g
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/db_xref="taxon:1395"
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US-09-823-649A-7 (1-11) x E05777 (1-1779)
US-09-823-649A-7 (1-11) x AX002395 (1-1880)
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                                                                                                                                                                                                                                                                                                                                                                                              Sequence 8 from Patent EP0875576
                                                                                                                                                                                                                                                 Bacillus stearothermophilus DNA polymerase I (klenow) clones including those with reduced 3'-to-5' exonuclease activity Patent: EP 0875576-A 8 04-NOV-1998;
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Tan, T.C. and Phang, S.M.
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Method for cloning of a gene for Pol I type DNA polymerase
Patent: US 5436326-A 16 25-JUL-1995;
                                                                                                                                                                                                                                       UNIV SINGAPORE (SG)
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Ishino,Y., Uemori,T.,
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425 c 529 g
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486 c 573 g
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PC C12N1
CC strap
CC topol
CC Featt
FH Key
FH CDS
 96303305
8740835
                                                                                            Geobacillus stearothermophilus
Bacteria; Firmicutes; Bacillales; Geobacillus
1 (bases 1 to 2631)
                                                                                                                                                                                          cds.
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DNA POLYMERASE GENE
Patent: JP 1993304964-A 4 19-NOV-1993;
TAKARA SHUZO CO LTD
PN JP 1993304964-A/4
                                     Thermostable Bst DNA polymerase I lacks a 3'-->5' proofreading exonuclease activity
                                                                                                                                                                                                    BSU33536 2631 bp DNA linear BCT 21-APR-1997
Bacillus stearothermophilus DNA polymerase I (polA) gene, complete:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PF PN NA
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JP 1993304964-A/4.
                                                                              Aliotta, J.M.,
                                                                                                                                    Geobacillus stearothermophilus.
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                           Genet. Anal.
                                                                  and Kong, H.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                topology: Linear;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product='DNA polymerase'
Location/Qualifiers
Location_2628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Geobacillus stearothermophilus"
/db_xref="taxon:1422"
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97.96%
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                                                                              Pelletier, J.J., Ware, J.I., Moran, L.S., Benner, J.S.
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Alignment Scores: Pred. No.:
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US-09-823-649A-7 (1-11) x BSU33536
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 LeuAlaGinAsnieuAsnile***ArgiysGlu 11
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Sequence 13 from patent US 5753482.
AR008368
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                                                                                                                                                                              1 (bases 1 to 2631)
Ishino,Y., Uemori,T., Fujita,K. and Kato,I.
Method for cloning of a gene for pol I type DNA polymerase
Patent: US 5753482-A 13 19-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
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GFQSFLEKMAAPAAEGEKPLEEMEFAIVDVITEEMLADKAALVVEVMEENYHDAPIVG
IALVNEHGRFYMRPEYALADSQFLAWLADETKKKSMFDAKRAVVALKWKGIELRGVAF
                                                                                      /organism="unknown"
638 c 774 g
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TLRVPLKVDYHYGPTWYDAK"
1 616 c 716 g 578 t
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TKTAMDIFHVSEEEVTANWRRQAKAVNFGIVYGISDYGLAQNLNITRKEAAEFJERYF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAAIWALEQPFMDDLRNNEQDQLLTKLEQPLAAILAEMEFTGVNVDTKRLEQMGSELA
EQLRAIEQRIYELAGQEENINSPKQLGVILFEKLQLPVLKKTKTGYSTSADVLEKLAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DILLAAYLLNPAQDAGDIAAVAKMKQYEAVRSDEAVYGKGVKRSLPDEQTLAEHLVRK
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YELDHYEADDIIGTLAARAEQEGFEVKIISGDRDLTQLASRHVTVDITKKGITDIEPY
TPETVREKYGLTPEQIVDLKGLKGDKSDNIPGVPGIGEKTAVKLLKQFGTVENVLASI
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/db_xref="G1:1205984"
/translation="MKKKIVLIDGNSVAYRAFFALPLLHNDKG1HTNAVYGFTMMLNK
                                                                                                                                                      Location/Qualifiers
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US-09-823-649A-7 (1-11) x AR008368 (1-2631)	x AR008368 (1-:	2631)	
Oy 1 LeualaGinAsnLeuasnIle***ArgLysGlu 11	uAsnIle***ArgLy	ysGlu 11	
Db 2164 TTGGCGCAAAACTTAAATATTTCACGCAAAGAG 2196 Search completed: January 16, 2003, 11:05:00	AAATATTTCACGCA	AAGAG 2196	
Search completed: January 16, 2003, 11:05:00 Job time: 1534.14 secs	16, 2003, 11	:05:00	

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Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                SPTREMBL_21:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_human:*
5: sp_manmal:*
7: sp_mhc:*
8: sp_organele:*
9: sp_blage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:
14: sp_unclassific
15: sp_archeap:*
16: sp_bacteriap:*
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Gapop 10.0 , Gapext 0.5
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2	48	98.0	877	2	024675	024675 bacillus st	
ω	40	81.6	866	16	6MIX8Ö	Q8xiw9 clostridium	
4	39	79.6	875	₽,	Q92BF0	Q92bf0 listeria in	
51	39	79.6	875	16	9M9A8Ö	Q8y6w6 listeria mo·	
6	39	79.6	876	26	Q9K854	Q9k854 bacillus ha	
7	37	75.5	388	æ	Q96LP7	Q961p7 homo sapien	
8	36	73.5	114	N	Q8VSV3	Q8vsv3 escherichia	•
9	36	73.5	114	2	Q8VSV2	Q8vsv2 escherichia	
10	36	73.5	114	N	Q8VLL0	Q8v110 escherichia	
11	36	73.5	114	N	Q8VL18	Q8v118 escherichia	
12	36	73.5	281	N	Q9AMB8	Q9amb8 burkholderi	
13	36	73.5	928	16	Q8X8H1	Q8x8hl escherichia	
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15	35	71.4	471	17	Q972J5	Q972j5 sulfolobus	
16	35	71.4	483	,		00:::::	

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	Q8rcm0 thermoanaer	campy loba	Q59599 neisseria g	Q9jxw8 neisseria m	Q8z2s2 salmonella	Q8rbe6 thermoanaer	Q8vp66 thermoanaer	Q8u6f8 agrobacteri	P90573 plasmodium	OD.	Q9szd0 arabidopsis	anabaena	Q9jzul neisseria m	Q9bk02 tribolium c		Q8wr84 tribolium c	062546 hydra atten	\sim	Q9w2j8 drosophila	drosophil) xenopus	٠.				arabidops	2326 arabidopsi	Q9z7b5 chlamydia p	

ALIGNMENTS

DR D	DR DR RET	R R R R R C C C C G G G	RESULT Q45458 ID Q AC Q DT 0 DT 0
InterPro; IPROO InterPro; IPROO InterPro; IPROO Pfam; pPO1357; Pfam; pF02739; Pfam; pF00446; PFINTS; PRO0868 SMART; SM00474; SMART; SM00475; SMART; SM00279; SMART; SM00279; SMART; SM00279; SMART; SM00279; SMART; SM00482; FIGRRAMS; TICRO PROSITE; PS0044 SEQUENCE 876	135 20 20	llus llus eria acil acil _Tax _Tax	21154 21154 21224
10513; EVA 10513; EXONUC 5_3_EXONUC 5_3_EXONUC 5_3_EXONUC 1052, EXONUC 1053, EXONUC 1053, EXONUC 1053, POLAC 11, DNA_POLAC 11, DNA_POLAC 11, DNA_POLAC 11, DNA_POLAC 11, DNA_POLAC	ble Bst DNA polymerase e activity."; 1. 12:185-195(1996). 36; AAB52611.1; 36; AXB52611.2; 37; AWL. 1PR002562; 3_exonucliter002562; 1XWL. 1PR002421; 5_3_exonucliter002089; DNA_pol_	rothermop micutes; 22; 1 N.A. Pelletie	PRELIMINARY; (Tremblrel 01, (Tremblrel 01, (Tremblrel 21,
DOLL. 2. 2. 2. 1. 1. 2. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1.	sc l	hilus. Bacillus/Clostridium group;	PRT; 876 AA. Created) Last sequence update) Last annotation update)
1. 1. E_A; 1. B981BCE95F1651A7	cks a	ridium q	876 AA. luence up
51A7 CRC64;	3'>5' proofreading	m group; Bacillales;	pdate) update)

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Matches
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Best Local
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SMART; SM00474; 35EXOC; 1.
SMART; SM00475; 53EXOC; 1.
SMART; SM00279; HhH2; 1.
SMART; SM00482; POLAC; 1.
                        Clostridium perfringens.
Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia; Clostridiales; Clostridiaceae; Clostridium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; 09308; AAB62092.1; -.
EMBL; 09308; AAB62092.1; -.
HSSP; P52026; 1XWL.
InterPro; IPR002562; 3_5_exonuclease.
InterPro; IPR002421; 5_3_exonuclease.
InterPro; IPR001098; DNA_pol.
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01-JAN-1998 (TrEMBLrel.
01-JAN-1998 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
                                                                DNA polymerase I. POLA OR CPE1994.
                                                                                         01-MAR-2002 (TrEMBLrel 01-MAR-2002 (TrEMBLrel 01-JUN-2002 (TrEMBLrel )
                                                                                                                               ; eMIXBO
                                                                                                                                                                                                                                                                                                                TIGREAMS; TIGR00593; pola; 1.
PROSITE; PS00447; DNA_POLYMERASE_A; 1.
SEQUENCE 877 AA; 99200 MW; 4B9639483FB41DHB CRC64;
NCBI_TaxID=1502; [1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA polymerase I gene.";
Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases
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Geobacillus
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PF01367; 5_3_exonuclease;
PF02779; 5_3_exonuc_N; 1.
PF004 5; DNA_pol_A; 1.
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90.9%;
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90.9%;
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Pred. No. 0.21;
0; Mismatches
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Best Local
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Pfam; PF02739; 5_3_exonuc_N; 1.
Pfam; PF00476; DNA_pol_A; 1.
PRINTS; PR00868; DNAPOLL;
SMART; SM00475; 53EXOC; 1.
SMART; SM00279; HHH2; 1.
SMART; SM00482; POLAC; 1.
TIGREAMS; TIGR00593; Pola; 1.
PROSITE; PS00447; DNA_POLYMERASE_A; 1.
                                                                                                             Baguero F., Herche P., Bloecker H., Brandt P., Chakraborty T., Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P., Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O., Entian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P., Gautter L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D., Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G., Madueno E., Maitournam A., Mata Vicence J., Ng E., Nedjari H., Madueno E., Maitournam A., Mata Vicence J., Ng E., Nedjari H., Mordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R., Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P., "Comparative genomics of Listeria species.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. STRAIN=13 / TYPE A; PubMed=11792842;
                                                                                       "Comparative genomics of Listeria Science 294:849-852(2001).
EMBL; AL596169; CAC96831.1; -.
                                                                                                                                                                                                                                                                                                                                          Listeria innocua.
Bacteria; Firmicutes; Bacillus/Clostridium
Listeriaceae; Listeria.
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InterPro; IPR000513;
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Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.;
"Complete genome sequence of Clostridium perfringens, an a
                     Listilist; LIN01600; ...
InterPro; IPR002421; 5.3_exonuclease.
InterPro; IPR001098; DNA_pol.
InterPro; IPR002298; DNA_pol.
InterPro; IPR002513; EXO_N_I.
                                                                                                                                                                                                                                                             Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
                                                                                                                                                                                                                                                                            STRAIN-CLIP 11262 / SEROVAR 6A; PubMed-11679669;
                                                                                                                                                                                                                                                                                                                                                                                POLA OR LIN1600.
                                                                                                                                                                                                                                                                                                                                                                                           DNA polymerase 1.
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Pfam; PF01367; 5_3_exonucle
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InterPro; IPR001098; DNA_pol.
 InterPro; IPRO
Pfam; PF01367;
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                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=1642;
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8; Conserv
             IPR003583; HHH_1
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(TrEMBLrel. 19, Last sequence update)
("FREMBL.rel. 21, Last annotation update)
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 5_3_exonuclease;
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72.7%;
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Best Local
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                                                                                                                                                                                                        Pfam; PF01367; 5_3_exonuclease; pfam; PF02759; 5_3_exonuc_N; 1. Pfam; PF00476; DNA_P01_A; 1. PRINTS; PR00868; DNAPOLI.
                                                                                                                                                                                                                                                                                                                                                                                    Vazquez-Boland J.-A., Voss H., Wehland J., C "Comparative genomics of Listeria species."; Science 294:849-852(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIKAIN=EGD-E / SEROVAR.1/2A;
MEDLINE-21537279; PubMed=116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales; Listeriaceae; Listeria.
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PROSITE; PS00447; DNA_POLYMERASE_A; UNKNOWN_1.
COmplete proteome.
SEQUENCE 875 AA; 98609 MW; 084F3936818D61E
                                                                                                                                                               SMART; SM00475;
SMART; SM00279;
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InterPro; IPR003584; HHH_2
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InterPro; IPR002421; 5_3_exonuclease.
InterPro; IPR001098; DNA_pol.
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                              Similarity
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875 AA;
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PS00447; DNA_POLYMERASE_A; 1.
                              Conservative
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                                                                                                                                                               35EXOC; 1.
53EXOC; 1.
HhH2; 1.
                                                                                                                                                 POLAC; 1.
                                                                                                                                                                                                                                                     _3_exonuclease; 1.
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                                                                                      98448 MW;
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72.7%;
                                           79.6%;
72.7%;
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Last sequence update)
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Pred. No. 15;
1; Mismatches
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Pred. No. 15
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                                                                                        94B541A6190D05CF CRC64;
                              Mismatches
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15;
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Best Local
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Q9K854;
Q1-QCT-2000 (TrEMBLrel. 15, Creation-cort-2000 (TrEMBLrel. 15, Last
Q1-JUN-2002 (TrEMBLrel. 21, Last
DNA polymerase 1 (EC 2.7.7.7).
POLA OR BH3153.
                                                                                                                                                                                                                                                                                                                                       SMART; SM00474; 35EXOC; 1.
SMART; SM00475; 53EXOC; 1.
SMART; SM00278; HhH1; 1.
SMART; SM00279; HhH2; 1.
SMART; SM00482; POLAC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam;
Pfam;
                                                                            Q96LP7;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam;
                  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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PROSITE; PS00447; DNA_POLYMERASE_A; 1.

Transferase; Nucleotidyltransferase; Complete proteome.

SEQUENCE 876 AA; 99545 MW; 3CAID7EBDB689617 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Takami H., Nakasone K., Takaki Y., Maeno G., So
Fuji F., Hirama C., Nakamura Y., Ogasawara N.,
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HSSP; P52026; 2BDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and genomic sequence comparison with Bacillus subtilis."; Nucleic Acids Res. 28:4317-4331(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacillus halodurans.
                                                        Homo sapiens (Human)
                                                                     CDNA FLJ25320 fis, clone TST00267 (Fragment).
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SEQUENCE FROM N.A
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PF02739; 5_3_exonuc_N; 1.
PF00476; DNA_pol_A; 1.
                                                                                                                                                                                                                                                                                                                                                                                                       PR00868; DNAPOLI
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                                                                                                                                                                                                                                              Conservative
                                                                                                                                   PRELIMINARY;
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72.78;
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., Kuhara S.,
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RESULT 9
Q8VSV2
ID Q8VS
AC Q8VS
AC Q8VS
DT 01-M
DT 01-M
DT 01-M
DT 01-M
DT 01-M
DE DNA
GN POLA
GN POLA
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Best Local S
Matches 7
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Matches 8; Conserv
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Q8VSV3;
01-MAR-2002
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Ishibashi T., Kanehori K., Yosida M., Watanabe S., Ishida S., Ono Y.,
Hotuta T., Hiraoka S., Murakawa K., Takiguchi S., Kusano J.,
Watanabe M., Fujimori K., Tanai H., Ishida M., Yamashita H., Chiba Y.,
Suzuki Y., Hata H., Nakagawa K., Mizuno S., Morinaga M., Kawamura M.,
Sugiyama T., Irie R., Otsuki T., Sugiyama S., Ishikawa T., Sugiyama A.,
Kawakami B., Nagai K., Isogai T., Sugano S.;
"NEDO human cDNA sequencing project.";
"NEDO human cDNA sequencing project.";
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
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SEQUENCE
                                                                                                                                                                                                                                                                                           NON_TER
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"Three R's of bacterial evolution: how replication, repair,
recombination frame the origin of species.";
Environ. Mol. Mutagen. 38:248-260(2001).
EMBL; AF359695; AAL59502.1; -.
EMBL; AF359695; DNA_pol.
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                                                          01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                               SEQUENCE
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01-JUN-2002
             Bacteria; Proteobacteria;
                       Escherichia coli
                                               DNA polymerase
                                                                                                Q8VSV2;
                                                                                                               Q8VSV2
                                                                                                                                                                                                                                                                                                                    PROSITE; PS00447; DNA_POLYMERASE_A; UNKNOWN_1
                                                                                                                                                                                                                                                                                                                                 SMART;
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F; SM00482; POLAC; 1.
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7; Conserv
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63.6%;
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              gamma subdivision; Enterobacteriaceae;
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Last annotation updat
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Q8VL18
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Q8VLL0;
01-MAR-2002
01-MAR-2002
01-JUN-2002
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Pfam; PF00476; DNA_pol_A; 1.
SMART; SM00482; POLAC; 1.
Q8VL18 PRELIMINARY, Q8VL18;
01-MAR-2002 (TremBLrel.
01-MAR-2002 (TremBLrel.
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EMBL; AF359736; AAL59543.1; -.
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MEDLINE=21610577; PubMed=11746762;
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Pred. No. 8.
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Last sequence update)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Three R's of bacterial evolution: how replication, repair, recombination frame the origin of species.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Brown E.W., LeClerc J.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=VARIOUS STRAINS;
MEDLINE=21610577; PubMed=11746762;
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AF359680; AAL59487.1;
AF359681; AAL59488.1;
AF459682; AAL59489.1;
AF359683; AAL59490.1;
AF359684; AAL59491.1;
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AF359731;
AF359732;
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AF359704;
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AF359702;
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AF359688;
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AAL59500.
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Q9AMB8;
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PROSITE; PS00716; SIGMA70_1; 1.

PKOSITE; PS00716; SIGMA70_2; 1.

PKOSITE; PS00716; SIGMA70_2; 1.

DNA-binding; DNA-directed RNA polymerase; Sigma factor;
                                                                                                                                                                                                                                                 InterPro; IPR000943; Sigma_70.
Pfam; PF00140; Sigma70; 1.
                                                                                                                                                                                                                                                                                                                                                               clinical PCR development.";
Submitted (DEG-2000) to the EMBL/GenHank/UDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                        Steiner B., Bowen M., Morrill W., Meyer R.; "Random segmenting of Burkholderia pseudomallei strain 69313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Burkholderia pseudomallei (Pseudomonas pseudomallei).
Bacteria; Proteobacteria; beta subdivision; Burkholderia group;
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                                                                                                                                                                Transcription regulation. SEQUENCE 281 AA; 31352 MW;
                                                                                                                                                                                                                                                                               HSSP; P00579;
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                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-G9313
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L; AF359738; AAL59545.1; -.
L; AF359742; AAL59549.1; -.
L; AF359742; AAL59550.1; -.
L; AF359744; AAL59551.1; -.
L; AF359746; AAL59553.1; -.
L; AF359746; AAL59553.1; -.
L; AF359747; AAL59555.1; --
L; AF359748; AAL595555.1; --
L; AF359748; AAL595555.1; --
L; AF359748; AAL59555.1; --
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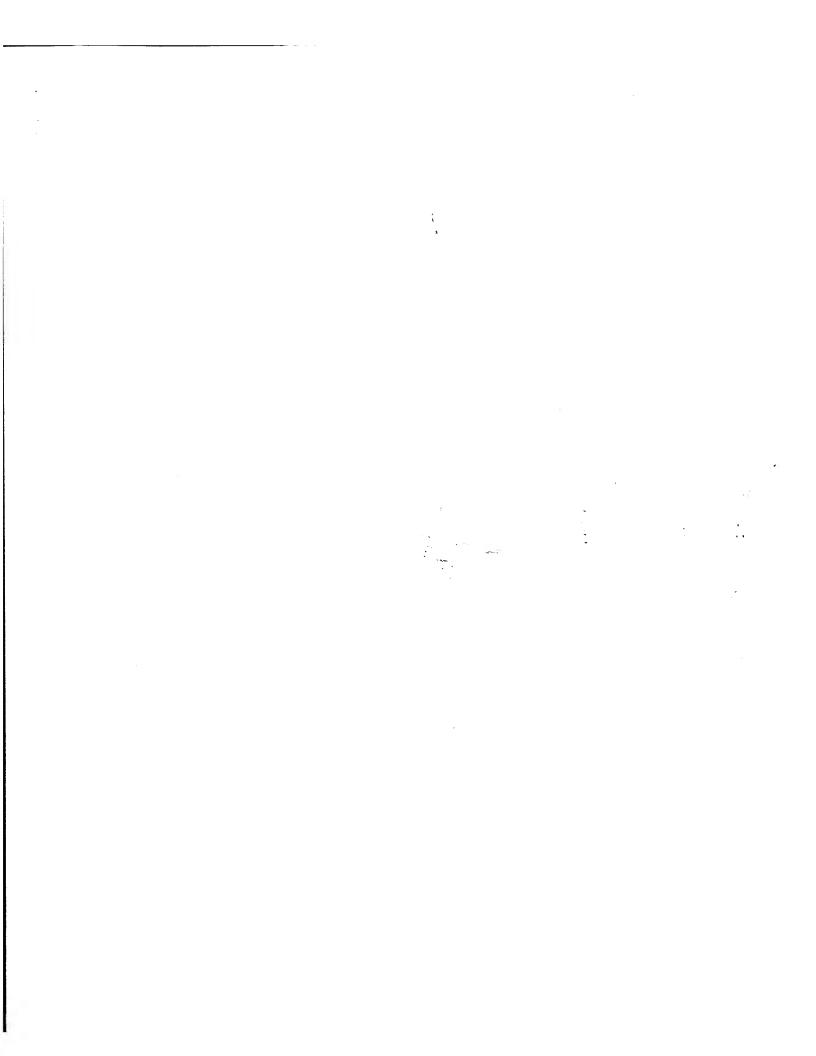
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POLA OR Z5398 OR ECS4786.
POLA OR Z5398 OR ECS4786.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Perna N.T., Pinkett G. III, Burland V., Mau B., Glasner J.D., Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A., Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L., Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K., Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C., Welch R.A., Blattner F.R.; "Genome sequence of enterohaemorrhagic Escherichia coli 0157:H7."; "Nature 409:529-533(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2002 (TrEMBLrel. 20, 01-MAR-2002 (TrEMBLrel. 20, 01-JUN-2002 (TrEMBLrel. 21, DNA polymerase I, 3'--> 5' E
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MEDLINE-21156331; PubMed-11258796;
Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
Kuhara S., Shiba T., Hattori M., Shinagawa H.;
Kuhara S., Shiba T., Hattori M., Shinagawa H.;
Tomplete genome sequence*of enterohemorrhagic Escherichia coli
0157:H7 and genomic comparison with a laboratory strain K-12.";
                 Q97L97;
01-OCT-2001 (TrEMBLrel. 18,
01-OCT-2001 (TrEMBLrel. 18,
01-DEC-2001 (TrEMBLrel. 19,
                                                                                       Q97L97
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MEDLINE=21074935; PubMed=11206551;
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DNA Res. 8:11-22(2001)
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ABC-type sugar transport system,
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r; SM00482; POLAC; 1.
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PF01367; 5_3_exonuclease; 1.
PF02739; 5_3_exonuc_N; 1.
PF00476; DNA_pol_A; 1.
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IPR002421; 5_3_exonuclease.
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Q972J5;
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109 AENLNIPREE 118
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6; Conserv
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"Tatusov R.L., Sabathe F., Dubois J., Qiu D., Hilli J., Wolf Y.I.,
Bennett G.N., Koonin E.V., Smith D.R.;
"Genome sequence and comparative analysis of the solvent-producing bacterium Clostridium acetobutylicum.";
J. Bacteriol. 183:4823-4838(2001).
EMBL; AE007582; AAK78642.1 -
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                                                                                                                                                                                     InterPro; IPR003439; ABC_transportr.
Pfam; PF00005; ABC_tran; 2.
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MEDLINE-21359325; PubMed=11466286;
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PROSITE; PS00211; ABC_TRANSPORTER; U
ATP-binding; Hypothetical protein; C
SEQUENCE 471 AA; 53267 MW; 57088
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EMBL; AP000985; BAB66171.1; ~.
                                                                                                                                                                                                                                                                            "Complete genome sequence of an aerobic thermoacidophilic Crenarchaeon, Sulfolobus toxodail strain7.";
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Search completed: January 15, 2003, 12:36:11 Job time: 33.5714 secs



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SAHH_SULTO
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YRY5_CAEEL
Y554_AQUAE
IDI2_RICCN
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YU52_ARCFU
YU53_YEAST
DF01_SALTY
CARB_NEIGO
CARB_NEIMB
RL29_RICGN
RL29_RICPR
RT29_RICPR
Y773_METJA
ASNA_CLOPE
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0.93md5 clostridium
0.29011 archaeoglob
p53148 saccharomyc
0.9f173 salmonella
0.5959 neisseria m
0.292x4 rickettsia
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0.58183 methanococc
0.8xi95 clostridium
0.18488 drosophila
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0.09355 caenorhabdi
0.66829 aquifex aeo
0.92hm7 rickettsia
0.975t0 sulfolobus
p14930 rickettsia
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p14930 nepptide m
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ntry is constituted instituted instituted instituted it instituted it statement a license to licens	C., Brame C., Brame C., Brame C., Brame C., Brame C., Brame C., Brame C., C., Brame C., P., C., C., C., C., C., C., C., C., C., C	95). APHY (2.1 AN PubMed=9016 C., Hansen (e L.s.; e thern e solution resolution 8(1997).	ubMed. ., Lo te se cteri	es; Bac:	34, Crean 36, Last 41, Last EC 2.7.7	DARD;	54444 500 54444 500 5444 500 500 500 500
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PFam; PFUZ/JJ; DNAFUL—
PFam; PFUZ/JJ; DNAFUL—
PRINTS; PRÜÜÖSS; DNAFUL—
SMART; SMÜÜ174; 35EXOC; 1.
SMART; SMÜÜ279; HhH2; 1.
SMART; SMÜÜ279; HHH2; 1.
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PROSITE; PS00447; DNA_POLYMERASE_A; 1.
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1 310 5'-3' EXONUCLEASE (BY SIMILARITY).
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  AAA85558.1;
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5_3_exonuc_N; 1.
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R -> H (IN STRAIN USED IN REF. 3/4).

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01-0CT-1993
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use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for compentities removed.
                                                                                                                                                                                                                                                                                                                        "Cloning of the DNA polymerase gene of Bacillus caldotenax characterization of the gene product.";
J. Blochem. 113:401-410(1993).
                                                                      This SWISS-PROF entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBI the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is
entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                            -i- FUNCTION: IN ADDITION TO FOLIMERASE ACTIVITY, THIS DNA POLYMERASE EXHIBITS 3' TO 5' AND 5' TO 3' EXONUCLEASE ACTIVITY.
-i- CATALYTIC ACTIVITY: N deoxymucleoside triphosphate = N diphosphate
                                                                                                                                                                                                                                                                                                                                                                                                             MEDIJINE=93252765; PubMed=8486614;
Uemori T., Ishino Y., Fujita K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacillus caldotenax.

Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus
                                                                                                                                                                                      -!- SUBUNIT: SINGLE-CHAIN MONOMER WITH MULTIPLE FUNCTIONS.
-!- SIMILARITY: BELONGS TO THE DNA POLYMERASE TYPE-A FAMILY.
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L. 27, Last sequence 1. 41, Last annotation (EC 2.7.7.7)
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D -> E (IN STRAIN USED IN REF. 3/4).

T -> M (IN STRAIN USED IN REF. 3/4).

SV -> NA (IN STRAIN USED IN REF. 3/4).

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RA Kunst F., Ogasawara N., Moszer I., Bloutin A., Borchert S.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
RA Denizot F., Devine A., Golightly E.J., Galderon N.,
RA Guiseppi G., Fujita Y., Fabret C., Ferrari E., Foulger D.,
RA Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Guiseppi G., Kasahara Y., Klaerr-Blanchard M., Klein C.,
RA Guiseppi S., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Kurita K., Lapidus A., Lavine A., Masuda S., Medina N., Meliado R., Mizuno M., Moestl D., Nakai S., Noback M.,
Medina N., Meliado R., Mizuno M., Moestl D., Nakai S., Noback M.,
Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
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pfam; PF01367; 5_3_exonuclease;
pfam PF02739; 5_3_exonucle; 1.
PRINTS; PR00868; DNAPOLI.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=98048467; PubMed=9387221;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DUN-2002 (Rel. 41, Last annotation update)
DNA polymerase I (EC 2.7.7.7) (POL I).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              034996;
15-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DPO1_BACSU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00447; DNA_POLYMERASE_A; 1.
Transferase; DNA-directed DNA polymerase; DNA replication;
Hydrolase; Exonuclease; DNA-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000513; Exo_N_I.
InterPro; IPR003584; HHH_2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lapidus A., Galleron N., Sorokin A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=1423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR003584;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               722 LAQNLNISRKE 732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 LAQNLNIXRKE 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 T; SM00475; 53EXOC; 1.
T; SM00279; HhH2; 1.
T; SM00279; POLAC; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IPR002562; 3_5_exonuclease. IPR002421; 5_3_exonuclease. IPR001098; DNA_pol. IPR002298; DNA_polI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TIGR00593; pola; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     469
877 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      311
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   877
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacillales; Bacillaceae; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5'-3' EXONUCLEASE (BY SIMILARITY).
3'-5' EXONUCLEASE (BY SIMILARITY).
POLYMERASE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 48; DB 1;
Pred. No. 0.026;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DASFC7F5B6DFA6F4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ehrlich S.D.;
n of the Bacillus subtilis genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               880 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              )_-.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              indeis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0,
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DA DA RE

SMX4_SCHMA STAI Q26603; 15-JUL-1999 (Rel. 15-JUL-1999 (Rel. 15-JUL-1999 (Rel.

STANDARD;

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Homeobox protein SMOX-4 (Fragment)

38, Created)
38, Last sequence update)
38, Last annotation updat

RESULT 4
SMX4_SCHMA

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                                                                                                                                           Query Match
Best Local (
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SMART; SM00474; 35EXOC; 1.
SMART; SM00475; 53EXOC; 1.
SMART; SM00278; 5HH1; 1.
SMART; SM00279; HHH2; 1.
SMART; SM00482; POLAC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y., Sato T., Scanna E., Schleich S., Schoeter R., Scoffone F., Seklyuchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo Scrokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K., Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A., Tosato V., Uchiyana S., Vandenbol M., Vannier F., Vassarotti A., Vandenbol V., Uchiyana S., Vandenbol M., Vannier F., Vassarotti A., Vandenbol V., Uchiyana S., Vandenbol M., Vanden
                                                                                                                                                                                                                         TIGREAMS; TIGROUS93; pola; 1.
PROSTIE; PSO0447; DNA.POLYMERASE.A; 1.
PROSTIES: DNA-directed DNA polymerase; DNA replication;
Hydrolase; Exonuclease; DNA-binding; Complete proteome.
SEQUENCE 880 AA; 99091 MW; AFB434AFDF25F488 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     modified and this statement is not removed. Usage by and for entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000513; Exo_N_I.
InterPro; IPR003583; HHH_1.
InterPro; IPR003584; HHH_2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Viari A., Wambutt R., Wedler E., Wedler H., Weitzenegger T.,
Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Parro V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SubtiList;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SUBUNIT: SINGLE-CHAIN MONOMER WITH MULTIPLE FUNCTIONS.
-!- SIMILARITY: BELONGS TO THE DNA POLYMERASE TYPE-A FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -i- FUNCTION: IN ADDITION TO POLYMERASE ACTIVITY, THIS DNA POLYMERASE EXHIBITS 3' TO 5' AND 5' TO 3' EXONUCLEASE ACTIVITY (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 390:249-256(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "The complete genome sequence of the Gram-positive bacterium Bacillus
725 LSQNLGITRKE 735
                                                                                                                                        Local
                                                  1 LAQNLNIXRKE 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PF00476; DNA_pol_A; 1.
PF01367; 5_3_exonuclease; 1.
PF02739; 5_3_exonuc_N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (N) {AND}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P52026;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AF008220; AAC00350.1; -.
                                                                                                           Similarity
8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              non-profit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IPR002562; 3_
IPR002421; 5_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IPR002298; DNA_polI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IPR001098;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pohl T.M., Portetelle D., Porwollik S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BG12656; polA
                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAB14869.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           institutions as long as its content
                                                                                                                                           79.6%;
72.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3_exonuclease
                                                                                                                                     Score 39; I
Pred. No. 2.
                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                There are no
                                                                                                                                                                   DB 1;
                                                                                                                                                                Length 880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Prescott A.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      restrictions
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                                                                                                                                                                                                                                                                           DNA repair;
                                                                                                           0,
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RESULT 5
CG12_YEAST
ID CG12_Y
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01-FEB-1996 (Rel. 33, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
G1/S-specific cyclin CLN2.
CLN2 OR YPL256C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   bilateral metazoan.";
Mech. Dev. 38:25-32(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Schistosoma mansoni (Blood fluke).
Eukaryota; Metazoa; Platyhelminthes;
Hadwiger J.A., Reed S.I., "Nucleotide sequence of the Saccharomyces cerevisiae CLN1 and
                                                                                                                                                                         {\tt Hadwiger\ J.A.,\ Wittenberg\ C.,\ Richardson\ H.E.,\ de\ Barros\ Lopes\ M.,\ Reed\ S.I.;}
                                                                                                                                                                                                                                                                                                                                         Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; M85302; AAA29931.1; -. HSSP; P14653; 1B72.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                            "A family of cyclin homologs that control the G1 phase in Proc. Natl. Acad. Sci. U.S.A. 86:6255-6259(1989).
                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                        Eukaryota; Fungi; l
Saccharomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P20438;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SUBCELLULAR LOCATION: Nuclear (Probable).
                                                    MEDLINE=90326560; PubMed=2197605;
                                                                               SEQUENCE FROM
                                                                                                                                                                                                                           MEDLINE=89345642; PubMed=2569741;
                                                                                                                                                                                                                                                                                                 NCBI_TaxID=4932;
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                                                                               I N.A.
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Pred. No.
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RESULT 6
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Bussey H., Slorms R.K., Ahmed A., Albermann K., Allen E., Ansore
Araujo R., Aparicio A., Barrell B.G., Badcock K., Benes V.,
Botstein D., Howman S., Bruckner M., Carpenter J., Cherry J.M.,
Chung E., Churcher C.M., Coster F., Davis K., Davis R.W.,
Dietrich F.S., Dellus H., Dipaolo T., Dubbis E., Duesterboeft A.
P00582;
21-JUL-1986 (Rel. 01, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00292; CYCLINS; 1.
Cyclin; Cell cycle; Cell division
SEQUENCE 545 AA; 61696 MW; D6
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"The nucleof ide seconds."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "The nucleotide sequence of Saccharomyces cerevisiae chromosome XVI.";
Nature 387:103-105(1997).
-1- FUNCTION: ESSENTIAL FOR THE CONTROL OF THE CELL CYCLE AT THE G1/S
(START) TRANSITION. INTERACTS WITH THE CDC28 PROTEIN KINASE TO
                                                                             DPO1_ECOLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00134; cyclin; 1.
SMART; SM00385; CYCLIN; 1
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Nucleic Acids Res. 18:4025-4025(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPRO04366; Cyclin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SGD; S0006177; CLN2
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                                                                                                                                                                                                                                 367 IASNLNISRK 376
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-1995) to the EMBL/GenBank/DDBJ databases
                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                        73.5%;
70.0%;
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PRESENTATION OF THE PRESEN
complexed with deoxynucleoside triphosphate and pyrophosphate." Biochemistry 32:14095-14101(1993).
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"Escherichia coll DNA polymerase I. Sequence characterization and secondary structure prediction.";
J. Biol. Chem. 257:1965-1972(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               coli
                                                                                                                                                                                                                                            MEDLINE=93227044; PubMed=8469987
Beese L.S., Derbyshire V., Steit:
                                                                                                                                                                                                                                                                                                                                                                                                                                      Beese L.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Structure of large fragment of Escherichia coli DNA polymerase complexed with dTMP.";
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15-JUN-2002 (Rel. 41, Last annotation update)
DNA polymerase I (EC 2.7.7.7) (POL I).
                                                Beese L.S., Friedman J.M., Steltz T.A.;
"Crystal structures of the Klenow fragment of DNA polymerase |
                                                                                                      MED1.INE=94083412;
                                                                                                                                   X-RAY CRYSTALLOGRAPHY (3.9 ANGSTROMS)
                                                                                                                                                                                      Science
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                                                                                                                                                                                                                                                                                                                                                                                                         "Structural basis for the 3'-5' exonuclease activity of Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-91114709; PubMed=1989886;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  [6]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPOSITION, AND PARTIAL SEQUENCE. MEDLINE-82120161; PubMed-7035456;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kelley W.S., Joyce C.M.;
"Genetic characterization of early
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=83189123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 284-350 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Joyce C.M., Grindley N.D.; "Identification of two genes immediately downstream from the gene of Escherichia coli.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=83056713; PubMed=6183253;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Plunkett G. III, Burland V.D., Daniels D.L., Blattner F.R.; "Analysis of the Escherichia coli genome. III. DNA sequence of the region from 87.2 to 89.2 minutes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. STRAIN-K12 / MG1655;
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JOyce C.M., Kelley W.S., Grindley N.D.F.;
"Nucleotide sequence of the Escherichia coli polA gene and primary
structure of DNA polymerase 1.";
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                                                                                                                                                                                                                                                                                                   -RAY CRYSTALLOGRAPHY (3.2 ANGSTROMS) OF KLENOW FRAGMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -RAY CHYSTALLOGRAPHY (2.6 ANGSTROMS)
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                                                                                                                                                                                         260:352-355(1993).
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                                                                                                         PubMed=8260491;
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PDB;

PDH;

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25-FEB-98

PDB;

2KZM; 2KZZ; 2KFN; 2KFZ;

16-FEB-99. 16-FEB-99. 11-NOV-98. 11-NOV-98.

10SL;

PDH; РЮВ; PDB; PDB;

30-JUN-99. 00 DEC-99. 02-DEC-99. 02-DEC-99.

SWISS-2DPAGE;

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PDB;
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"Sequential proton NMK resonance assignments, circular dichroism, and structural properties of a 50-residue substrate-binding peptide from DNA polymerase I.";
                                                                                                                                                                           PDB;
                                                                                                                                                                                                                                                                                                                                              entities requires a license care-ment (See http://www.isb-sib.ch/announce/or send an emain to license isb sib ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Brautigam C.A., Sun S., Piccirilli J.A., Steitz T.A.; "Structures of normal single-stranded DNA and deoxyribo-3/-S-phosphorothiolates bound to the 3/-5' exonucleolytic active s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         activity of Escherichia coli
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                                                                                                                                                                                                        ; सदाब
                                                                                                                                                                                                                                                                                             EMBL.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PUNCTION: IN ADDITION TO POLYMERASE ACTIVITY, THIS DNA POLYI ETUNCTION: IN ADDITION TO POLYMERASE ACTIVITY, IT IS A EXHIBITS 3' TO 5' AND 5' TO 3' EXOUCLEASE ACTIVITY, IT IS A TOUTLILIE NICKED CIRCULAR DIPLEX DNA AS A TEMPLATE AND CAN UNWIND THE PARENTAL, DNA STRAND FROM ITS TEMPLATE.

CATALITIC ACTIVITY: N deoxynucleoside (riphosphate = N diphosphate)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WWW="http://www.worthington-blochem.com/manual/D/DNAP.html"
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J01664; AAA24404.1;
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                                                                                                                                                                                                                                                                                                                     V00417; ('AA23607.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SINGLE-CHAIN MONOMER WITH MULTIPLE FUNCTIONS
                                                                                                                                                                                                                                  S40809
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Pfam; PF01612; 3_5_exonuclease; 1
Pfam; PF02739; 3_5_exonuc_N; 1.
PRINTS; PR00868; DNAPOLI.
SMART; SM00474; 35EXOC; 1.
SMART; SM00278; HhH1; 1.
SMART; SM00278; HhH1; 1.
SMART; SM00279; HhH2; 1.
SMART; SM00279; HhH2; 1.
between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                    MEDLINE=21235186; PubMed=11337471;
Bolotin A., Wincker P., Mauger S., Jaillon O., Malarme K.,
Weissenbach J., Ebrlich S.D., Sorokin A.;
"The complete genome sequence of the lactic acid bacterium Lactococcus lactis ssp. lactis IL1403.";
Genome Res. 11:731-753(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LACLA
                                                                                                                                                                                                                                                                                                                                                                              Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactoroccus.
                                                                                                                                                                                                                                                                                                                                                                                                               POLA OR LL2142.
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16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
DIA polymerase I (EC 2.7.7.7) (POL I).
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InterPro; IPR002562; 3_5_exonuclease.
InterPro; IPR002421; 5_3_exonuclease.
InterPro; IPR001098; DNA_pol.
                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                          SUBUNIT: SINGLE-CHAIN MONOMER WITH MULTIPLE FUNCTIONS. SIMILARITY: BELONGS TO THE DNA POLYMERASE TYPE-A FAMILY.
                                                                                                                                                        CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
                                                                                                                                                                                         FUNCTION: IN ADDITION TO POLYMERASE ACTIVITY, THIS DNA POLYMERASE EXHIBITS 3' TO 5' AND 5' TO 3' EXONUCLEASE ACTIVITY (BY
                                                                                                                                           + {DNA}(N).
                                                                                                                                                                            SIMILARITY).
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IPR000513; Exo_N_I.
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3'-5' EXONUCLEASE.
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PRO0868; DNAPOLL.
SMART; SM00474; 35EXOC; 1.
SMART; SM00475; 53EXOC; 1.
SMART; SM00279; HhHZ; 1.
SMART; SM00482; POLAC; 1.
                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                          J. Bacteriol. 179:4473-4479(1997).

-i- FUNCTION: IN ADDITION TO POLYMBRASE ACTIVITY,
-i- EXHIBITS 3' TO 5' AND 5' TO 3' EXONUCLEASE ACTIVITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transferase; DNA-directed DNA polymerase; DNA replication; DNA repair; Hydrolase; Exonuclease; DNA-binding; Complete proteome. SEQUENCE 877 AA; 98732 MW; A5C2BEB92FF98FB2 CRC64:
                          EMBL; U78771; AAB64184.1; HSSP; P52026; 1XWL.
                                                                 entities requires a license agreement (Son send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                       STRAIN-MC1363;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-DEC-1998 (Hel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DUN-2002 (Rel. 41, Last annotation update)
DNA polymerase I (EC 2.7.7.7) (POL I).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00476; DNA_pol_A; 1. pfam; PF01367; 5_3_exonuclease; pfam; PF02739; 5_3_exonuc_N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro: IPR001098; DNA_pol.
InterPro: IPR002298; DNA_polI.
InterPro: IPR000513; Exo_N_I.
InterPro: IPR000594; HHH_2.
                                                                                                                                                                                                                                                                                                                                                     MEDLINE~97369814; PubMed=9226255;
                                                                                                                                                                                                                                                                                                                                                                                                                        Lactococcus lactis (subsp. cremoris) (Streptococcus cremoris).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DPO1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                     "Characterization of Lactococcus
                                                                                                                                                                                                                                                                                                                                    Duwat P., Cochu A., Ehrlich S.D.,
                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID-1359;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            POLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00447; DNA_POLYMERASE_A; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TIGREAMS; TIGRO0593; pola; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; 1PR002421;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR002562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         722 LARNLGITRKD 732
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 LAQNLNIXRKE 11
                                                                                                                                                                              + {DNA}(N).

SUBJUNT: SINGLE-CHAIN MONOMER WITH MULTIPLE FUNCTIONS.

SIMILARITY: BELONGS TO THE DNA POLYMERASE TYPE-A FAMILY.
                                                                                                                                                                                                                              CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LACIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P52026;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98732 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               71.4%;
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5_3_exonuclease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   _3_exonuclease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 35; DB
Pred. No. 14;
2; Mismatches
                                                                                                                                                                                                                                                                                                                      lactis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                877
                                                                                (See http://www.isb-sib.ch/announce/
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14;
                                                                                                                                                                                                                                                                                                                      A.;
UV-sensitive mutants obtained
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA.
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                                                                                                                                                                                                                                                              ACTIVITY
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                                                                                                                                                                                                                                                           THIS DNA POLYMERASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
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InterPro; IPR002562;

IPR002562; 3_5_exonuclease. IPR002421; 5_3_exonuclease.

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TYAO7,

TYAO7,
                                      RA Oliver K., O'Neil S., Pearson D., Quali M.A., Rabbinowitsch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Wueller Auer S.,
RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Wueller Auer S.,
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Borzym K., Janger I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Borzym K., Langer I., Joreano S., Gloux S., Lelaure V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
RT "The genome sequence of Schizosaccharomyces pombe.";
RT Nature 415:871-880(2002).
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01-FEB-1996 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mooney P.,
Oliver K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A., Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G., Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A., Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S., Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Fungi; Ascomycota; Schizosaccharomycete Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YAO7_
-!- SUBCELLULAR LOCATION: Nuclear (Probable)
-!- SIMILARITY: CONTAINS 1 2N(2)-CYS(6), FUN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   James K., Jones L., Jones M., Leather S., McDonald S., McLean J., McOney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Schizosaccharomycetales; Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Putative transcriptional regulatory protein C11D3.07c. SPAC11D3.07C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-OCT-2001 (Rel. 40, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SCHPO
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PROSITE; PS00447; DNA_POLYMERASE_A; 1.

Transferase: DNA-directed DNA polymerase; DNA replication;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-21848401; PubMed=11859360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=4896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Schizosaccharomyces pombe (Fission yeast)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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; SM00475; 53EXOC; 1.
; SM00279; HhH2; 1.
; SM00482; POLAC; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Exonuclease; DNA-binding, 877 AA; 98895 MW; EA80:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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Pred. No.
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  FUNGAL-TYPE BINUCLEAR
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RESULT 10
DPO1_STRPN
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Query Match
Best Local Similarity
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Tettelin H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.D., Peterson S., Heidelberg J., DeBoy R.T., Haft D.H., Dodson R.J., Durkin A.S., Gwinn M., Kolonay J.E., Nelson W.C., Peterson J.D., Umayam L.A., White O., Salzberg S.L., Lewis M.R., Radune D., Umayam L.A., White O., Salzberg S.L., Lewis M.R., Radune D., McDonald L.A., Feldblyum T.V., Angiuoli S., Dickinson T., Hickey Holt I.E., Loftus B.J., Yang F., Smith H.O., Venter J.C., Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M.; "Complete genome sequence of a virulent isolate of Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-89139504; PubMed=2537309; Lopez P., Martinez S., Diaz A., Espinosa M., Lacks S.A.; Characterization of the polA gene of Streptococcus pneumoniae and comparison of the DNA polymerase I it encodes to homologous enzymes from Escherichia coli and phage T7."; J. Biol. Chem. 264:4255-4263(1989).
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16-0CT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
DNA polymerase I (EC 2.7.7.7) (POL I).
                                                                                          Science 293:498-506(2001).

-:- FUNCTION: IN ADDITION TO POLYMERASE ACTIVITY, THIS DNA POLYMERASE EXHIBITS 3, TO 5, AND 5, TO 3. EXONUCLEASE ACTIVITY.

-:- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical protein; Transcription regulation; DNA-binding; Nuclear protein; Zinc; Metal-binding.

DNA_BIND 7 34 ZN(2)-CYS(6), FUNCAL-TYPE (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001138; Fungi_TrN. Pfam; PF00172; Zn_clus; 1. SMART; SM00066; GAL4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the European Bioinformatics Institute. There are no rest
use by non-profit institutions as long as its content
modified and this statement is not removed. Usage by ar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; Z68166; CAA92308.2; -. HSSP; P08657; ICLD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entities requires a license agreement (See http://www.isb-sib ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                          pneumoniae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-TIGR4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=1313;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POLA OR SP0032.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              282 MAQQLNLHRKQ 292
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SUBUNIT: SINGLE-CHAIN MONOMER WITH MULTIPLE FUNCTIONS. SIMILARITY: BELONGS TO THE DNA POLYMERASE TYPE-A FAMILY
                                                                + (DNA)(N)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PS00463; ZN2_CY6_FUNGAL_1; 1.
PS50048; ZN2_CY6_FUNGAL_2; 1.
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54.58;
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Pred. No. 16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AΑ
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                                                                                                                                                                                                                                                                                                                                              E.K.,
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s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its

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Matches
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16-OCT-2001
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MEDIINE-20196006; PubMed=10731132;
Addams M.D., Celniker S.E., Holt R.A., Ev
Amanatides P.G., Scherer S.E., Li P.W.,
George R.A., Lewis S.E., Richards S., As
                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PRO0868; DNAPOLI.
SMART; SM00474; 35EXOC; 1.
SMART; SM00475; 53EXOC; 1.
SMART; SM00279; HhH2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical CG10805,
                                                                                                                                      STRAIN=Berkeley;
                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster (Fruit fly)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BP28_DROME
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                                                                                                                                                                                                                                            NCBI_TaxID=7227;
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AE007320; AAK74222.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7; Conserv
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32 32. * V -> A (IN REF. 1).
109 109 D -> E (IN REF. 1).
292 292 V -> M (IN REF. 1).
298 300 SES -> AEG (IN REF. 1).
338 338 V -> A (IN REF. 1).
344 344 K -> O (IN REF. 1).
493 493 M -> V (IN REF. 1).
697 D -> N (IN REF. 1).
790 790 R -> A (IN REF. 1).
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IPR002298; DNA_pol1.
IPR000513; Exc_N_I.
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IPR002421; 5_3_exonuclease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                            (Rel. 40, Created)
(Rel. 40, Last sequence update)
(Rel. 40, Last annotation update)
protein CG10805.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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63.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 34; DB Pred. No. 23;
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Evans C.A., Gocayne J.D.,
1., Hoskins R.A., Galle R.F.
Ashburner M., Henderson S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1;
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RA Borkova D., Botchan M.R., Bouck J., Frokstein P., Botshand R., Botchan M.R., Bouck J., Frokstein P., Brotther P., RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., Page P., Brotther R., Deng Z., Mays A.D., Dew I., Dietz S.M., Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., RA Dodson K.J., Evangelista C.C., Ferriaz C., Ferriaz S., Fleischmann W., RA Fosler C., Gabrielian A.E., Garg M.S., Gelbart W.M., Glasser K., RA Clodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., RA RA Liux L., Harvey D., Helman T.J., Hernandez J.R., Houck J., RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibouck J., RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Lai Z., Lai Z., Lai Z., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., RA Merkalov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A., RA Merkalov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A., RA Reinert K., Remington K., Sunders K.D.C., Scheeler F., Shen H., RA Shue B.C., Siden Kiamos I., Simpson M., Skupskin M.P., Smith T., RA Ra Razzolo M., Pittnan G.S., Pan S., Pollard J., Puri V., Reese M.G., RA Ranger E., Spradling A.C., Slapleton M., Skupskin M.P., Smith T., RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., RA Spier E., Spradling A.C., Slapleton M., Skupskin M.P., Smith H.O., RA Zheng X.H., Zhong F. N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O., Zheng S., Yao Q.A., Then Gibbs R.A., Myers E.W., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O., Find Gibbs R.A., Myers E.W., Zhong W., Zhou X., Smith H.O., Find Gibbs R.A., Myers E.W., Moshin G.M., Venter J.C., Find Language G. F., Walley B., Walley G., Find G. S., Find M., 
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Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfelffer B.D.,
Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.
Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
                                                                                                                                                                                                                                                                               use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                 entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Qy Best Matches Query Match SEQUENCE Hypothetical protein. REPEAT PROSITE; FlyBase; EMBL; AE003615; AAF52447 InterPro; IPR000357; HEAT_repeat 510 LLQNLNVTKK 519 Local 1 LAQNLNIXRK Similarity 6; Conserv PS50077; HEAT_REPEAT; FALSE_NEG FBgn0031864; CG10805 2096 AA; Conservative 10 2094 69.4%; 60.0%; 237217 WW; 2; Mismatches Score 34; Pred. 3E7B3C67CE6DF62C CRC64; NO. 61; DB 1; Length 2096; Indels 0;

0;

TUD_DROME RESULT 12 P25823; 01-MAY-1992 01-MAY-1992 15-JUN-2002 Drosophila melanogaster (Fruit fly) TUD_DROME Maternal tudor protein. (Rel. 22, Created)
(Rel. 22, Last sequence update)
(Rel. 41, Last annotation update) STANDARD; 2515 ĀĀ

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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -1- FUNCTION: REQUIRED DURING OOGENESIS FOR THE FORMATION OF PRIMORDIAL GERM CELLS AND FOR NORMAL ABDOMINAL SEGMENTATION.
-1- DEVELOPMENTAL STAGE: EXPRESSED THROUGHOUT THE LIFE CYCLE.
-1- MISCELLANEOUS: THE TUD MRNA ACCUMULATES WITHIN THE POSTERIOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Golumbeski G.S., Bardsley A., Tax F., Boswell R.E.;
"Tudor, a posterior-group gene of Drosophila melanogaster, encodes novel protein and an mRNA localized during mid-oogenesis.";
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SEQUENCE FROM N.A.
                                    Clostridium
                                                Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
                                                            Plasmid pCP13
                                                                        Clostridium perfringens.
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                                                                                                 Hypothetical protein PCP12
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InterPro; iPR002999; Tudof.
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                        NCBI_TaxID=1502;
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                                             entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                   This {\tt SWISS-PROT} entry is copyright. It is produced through a collaboration between the {\tt Swiss} Institute of Bioinformatics and the {\tt EMBL} outstation -
                                                                                                                                                                                                                "The complete genome sequence of the hyperthermophilic, sulphate-reducing archaeon Archaeoglobus fulgidus.";
Nature 390:364-370(1997).
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16-OCT-2001
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Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(200-i-SIMILARITY: "FO C.perfringens piv404 ORP6.
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Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.;
"Complete genome sequence of Clostridium perfringens, an anaerobic
                                                                                use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=VC-16 / DSM 4304 / ATCC 49558;
MEDLINE-98049343; PubMed-9389475;
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SEQUENCE 1
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PubMed=11792842;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_'faxID=2234;
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61 AA; 19180 MW; DBE5BE41BBE4CEDE CRC64;
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Pred. No. 5.9;
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TIGR; AF1257;

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RESULT 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA polymerase that is modified (see AAV91930) so that during DNA sequencing, it effectively incorporates all four fluorescent dye-lal dideoxynucleotide triphosphates (ddNTP), or their analogs, and reduthe discrimination, observed with the unmodified enzyme, for incorporation of labeled ddCTP and ddATP, is new. The modified DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                               02-MAR-2000; 2000US-0517871
                                                                                 28-FEB-2001; 2001WO-US06571.
                                                                                                                                                  WO200164954-A1
                                                                                                                                                                                Bacillus stearothermophilus
                                                                                                                                                                                                                                                              Bacillus stearothermophilus (Bst) DNA polymerase 1 protein fragment.
                                                                                                                                                                                                                                                                                                                                     AAE11060;
                                                                                                                                                                                                                                                                                                                                                                   AAE11060 standard; Protein; 587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 82-90; 109pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New DNA polymerase, useful particularly in DNA sequencing, incorpora-
all four dideoxynucleotide triphosphate terminators with about equal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAA08545.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-283563/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200017330-A1
               (PROM-) PROMEGA CORP
                                                                                                                                                                                                                  Bst; enzyme; amplification; hybridisation.
                                                                                                                                                                                                                                Reverse transcription; DNA polymerase 1; Bacillus stearothermophilus;
                                                                                                                                                                                                                                                                                                   18-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (SHAN-) SHANGHAI INST BIOCHEMISTRY CHINESE ACAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                     432 LAQNLNITRKE 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 LAQNLNIXRKE 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        present sequence shows a wild type Bacillus stearothermophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Huang W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        K87 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98US-0157397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99WO-IB00146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "F421Y in AAY91930"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 48; DB 21; Length 587; Pred. No. 0.2;
                                                                                                                                                                                                                                                                                                                                                                     8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        incorporates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and reduces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       dye-labeled
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 8
AAR80140
Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                             24-FEB-1995;
01-APR-1994;
16-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                              Bacillus stearothermophilus; thermostable DT. polymerase; PCR; primer; amplification; probe; Bacillus caldotenax; exonuclease; recombination; sequencing; polymerase chain reaction.
       Bacillus stearothermophilus DNA encoding thermostable polymerase for nucleic acid sequencing and amplification % \left( 1\right) =\left\{ 1\right\} 
                                                                                                           Riggs MG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                             N-PSDB; AAT04803.
                                                                            WPI; 1995-373510/48
                                                                                                                                             (GENP-) GEN-PROBE INC
                                                                                                                                                                                                                                                30-MAR-1995;
                                                                                                                                                                                                                                                                                  12-OCT-1995
                                                                                                                                                                                                                                                                                                                  WO9527067-A1
                                                                                                                                                                                                                                                                                                                                                 Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                               B.stearothermophilus DNA polymerase encoded by clone Bst3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-MAY-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR80140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR80140 standard; Protein; 588 AA
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뮍 Qy

ID

Sivaram M,

95US-0394232 94US-0222612 94US-0307410

95WO-US04080

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at each cooling step. The invention contemplates single-reaction RT-PCR wherein reverse transcription and amplification are performed in a single continuous procedure. Primers, template, nucleoside triphosphates, appropriate reaction buffer having magnesium ions, reaction conditions, and polymerase are used in the PCR process, which involves denaturation of target DNA, hybridisation of primers and synthesis of complementary strands. The present sequence is Bacillus stearothermophilus (Bst) DNA polymerase 1 protein fragment which lacks 5' to 3' exonuclease activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Reverse transcription of RNA using Tvu and Bst DNA polymerase, comprises combining the polymerase, RNA containing sample, a primer and reaction buffer having magnesium ions and reacting the mixture to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     thermostable DNA polymerase such as Thermoactinomyces vulgaris (Tvu) and Bacilius stearothermophilus (BSt) DNA polymerase. Tvu and Bst DNA polymerase are useful for reverse transcription reactions which allows repetitive heating/cooling cycles without the requirement of fresh enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to reverse transcription of RNA templates using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 29; Fig 10; 118pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAD18459
432 LAQNLNJTRKE 442
                                                                                                                                                                       Local Similarity
                                                               1 LAQNLNIXRKE 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2001-589872/66.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Huang F, Hartnett JR;
                                                                                                                                     10;
                                                                                                                                                                                                                                                                              587 AA;
                                                                                                                                     Conservative
                                                                                                                                                                       98.0%;
                                                                                                                                     0;
                                                                                                                                                                   Score 48; DB Pred. No. 0.2;
                                                                                                                                     Mismatches
                                                                                                                                                                                                    22;
                                                                                                                                 <u>..</u>
                                                                                                                                                                                                Length 587;
                                                                                                                                     Indels
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RESULT AAXSULJY AAXY9193 ID WAX AAC AAA AAC AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ş
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
The present sequence of the polymerase that, during DNA sequencing, effectively DNA polymerase that, during DNA sequencing, effectively incorporates all four fluorescent dye-labeled dideoxynucleotide triphosphates (ddNTP), or their analogs, and reduces the discrimination, triphosphates (ddNTP), or their analogs, and reduces the discrimination, with the unmodified enzyme, for incorporation of labeled
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene (AAT04801) to remove a 195 bp HincII-PwIII fragment from the region encoding the 5'-3' exonuclease. The deleted fragment removes 65 amino acids (residues 178-242 of the protein) including 2 Gly residues though to correspond to 2 amino acids in the E.coli DNA polymerase I necessary for 5'-3' exonuclease activity. The modified DNA polymerase can be used in primer extension reactions such as DNA sequencing or polymerase chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hong
                                                                                                           The present sequence shows a modified Bacillus stearothermophilus DNA polymerase that, during DNA sequencing, effectively
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This is the amino acid sequence of the modified Bacillus stearothermophilus thermostable DNA polymerase encoded by the clone Bst3 which contains a deletion in the 5^{\circ}-3' exonuclease domain. The correspondence was constructed by digestion and recombination of the full length
                                                                                                                                                                                                    Claim 7; Page 95-103; 109pp; English.
                                                                                                                                                                                                                                                                                      New DNA polymerase, useful particularly in DNA sequencing, incorporates all four dideoxynucleotide triphosphate terminators with about equal
                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAA08544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        B. stearothermophilus 320 modified DNA polymerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY91930;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (SHAN-) SHANGHAI INST BIOCHEMISTRY CHINESE ACAD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200017330-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             random primer labeling; site-directed mutagenesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Modified DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY91930 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 reaction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 433 LAQNLNITRKE 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity nes 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 LAQNLNIXRKE 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ģ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          stearothermophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        588 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            polymerase; DNA sequencing; 3' to 5' exonuclease activity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   87-90; 135pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98US-0157397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99WO-IB00146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     342..344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "F422Y substitution
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "wild type sequence is Leu-Glu-Glu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein; 588 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 48;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         from wild type"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 588;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
      The invention relates to reverse transcription of RNA templates using thermostable DNA polymerase such as Thermoactionwyces vulgaris (Tvu) and Bacillus stearothermophilus (Bst) DNA polymerase. Tvu and Bst DNA polymerase are useful for reverse transcription reactions which allows repetitive heating/cooling cycles without the requirement of fresh enzyme at each cooling step. The invention contemplates single-reaction RT-PCR wherein reverse transcription and amplification are performed in a single continuous procedure. Primers, template, nucleoside triphosphates, and polymerase are used in the PCR process, which involves denaturation of target DNA, hybridisation of primers and synthesis of complementary extrand The process of primers and synthesis of complementary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ddCTP and ddATP, is new. The modified DNA polymerase, has proofreading 3'-5' exonuclease activity during DNA sequencing from a template and the polymerase excises mismatched nucleotides from the 3' terminus at a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         faster rate than it removes correctly matched nucleotides. The polymerase is used particularly for DNA sequencing, also for filling in 5'-overhangs, synthesis of DNA probes by random primer labeling and in
                                                                                                                                                                                                                                                       Reverse transcription of RNA using Tvu and Bst DNA polymerase, comprises combining the polymerase, RNA containing sample, a primer and reaction buffer having magnesium ions and reacting the mixture to
                                                                                                                                                                                                           Claim 7; Fig 6; 118pp; English.
                                                                                                                                                                                                                                            obtain cDNA
                                                                                                                                                                                                                                                                                                                                                                                                          (PROM-) PROMECA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                        02-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-FEB-2001; 2001WO-US06571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-SEP-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Misc-difference 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Thermoactinomyces vulgaris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   enzyme;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Reverse transcription;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Thermoactinomyces vulgaris Tvu DNA polymerase T289M truncated mutant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAE11058;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAE11058 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         site-directed mutagenesis, (claimed).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               433 LAQNLNITRKE 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 LAQNLNIXRKE 11
                                                                                                                                                                                                                                                                                                                          2001-589872/66.
DB; AAD18445.
                                                                                                                                                                                                                                                                                                                                                                          Huang F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amplification; hybridisation; mutant; mutein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             588 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                        2000US-0517871.
                                                                                                                                                                                                                                                                                                                                                                          Hartnett JR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "Encoded by Ang"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA polymerase; Thermoactinomyces vulgaris; Tvu;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 48;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 0.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 588;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
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strands. The

present sequence is Thermoactinomyces vulgaris Tvu DNA

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SSX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            888
                                                                                          The invention provides compositions comprising thermostable DNA copymerases derived from hyperthermophilic eubacteria, in particular, a purified and isolated Thermoactinomyces vulgaris (Tvu) DNA polymerase can be aving DNA synthesis activity. It is useful for determining the nucleotide base sequence of a DNA molecule. Tvu DNA polymerase can be used for processes of high temperature nucleic acid amplification and coule for processes of high temperature reverse transcription in the sequencing without substantial loss of DNA synthesis activity. The enzyme can be used to perform high temperature reverse transcription in the casence of manganese ions and in high throughput robotically manipulated procedures because greater enzymatic stability is retained at room temperature. Using the Tvu DNA polymerase, reverse transcription reactions can be conducted at increased temperatures so that secondary controlled sequence of a 5'-3' exonuclease deletion mutant form of two DNA polymerase called T289M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local
   Matches
                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           polymerase T289M truncated mutant. This Tvu T289M mutant is obtained by deleting 288 amino acids from the N-terminal end of wild-type T.
                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                            Claim 13; Fig 8; 113pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                               amplification, reverse transcription and sequencing reactions
                                                                                                                                                                                                                                                                                                                                                                                                                             vulgaris for us in many recombinant DNA techniques, including
                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel thermostable DNA polymerase derived from Thermoactinomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAH47392.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02-MAR-2000; 2000US-0517439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-FEB-2001; 2001WO-US06436.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200164838-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Thermoactinomyces vulgaris.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          deletion mutant; T289M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tvu DNA polymerase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Thermostable; DNA polymerase; hyperthermophilic; DNA synthesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tvu DNA polymerase deletion mutant T289M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB85951 standard; Protein; 588 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            vulgaris Tvu DNA polymerase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (PROM-) PROMEGA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      433 LAQNLNITRKE 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
Local Similarity
les 10; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 LAQNLNIXRKE 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2001-557768/62.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Huang F, Hartnett JR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             588 AA;
                                                                  588 AA;
 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nucleic acid amplification; reverse transcription;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98.0%;
              90.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 48;
Pred. No.
Score 48; DB 22; Length 588; Pred. No. 0.2; 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 588;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
Gaps
                                                                                                                                                                                                                                       enzyme
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AAR80141
ID AAR8
XX
AC AAR8
XX
DT 30-1
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                                                                                             RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW30094
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 12
                                                                                                                                                                                             Matches
                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                       This is the protein sequence (589 amino acids) of the Bacillus stearothermophilus strain DNA polymerase. The heat stable DNA polymerase can be used in a method for the replication of a DNA chain. It can also be used in a method for the determination of the sequence of DNA chain. As the DNA polymerase has a proof reading 3'-5' exonuclease activity, possible mismatches of base pairing that occurs in current methods of DNA sequence determination of a DNA clone can be avoided.
                                                                                                                                                                                                                                                                                                                                                                                   Claim 9; Pages 29-30; 32pp; Japanese.
           30-MAY-1996 (first entry)
                                                                  AAR80141 standard; Protein; 590 AA
                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA polymerase from Bacillus stearothermophilus - used in DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacillus stearothermophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacillus stearothermophilus; DNA polymerase; DNA amplification; DNA replication; exonuclease; proof reading.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacillus stearothermophilus DNA polymerase (peptides 1-589).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW30094;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW30094 standard; Protein; 589 AA.
                                       AAR80141;
                                                                                                                                                                                                                                                                                                                                                                                                                             amplification and sequencing methods having lower frequency
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAT90820.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1997-474304/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hong GF, Huang W, Zhai F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (SHAN-) SHANGHAI INST BIOCHEMISTRY CHINESE ACAD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (ZHAI/) ZHAI F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HUAN/) HUANG W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HONG/) HONG G F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             03-MAY-1996;
18-OCT-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JP09220087-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14-APR-1998 (first entry)
                                                                                                                                   434 LAQNINITRKE 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               433 LAQNINITRKE 443
                                                                                                                                                               1 LAQNLNIXRKE 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 LAQNLNIXRKE 11
                                                                                                                                                                                                          ocal
                                                                                                                                                                                            10;
                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                               589 AA;
                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95US-0544643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96JP-0160402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96US-0642684
                                                                                                                                                                                                       98.08;
                                                                                                                                                                                          0;
                                                                                                                                                                                                     Score 48; DB
Pred. No. 0.2;
                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                   DB 18; Length 589;
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RESULT 14
AAE11057
ID AAE11
XX AAE11
XX AAE11
XX Therm
DT 18-DE
XX Therm
XX Rever
KW Rever
KW enzym
XX Therm
XX Therm
XX UO200
XX WO200
XX O7-S1
                                                                                                                                                                                                                                                                                                                               B
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This is the amino acid sequence of the modified B.stearothermophilus thermostable DNA polymerase encoded by the clone Bst4. This clone encodes the sequence of a natural degradation product obtained when the DNA polymerase clone Bst3 (AAT04803) is expressed in E.coli. The same sequence is found when the full length clone (AAT04801) is expressed and cleaved with subtilisin to produce a "Rienow-Type" DNA polymerase. This sequence starts with the Val residue at pos. 287 of the full length protein. This contrasts with a commercially available B.stearothermophilus DNA polymerase subtilisin fragment where the protein sequence starts with the Ala residue corresp. to pos. 290. The modified DNA polymerase can be used in primer extension reactions such as DNA sequencing or polymerase chain reaction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24-FEB-1995;
01-APR-1994;
16-SEP-1994;
   07-SEP-2001
                                                              Synthetic.
                                                                         Thermoactinomyces vulgaris
                                                                                                        Reverse transcription; DNA polymerase; Thermoactinomyces vulgaris; Tvu; enzyme; amplification; hybridisation; mutant; mutein.
                                                                                                                                                                                                                     AAE11057;
                                WO200164954-A1
                                                                                                                                                      Thermoactinomyces vulgaris Tvu DNA polymerase M285 truncated mutant
                                                                                                                                                                                                                                                 AAE11057 standard; Protein; 592 AA.
                                                                                                                                                                                      18-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 9; Page 92-94; 135pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Riggs MG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacillus stearothermophilus; thermostable DNA polymerase; PCR; primer; amplification; probe; Bacillus caldotenax; exonuclease; recombination; sequencing; polymerase chain reaction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             B.stearothermophilus DNA polymerase encoded by clone Bst4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacillus stearothermophilus DNA encoding thermostable polymerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (GENP-) GEN-PROBE INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-MAR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      W09527067-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                                                                                                                              435 LAQNLNITRKE 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     for nucleic acid sequencing
                                                                                                                                                                                                                                                                                                                                                           1 LAQNLNIXRKE 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1995-373510/48.
                                                                                                                                                                                                                                                                                                                                                                                          10;
                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sivaram M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                     590 AA;
                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95US-0394232.
94US-0222612.
94US-0307410.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95WO-US04080
                                                                                                                                                                                                                                                                                                                                                                                                      98.0%;
                                                                                                                                                                                                                                                                                                                                                                                                       Score 48;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                          0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and amplification
                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                       0.2;
                                                                                                                                                                                                                                                                                                                                                                                                                      DB 16;
                                                                                                                                                                                                                                                                                                                                                                                                                      Length 590;
                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                       0;
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RESULT 15
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Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
 Gu T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            at each cooling step. The invention contemplates single-reaction RT-PCR wherein reverse transcription and amplification are performed in a single continuous procedure. Primers, template, nucleoside triphosphates, appropriate reaction buffer having magnesium in reaction conditions, and polymerase are used in the PCR process, which involves denaturation of target DNA, hybridisation of primers and synthesis of complementary strands. The present sequence is Thermoactinomyces vulgaris Twu DNA polymerase M285 truncated mutant. This Tvu M285 mutant is obtained by deleting 284 amino acids from the N-terminal end of wild-type T. vulgaris
                                                                                                                                                                                                                Tvu DNA polymerase; deletion mutant; M2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       thermostable DNA polymerase such as Thermoactinomyces vulgaris (Tvu) and Bacillus stearothermophilus (Bst) DNA polymerase. Tvu and Bst DNA polymerase are useful for reverse transcription reactions which allows
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Reverse transcription of RNA using "Yu and Bst DNA polymerase, comprises combining the polymerase, RNA containing sample, a prime reaction buffer having magnesium ions and reacting the mixture to
                                                          02-MAR-2000; 2000US-0517439
                                                                                          28-FEB-2001; 2001WO-US06436
                                                                                                                                                       WO200164838-A2
                                                                                                                                                                                   Thermoactinomyces vulgaris
                                                                                                                                                                                                                                                                                                            30-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 7; Fig 4; 118pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gu T,
                                                                                                                                                                                                                                              Thermostable; DNA polymerase;
                                                                                                                                                                                                                                                                           Tvu DNA polymerase deletion mutant M285.
                                                                                                                                                                                                                                                                                                                                          AAB85950;
                                                                                                                                                                                                                                                                                                                                                                    AAB85950 standard; Protein; 592 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tvu DNA polymerase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to reverse transcription of RNA templates using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAD18444.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        02-MAR-2000; 2000US-0517871
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-FEB-2001; 2001WO-US06571.
                                (PROM-) PROMEGA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                437 LAQNIAUTEKE, 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         repetitive heating/cooling cycles without the requirement of fresh enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 LAQNLNIXRKE 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2001-589872/66.
Huang F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Huang F, Hartnett JR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      592 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                   M285.
                                                                                                                                                                                                                           olymerase; hyperthermophilic; DNA synthesis; nucleic acid amplification; reverse transcription;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 48; DB
Pred. No. 0.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               primer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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and

Hartnett JR;

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Search completed: January 15, 2003, 11:20:24
Job time: 31.2857 secs
                                                                                       Вþ
                                                                                                                             δÃ
                                                                                                                                                                                                                                                                                                           The invention provides compositions comprising thermostable DNA

C polymerases derived from hyperthermophilic eubacteria, in particular,

C a purified and isolated Thermoactinomyces vulgaris (Tvu) DNA polymerase

C having DNA synthesis activity. It is useful for determining the

C nucleotide base sequence of a DNA molecule. Tvu DNA polymerase can be

C used for processes of high temperature nucleic acid amplification and

C sequencing without substantial loss of DNA synthesis activity. The enzyme

C can be used to perform high temperature reverse transcription in the

C absence of manganese lons and in high throughput robotically manipulated

C procedures because greater enzymatic stability is retained at room

C temperature. Using the Tvu DNA polymerase, reverse transcription

C reactions can be conducted at increased temperatures so that secondary

C structure is removed or limited. The present sequence represents the

amino acid sequence of a 5'-3' exonuclease deletion mutant form of
                                                                                                                                                                   Query Match 98.0
Best Local Similarity 90.9
Matches 10; Conservative
                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 13; Fig 6; 113pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel thermostable DNA polymerase derived from Thermoactinomyces vulgaris for us in many recombinant DNA techniques, including amplification, reverse transcription and sequencing reactions -
                                                                                                                                                                                                                                                                                                  Tvu DNA polymerase called M285.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAH47392.
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                                                                                437 LAQNINITRKE 447
                                                                                                         1 LAQNLNIXRKE 11
                                                                                                                                                                                                                                                        592 AA;
                                                                                                                                                                                       98.0%;
90.9%;
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                                                                                                                                                                     0,
                                                                                                                                                                                       Score 48; DB 22; Length 592; Pred. No. 0.2;
                                                                                                                                                                     Mismatches
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Result
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Maximum DB seq length: 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is dcrived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         January 15, 2003, 11:17:28; Search time 9.28571 Seconds (without alignments) 34.855 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query
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     Issued_Patents_AA:*
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Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
     US-09-057-969-7
US-09-057-969-6
US-09-057-969-4
US-09-057-969-4
US-08-642-644-2
US-08-436-664-23
US-08-394-232A-23
US-09-135-642-25
US-09-135-642-25
US-09-135-642-25
US-09-135-642-25
US-09-135-642-27
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                                  Sequence 4, Appli
Sequence 5, Appli
Sequence 25, Appli
Sequence 27, Appli
Sequence 27, Appl
Sequence 27, Appl
Sequence 27, Appl
Sequence 27, Appli
Sequence 4, Appli
Sequence 17, Appli
Sequence 17, Appli
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Sequence 22, Appl
Sequence 23, Appl
Sequence 25, Appl
Sequence 25, Appl
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Sequence 23, Appl
Sequence 23, Appl
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Sequence 6, Appli
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                  Qy
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; Patent No. 6013451
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US-09-057-969-7
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TITLE OF INVENTION:
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41 42 43 43 48 44 48																. 29 4	28 4
	0.86											8 98.0					
954	877	877	876	876	876	876	876	876	876	876	876	876	876	876	876	876	876
3 115-09-057-969-2	1 US-08-428-823-14	1 US-08-208-036-14	5 PCT-US95-04080-34	5 PCT-US95-04080-32	5 PCT-US95-04080-20	4 US-09-517-871-20	4 US-09-517-871-2	3 US-08-394-232A-34	3 US-08-394-232A-32	3 US-08-394-232A-20	3 US-09-135-642-34	3 US-09-135-642-32	3 US-09-135-642-20	2 US-08-436-664-34	2 US-08-436-664-32	2 US-08-436-664-20	2 US-08-633-476-2
Sequence 2, Appli	Sequence 14, Appl	Sequence 14, Appl	Sequence 34, Appl	`	Sequence 20, Appl	Sequence 20, Appl	Sequence 2, Appli	Sequence 34, Appl	Sequence 32, Appl	Sequence 20, Appl	Sequence 34, Appl	Sequence 32; Appl	Sequence 20, Appl	Sequence 34, Appl	`	$\overline{}$	Sequence 2, Appli

ALIGNMENTS

PHANG, SENG MENG TAN, TIEN CHYE

BACILLUS STEAROTHERMAPHILUS DNA
POLYMERASE I (KLENOW) CLONES INCLUDING THOSE REDUCED
3'-TO-5' EXONUCLEASE ACTIVITY

VICTOR THI WONG

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US-09-057-969-7
                                                           Query Match
Best Local Similarity
                                               Matches 10; Conservative
                                                                                                                                                                                                                            TELEFAX: 212-588-0500 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: 18M PC compa
OPERATING SYSTEM: PC-D
SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
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ADDRESSEE: FROMMER LAWRENCE & HAUG LLP
                                                                                                                           TOPOLOGY: linear MOLECULE TYPE: amino acid
                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 294 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 67
TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION: NAME: KOWALSKI, THOMAS J
1 LAQNLNIXRKE 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: NEW YORK
STATE: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/09/057,969 FILING DATE: 09-APR-1998
                                                                                                                                                             STRANDEDNESS:
                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
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                                                                                                                                                                            amino acid
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                                                                                                                                                                                            294 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   E: Floppy disk
                                                                                                                                                                                                                                                            212-588-0800
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                                                                                                                                                                                                                                                                                                                                                         435
5
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                                                              98.0<del>8</del>;
90.9<del>8</del>;
                                                                                                                                                                                                                                                                                                     32, 147
                                               0;
                                                                                                                                                                                                                                                                                          674507-2001
                                                              Score 48; DB 3;
Pred. No. 0.024;
                                             Mismatches
                                                                             DB 3;
                                                                             Length 294;
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109 LAQNLNITRKE 119

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                                                                                                                                                                                                                                                                                 us-09-057-969-5
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Best Local Similarity
Matches 10; Conserva
                                                                                                                                                                                                                                        Sequence 5, Applic Patent No. 6013451
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                                                                      CORRESPONDENCE ADDRESS:
                                                                                        TITLE OF INVENTION: BACILLUS STEAROTHERMAPHILUS DNA
TITLE OF INVENTION: POLYMERASE I (KLENOW) CLONES INCLUDING THOSE REDUCED TO
TITLE OF INVENTION: 3'-TO-5' EXONUCLEASE ACTIVITY
NUMBER OF SEQUENCES: 17
                                                                                                                                                              APPLICANT: WONG, VICTOR THI WONG
APPLICANT: PHANG, SENG MENG
APPLICANT: TAN, TIEN CHYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: 212-588-0800
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APPLICATION NUMBER: US/09/057,969
FILING DATE: 09-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: BACILLUS STEAROTHERMAPHILUS DNA
TITLE OF INVENTION: POLYMERASE I (KLENOW) CLONES INCLUDING THOSE REDUCED TO
TITLE OF INVENTION: 3'-To-5' EXONUCLEASE ACTIVITY
NUMBER OF SEQUENCES: 17
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                                                                                                                                                                                                                                                                                                                                                        193 LAQNENITRKE 203
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   STATE:
                                                      ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: sir
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STATE: NEW YORK
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                                     STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 32,147
REFERENCE/DOCKET NUMBER: 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: KOWALSKI, THOMAS U
REGISTRATION NUMBER: 32,
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                                                                                                                                                                                                                                                                                                                                                                                           1 LAQNLNIXRKE 11
                                                                                                                                                                                                                                                              Application US/09057969
NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 378 amino acids
                                     745 FIFTH AVENUE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PatentIn Release #1.0, Version #1.30
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                                                      FROMMER LAWRENCE & HAUG LLP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                98.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 48;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                0.031;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 378;
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RESULT 4
US-09-057-969-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Patent No. 6013451
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4,
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              TELEFAX: 212-588-0500 INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: KOWALSKI, THOMAS J.
REGISTRATION NUMBER: 32,147
REFERENCE/DOCKET NUMBER: 6745
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-588-0800
TELEPHONE: 212-588-0800
                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: TAN, TIEN CHYE
TITLE OF INVENTION: BACILLO
TITLE OF INVENTION: POLYMER
TITLE OF INVENTION: 3'-TO-5
NUMBER OF SEQUENCES: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 5:
                              TELEPHONE: 212-588-0800
TELEPAX: 212-588-0500
                                                                                                                              CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 457 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              272 LAQNINITRKE 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              y Match 98.0%;
Local Similarity 90.9%;
                                                                              REFERENCE/DOCKET NUMBER: 67.
                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                     COMPUTER: IBM PC OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                       CITY: NEW YORK
STATE: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                        STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER:
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                                                                                                                 NAME: KOWALSKI, THOMAS J
                                                                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 LAQNLNIXRKE 11
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                                                                                                                                                                                                                                                                                                                                                                       745 FIFTH AVENUE
                                                                                                                                                                                                                                                                                                                        USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WONG
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IBM PC compatible
                                                                                                                                                                                                                                                   E: Floppy disk
IBM PC compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VICTOR THI WONG
                                                                                                                                                                                                                                                                                                                                                                                                                                       BACILLUS STEAROTHERMAPHILUS DNA
POLYMERASE I (KLENOW) CLONES INCLUDING THOSE REDUCED TO
3'-TO-5' EXONUCLEASE ACTIVITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PC-DOS/MS-DOS
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; Sequence 23, Application US/08436664
; Patent No. 5874282
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                                 US-08-436-664-23
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                                                                                                                                                          Matches
                                                                                                                                                                                        Query Match
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                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
ATTORNEY/ACENT INFORMATION:
NAME: CHAPIN, MARLANA K.
REGISTRATION NUMBER: 35,843
REFERENCE/DOCKET NUMBER: 4694
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: A NEW DNA POLYMERASE WITH PROOF-READING TITLE OF INVENTION: 3'-5' EXONUCLEASE ACTIVITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
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                                                                                             432 LAQNLNITRKE 442
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                           1 LAQNENIXRKE 11
                                                                                                                                                         Local Similarity
les 10; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: WASHINGTON
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Local Similarity 90.9%;
les 10; Conservative
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FENG, ZHAI
                                                                                                                                                                                                                                                      linear
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                                                                                                                                                                       Score 48; DB 2;
Pred. No. 0.049;
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                                                                                                                                                                                      DB 2; Length 587;
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US-08-436-664-23
                                                                                                                                    Patent No. 6066483
GENERAL INFORMATION:
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Matches 10; Conservative
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APPLICANT: RIGGS, MICHAEL G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: NAME OF THE SENSE: NO
                APPLICANT: RIGGS, MICHAEL G.
APPLICANT: SIVARAM, MATHOOR
APPLICANT: TUDOK, STARLA D.
TITLE OF INVENTION: PURIFED DNA POLYMERASE FROM BACILLUS
TITLE OF INVENTION: STEAROTHERMOPHILUS
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                 FRAGMENT TYPE:
ORIGINAL SOURCE:
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MEDIUM TYPE: Diskett
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                                                                                                                                                                                                                                                          432 LAQULNITRKE 442
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                                                                                                                                                                                                                                                                                           1 LAQNLNIXRKE 11
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ADDRESSEE: Gen-Probe Incorporated
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Pred. No. 0.049;
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Best Local Similarity 90.9%;
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                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                      APPLICANT: RIGGS, MICHAEL G. APPLICANT: SIVARAM, MATHOOR APPLICANT: TUDOR, STARLA D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FRAGMENT TYPE:
ORIGINAL SOURCE:
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HYPOTHETICAL:
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                                                                                                                                                                        CORRESPONDENCE ADDRESS
                                                                                                                                                                                       NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                 432 LAQNLNITRKE 442
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APPLICATION NUMBER:
                                COMPUTER:
                                                                                         COUNTRY:
                                                                                                           STATE:
                                                                                                                       CITY: San Diego
                                                                                                                                        STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/09/135,642
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SOFTWARE:
             OPERATING SYSTEM:
                                                                             ZIP:
                                                                                                                                                       ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 619-546-7929
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FastSEQ Version 1.5
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                          IBM Compatible
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                                                                                                                                                         Gen-Probe Incorporated
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                                               Diskette
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                                                                                                                                                                                                        PURIFED DNA POLYMERASE FROM BACILLUS STEAROTHERMOPHILU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
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APPLICANT: HUANG, WEI-HUA
FITTE OF INVENTION: DNA POLYMERASE HAVING ABILITY TO REDUCE INNATE
FITTE OF INVENTION: DYE LABELED DIDENSYNDCLEOFIDES
FILE OF INVENTION: DYE LABELED DIDENSYNDCLEOFIDES
FILE REFERENCE: houge-generice listing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-157-397-2
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                                                                                                                                   ; ORGANISM: Bacillus stearothermophilus US-09-157-397-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 9
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                                                                                                                                                                                                      SOFTWARE: Patentin Ver. 2.0 - beta SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/09157397 Patent No. 6165765
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                                                                    Matches
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                                                                                               Query Match
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                                                                                                                                                                                                                                                                                                     CURRENT FILING DATE: T998-09-21
EARLIER APPLICATION NUMBER: 08/544,643
                                                                                                                                                                                                                                        NUMBER OF SEQ 1D NOS: 11
                                                                                                                                                                                                                                                       EARLIER APPLICATION NUMBER: 08/642,684 EARLIER FILING DATE: 1996-05-03
                                                                                                                                                                                                                                                                                         EARLIER FILING DATE: 1995-10-
                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/157, 397
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                                                                                                                                                                    TYPE: PRT
                                                                                                                                                                                      LENGTH: 587
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'- TELEPHONE: 619-535-2807
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432 LAQNLNITRKE 442
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                                                                                  Local Similarity
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                              1 LAQNLNIXRKE 11
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                                                                               98.0%;
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                                                                               Score 48; DB 4;
Pred. No. 0.049;
                                                                  Mismatches
                                                                                               DB 4; Length 587;
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                                                                                                                     US-08-436-664-25
                                                                                                                                                                                                                                                                                                                    PCT-US95-04080-23
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US-09-517-871-22
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LENGTH: 587
TYPE: PRT
                                                                                    Sequence 25, Appli Patent No. 5874282
                                                                                                                                                                                                                                                        Matches
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Best Local Similarity
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GENERAL INFORMATION: RIGGS, MICHAEL G.
APPLICANT: RIGGS, MATHOOR
APPLICANT: TUDOK, STARLA D.
TITLE OF INVENTION: PURIFED DNA POLYMERASE FROM BACTILUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/517,871
CURRENT FILING DATE: 2000-03-02
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver: 2.0
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APPLICANT: Gu, Trent
TITLE OF INVENTION: Method of Reverse Transcription
FILE REFERENCE: PRMG-03833
                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO:
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LENGTH: 587 amino acid
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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                                                                                                                                                                                    432 LAQNLNITRKE 442
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OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                          1 LAQNLNIXRKE 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: PCT/US95/04080
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                                                                                                    Application US/08436664
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Pred. No. 0.049;
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RESULT 13
US-09-135-642-25
; Sequence 25, Ap
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Matches 10; Conserv
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                                                                                                                                                                                                       GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 08/22,612
FILING DATE: 16-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Fisher, Carlos A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM
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                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Gen-Probe Incorporated
STREET: 9880 Campus Point Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-535-2807
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APPLICATION NUMBER:
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                                                                                                                           APPLICANT: SIVARAM, MATHOOR APPLICANT: TUDOR, STARLA D. TITLE OF INVENTION: PURIFED TITLE OF INVENTION: STEAROTH
                                                                                                                                                                                       APPLICANT:
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                                                                                                           NUMBER OF SEQUENCES:
COUNTRY: US
ZIP: 92121
                                                                                                                                                                                                                                                                                                                   433 LAQNLNITRKE 443
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CITY: San Diego
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                                  STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                1 LAQNLNIXRKE 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 619-546-7929
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
                             San Diego
                                                                                                                                                                                                                        6066483
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amino acid
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                                                                                                                                                                                                                                     Application US/09135642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    588 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: Gen-Probe Incorporated 9880 Campus Point Drive
                USA
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                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                        RIGGS, MICHAEL G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FastSEQ Version 1.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       single
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90.9%;
                                                                                                                          PURIFED DNA POLYMERASE FROM BACILLUS STEAROTHERMOPHILUS
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                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                             Score 48; DB 2;
Pred. No. 0.049;
                                                                                                                                                                                                                                                                                                                                                                                                          Length 588;
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US-08-94-232A-25
US-08-964-232A-25
Sequence 25, Application US/08394232A
Patent No. 6100078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; FRAGMENT TYPE:
; ORIGINAL SOURCE:
US-09-135-642-25
                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 14
                                                                                                                                                                                                                                                                                                                                                                Patent No. 6100078
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 08/307,410
APPLICATION NUMBER: 08/307,410
FILING DATE: 16-SEP-1994
APPLICATION NUMBER: 08/222,612
APPLICATION NUMBER: 08/222,612
APPLICATION NUMBER: 08/222,612
APPLICATION NUMBER: 08/222,612
APPLICATION NUMBER: 08/307,410
                                                             SOFTWARE: FastSEQ Version 1.5 CURRENT APPLICATION DATA:
PRIOR APPLICATION DATA:
                                                                                                                                                COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: PURIFED DNA POLYMERASE FROM BACILLUS STEAROTHERMOPHILU NUMBER OF SEQUENCES: 34
                                                                                                                                                                                                                                                                                                                APPLICANT: RIGGS, MICHAEL G.
APPLICANT: SIVARAM, MATHOOR
APPLICANT: TUDOR, STARLA D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HYPOTHETICAL:
ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: FastSEQ Version 1.5 CURRENT APPLICATION DATA:
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MEDIUM TYPL: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    433 LAQNLNITRKE 443
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                                                                                               OPERATING SYSTEM:
                                                                                                                COMPUTER:
                                                                                                                                                                  COUNTRY: U
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                             FILING DATE:
                                             APPLICATION NUMBER: US/08/394,232A
                                                                                                                              MEDIUM TYPE:
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                                                                                                                                                                                                                              ADDRESSEE: Gen-Probe Incorporated STREET: 9880 Campus Point Drive
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TELEFAX: 619-546-7929
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                                                                                                                                                                                                                San Diego
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                                                                                             PE: Diskette
IBM Compatible
SYSTEM: DOS
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90.9%;
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; ORIGINAL SOURCE:
US-08-394-232A-25
                                      Search completed: January 15, 2003, 12:38:26 Job time: 10.2857 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      В
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Matches 10; Conserv
                                                                                                                                                                                          Query Match
Best Local Similarity
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                                                                                                                                                                            Matches
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                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ 10 NOS: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: P
HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                         433 LAQNLNITRKE 443
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                                                                                                                                     1 LAQNLNIXRKE 11
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APPLICATION NUMBER: 08/222,612
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; SOFTWARE: Patentin Ver. 2.0 - beta
; SEQ ID NO 4
; LENGTH: 588
; TYPE: PRT
; ORGANISM: Bacillus stearothermophilus
US-09-157-397-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4, Application US/09157397 Patent No. 6165765
                                                                                                                                                                                                                                       EARLIER FILING DATE: 1995-10-18
EARLIER APPLICATION NUMBER: 08/642,684
EARLIER FILING DATE: 1996-05-03
                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: DNA POLYMERASE HAVING ABILITY TO REDUCE INNATE TITLE OF INVENTION: SELECTIVE DISCRIMINATION AGAINST FLUORESCENT TITLE OF INVENTION. DVE-LABBLED DIDEOXYNUCLEOTIDES FILE REFERENCE: hongsequencelisting CURRENT APPLICATION NUMBER: US/09/157,397 CURRENT APPLICATION NUMBER: US/09/157,397 CURRENT APPLICATION NUMBER: 08/544,643
                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: HONG, GUOFAN APPLICANT: HUANG, WEI-HUA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KEGISTRATION NUMBER: 36,510
REFERENCE/DOCKET NUMBER: GPS
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 16-SEP-1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Fisher, Carlos A REGISTRATION NUMBER: 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: 619-535-28 TELEFAX: 619-546-7929
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      Conservative
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  Score 48; DB 4; Length 588; Pred. No. 0.049; 0; Mismatches 1; Indels
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Gaps
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Result
No.
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-DB=1ssued_patents_NA -QFMT=fastap -SUFFIX=rn1 -MINMARCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -STRAT=1 -END=-1 -MARTHIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -QUTFMT=pto -NORMe=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
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-NO_KIDPX -NO_MAAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LOORGCO -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOD=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OM protein - nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
                                                                                                                                                                                                                                                                                                  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                      Score
     Xgapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
                                                                                                                                                                                                                      Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              January 15, 2003, 12:36:21; Search time 26 Seconds (without alignments) 129.748 Million cell updates/sec
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   Issued_Patents_NA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             441362 seqs, 153338381 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-823-649A-7
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Listing first 45 summaries
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Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                 /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/Dackfiles1.seq:*
                                                                                                                                                                                                                     Length DB
   1142
1379
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US-09-057-969-12

US-09-057-969-11

US-09-057-969-10

US-09-057-969-9

US-08-642-684-1

US-08-436-646-22

US-09-135-642-22

US-09-135-642-22

US-09-157-397-1

US-09-157-397-3

US-09-157-397-3

US-09-517-37-21

US-09-517-871-21

US-09-517-871-21

US-09-517-871-21
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US-09-057-969-12
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APPLICANT:
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                                                                                                                                                                                                                                                                                COUNTRY:
ZIP: 101
              TELEFAX:
                                                                                                                                                                                                                                                                                                                  STATE:
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                                                                                                                                                                                                                                                                                                USA
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equence 19,	19,	Sequence 33, Appl	ω,	m ·	e 19.		33,	31,	21,		ω 1	21.	ω	31, App	21 App		13	13	8, Appl	3, Appl	Sequence 16, Appl	16, App	26		26.	•		24. App	ر س	24, App	e 24	4

ALIGNMENTS

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Sequence 12, Application US/09057969 Patent No. 6013451
INFORMATION FOR SEQ ID NO:
                                      FILING DATE: 09-APR-1998
CLASSIFICATION: 435
ATTORNEY_AGENT INFORMATION:
NAME: KOWALSKI, THOMAS J.
REGISTRATION NUMBER: 32,147
REFERENCE/DOCKET NUMBER: 6745
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-588-0800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FOR COMPACTIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                APPLICATION NUMBER: US/09/057,969 FILING DATE: 09-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                    3: FROMMER LAWRENCE & HAUG LLP
745 FIFTH AVENUE
                           212-588-0500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PHANG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VICTOR THI WONG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BACILLUS STEAROTHERMAPHILUS DNA
POLYMERASE I (KLENOW) CLONES INCLUDING THOSE REDUCED
3'-TO-5' EXONUCLEASE ACTIVITY
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    12:
                                                                                     674507-2001
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Percent Similarity:
Best Local Similarity:
                                                                                        Pred. No.:
                                                                                                      Alignment Scores:
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Patent No. 6013451
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INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
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APPLICANT: TAN, TIEN CHYE
TITLE OF INVENTION: BACILLUS STEAROTHERMAPHILUS DNA
TITLE OF INVENTION: POLYMERASE I (KLENOW) CLONES INCLUDING THOSE REDUCED TO
TITLE OF INVENTION: 34-To-5' EXONUCLEASE ACTIVITY
                                                                                                                                                                                                                                                                                           TELEPHONE: 212-588-0800
                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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ADDRESSEE: FROMMER LAWRENCE & HAUG LLP
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                                                                                                                                                                                        STRANDEDNESS: single
                                                                                                                                                                                                         LENGTH: 1142 base pairs TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                          NAME: KOWALSKI, THOMAS J.
REGISTRATION NUMBER: 32,147
REFERENCE/DOCKET NUMBER: 674507-2001
                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/09/057,969
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: NEW YORK
STATE: NEW YORK
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Gaps:
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GENERAL INFORMATION:
APPLICANT: WONG, V
APPLICANT: PHANG, APPLICANT: TAN, TI
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Percent Similarity:
Best Local Similarity:
Query Match:
; Sequence 9, Application US/09057969
; Patent No. 6013451
                                   US-09-057-969-9
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INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
SEQUENCE 1379 base pairs
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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STREET: /**
CITY: NEW YORK
CTATE: NEW YORK
TISA
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ATTORNEY/AGENT INFORMATION:
NAME: KOWALSKI, THOMAS J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: TAN, TIEN CHYE
TITLE OF INVENTION: BACILLUS STEAROTHERWAPHILUS DNA
TITLE OF INVENTION: POLYMERASE I (KLENOW) CLONES INCLUDING THOSE REDUCED TO
TITLE OF INVENTION: 3'-TO-5' EXONUCLEASE ACTIVITY
NUMBER OF SEQUENCES: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION: TELEPHONE: 212-588-0800
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                                                                                 577 CTGGCGCAAAACTTGAACATTACGCGCAAAGAA 609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/09/057,969 FILING DATE: 09-APR-1998
                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE:
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Conservative:
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WONG, VICTOR THI WONG PHANG, SENG MENG TAN, TIEN CHYE

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US-08-642-684-1
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                                                                                                                                                                                                                                                                                                                                        Patent No. 5834253
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                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: KOWALSKI, THOMAS J.
REGISTRATION NUMBER: 32,147
REFERENCE/DOCKET NUMBER: 674507-2001
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                 1060 CTGGCGCAAAACTTGAACATTACGCGCAAAGAA 1092
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LENGTH: 1625 base pairs
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                                                                                                                                                                                                                                 TITLE OF INVENTION: A NEW DNA POLYMERASE WITH PROOF-READING TITLE OF INVENTION: 3'-5' EXONUCLEASE ACTIVITY
                                                                                                                                                                                                                                                                   APPLICANT: FENG, ZHAI
APPLICANT: HUANG, WEI-HUA
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                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                         APPLICANT:
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 MEDIUM TYPE: Floppy disk
COMPOTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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                                                                                        ZIP: 20005
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                                                                                                           COUNTRY:
                                                                                                                            STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IBM PC compatible
                                                                                                                                                                                CUSHMAN, DARBY & CUSHMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BACILLUS STEAROTHERMAPHILUS DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patent No. 5874282
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 22, Application US/08436664 Patent No. 5874282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1294 TTGGCGCAAAACTTGAACATTACGCGCAAAGAA 1326
                                                  FILING DATE: 16-SEP-1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: PURIFIED DNA FOLYMER TITLE OF INVENTION: STEAROTHERWOPHILUS NUMBER OF SEQUENCES: 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: SIVARAM, MATHOOR APPLICANT: TUDOR, STARLA D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: DNA (genomic)
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                                                                                                                                                                            CLASSIFICATION: 536 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
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                                                                                                   FILING DATE:
APPLICATION NUMBER:
FILING DATE: 16-SEE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
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               NAME: Fisher, Carlos A REGISTRATION NUMBER: 3
                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                   SOFTWARE:
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STRANDEDNESS: single
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                                                                                  APPLICATION NUMBER: 08/222,612
                                                                                                                                                             APPLICATION NUMBER:
                                                                                                                                                                                                                               APPLICATION NUMBER:
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REFERENCE/DOCKET NUMBER:
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                                                                                                                        08/307,410
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                36,510
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GP94003.CP2
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Matches:
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Indels:
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 22,
                                         APPLICATION NUMBER: 08/307,410
APPLICATION NUMBER: 08/307,410
APPLICATION NUMBER: 08/22,612
APPLICATION NUMBER: 08/22,612
TTMT DATE: 16-SEP-1994
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            FILING DATE: 16-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Fisher, Carlos A
REGISTRATION NUMBER: 36,5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: FastSEQ Version 1.5 CURRENT APPLICATION DATA:
                                                                                                                                                             PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: RIGGS, MICHAEL G.
APPLICANT: SIVARAM, MATHOOR
APPLICANT: TUDOR, STARLA D.
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LENGTH: 1764 base pairs
TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
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TELEPHONE: 619-535-2807
TELEFAX: 619-546-7929
                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                COMPUTER:
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                                                                                                                                                                                                                                                                                                                                                                STATE:
REFERENCE/DOCKET NUMBER: GP94003.CP2
                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                              MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Gen-Probe Incorporated STREET: 9880 Campus Point Drive
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             36,510
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US-08-394-232A-22
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             APPLICATION NUMBER: 08/222,612
FILING DATE: 16-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Fisher, Carlos A
REGISTRATION NUMBER: 36,510
REFERENCE/DOCKET NUMBER: GP94003
TELEPHONE: 619-535-2807
TELEPHONE: 619-535-2807
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APPLICANT: KIGGS, MICHAEL, G.
APPLICANT: STARRAM, MATHOOR
APPLICANT: TUDOR, STARLA D.
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                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/3
FILLING DATE: 16-SEP-1994
                                                                                                                                                                                                                                                                              SOFTWARE: FastSEQ Version 1.5 CURRENT APPLICATION DATA:
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MEDIUM TYPE: Diskett
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: PURIFED DNA POLYMERASE FROM BACILLUS STEAROTHERMOPHILU NUMBER OF SEQUENCES: 34
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                                                                                                                                                                                                                      CLASSIFICATION: 435
                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/394,232A
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TOPOLOGY: linear
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619-546-7929
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Conservative:
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RESULT 10
US-09-157-397-3
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Best Local Similarity:
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Best Local Similarity:
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APPLICANT: HEARD, WEIT-HUA
APPLICANT: HEARD, WEIT-HUA
TITLE OF INVL.ITON: DAR POLYMERASE HAVING ABILITY TO REDUCE INNATE
TITLE OF INVENTION: SELECTIVE DISCRIMINATION AGAINST FLUORESCENT
TITLE OF INVENTION: DYE-LABELED DIDEOXYNUCLEOTIDES
FILE REFERENCE: hongsequencelisting
CURRENT APPLICATION NUMBER: US/09/157,397
CURRENT APPLICATION NUMBER: US/09/157,397
CURRENT APPLICATION NUMBER: US/09/157
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                                                                                                                                                                                                                                                                                                                                                                                                                                    EARLIER APPLICATION NUMBER: 08/544,643
EARLIER FILING DATE: 1995-10-18
EARLIER APPLICATION NUMBER: 08/642,684
EARLIER FILING DATE: 1996-05-03
NUMBER OF SEQ ID NOS: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/09157397 Patent No. 6165765
                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Ver. 2.0 - beta
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                                                     1294 TIGGCGCAAAACTTGAACATTACGCGCAAAGAA 1326
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US-09-823-649A-7 (1-11) x US-09-517-871-21 (1-1764)
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PCT-US95-04080-22
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Best Local Similarity:
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US-09-157-397-3
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; Patent No. 643667;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Hartnett, John R.
APPLICANT: Huang, Fen
APPLICANT: Gu, Trent
TITLE OF INVENTION: Method of Reverse Transcription
FILE REFERENCE: PRMG-03833
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                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ 1D NOS: 24
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT FILING DATE: 2000-03 02
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                                                   1294 TTGGCGCAAAACTTGAACATTACGCGCAAAGAA 1326
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Matches:
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US-09-823-649A-7 (1-11) x PCT-US95-04080-22 (1-1764)
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                                                            CLASSIFICATION: 536 PRIOR APPLICATION DATA:
                                                                                                                           SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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TYPE: nucleic acid
STRANDEDNESS: single
FILING DATE:
                                              APPLICATION NUMBER:
                                                                                             APPLICATION NUMBER: FILING DATE: 08-MA
                                                                                                                                                            OPERATING SYSTEM:
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ZIP: 92121
                                                                                                                                                                                                                                                                STATE:
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                             FILING DATE:
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               CATION NUMBER:
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               08/307,410
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                                              08/394,232
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RESULT 14
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APPLICANT: RIGGS, MICHAEL G.

APPLICANT: SIVAKAM, MATHOOR

APPLICANT: TUDOR, STARLA D.

TITLE OF INVENTION: PURIFED DNA POLYMERASH FROM BACILLUS

TITLE OF INVENTION: STEAROTHERMOPHILUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                          ZIP: 92121
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                         COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOTTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1297 CTGGCGCAAAACTTGAACATTACGCGCAAAGAA 1329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: GP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-535-2807
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LENGTH: 1767 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 08/2: FILING DATE: 16-SEP-1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
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                                                                                                 APPLICATION NUMBER: US/09/135,642 FILING DATE:
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OTHER INFORMATION:
APPLICATION NUMBER: 08/3 FILING DATE: 16-SEP-1994
                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                  STATE:
                                                                                                                                                                                                                                                                            CITY: San Diego
                                                                                                                                                                                                                                                                                          ADDRESSEE: Gen-Probe Incorporated STREET: 9880 Campus Point Drive
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Fisher, Carlos REGISTRATION NUMBER:
                                  FILING DATE:
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                                              08/394,232
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US-08-394-232A-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity:
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APPLICANT: RIGGS, MICHAEL G.
APPLICANT: SIVARAM, MATHOOR
APPLICANT: TUDOR, STARLA D.
TITLE OF INVENTION: PURIFED DNA POLYMERASE FROM BACHILUS STEAROTHERMOPHILU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 1767 base pairs
TYPE: nucleic acid
                             PRIOR APPLICATION NUMBER: 08/307,410
FILING DATE: 16-SEP-1994
APPLICATION NUMBER: 08/222,612
                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Gen-Probe Incorporated
                                                                                                                                                SOFTWARE: FastSEQ Version 1.5 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1297 CTGGCGCAAAACTTGAACATTACGCGCAAAGAA 1329
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REFERENCE/DOCKET NUMBER: GP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-535-2807
ATTORNEY/AGENT INFORMATION:
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ATTORNEY/AGENT INFORMATION:
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                                                                                                FILING DATE:
CLASSIFICATION: 435
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               FILING DATE:
                                                                                                                                  APPLICATION NUMBER: US/08/394,232A
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                                                                                                                                                                                                                                                                                                                   9880 Campus Point Drive
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Search completed: January 15, 2003, 12:58:58 Job time: 30 secs
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                                                                                                                                                                                                               Pred. No.:
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                                                                                                                                                                                                                                                        US-08-394-232A-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO:
                                                    1297 CTGGCGCAAAACTTGAACATTACGCGCAAAGAA 1329
                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: CL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: GP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-535-2807
                                                                                                                                                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                          FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                     ANTI-SENSE: NO
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                                                                                                                                                                                                                                                                                 NAME/KEY: Coding Sequence LOCATION: 1...1764
                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Fisher, Carlos A
REGISTRATION NUMBER: 36,510
                                                                                                                                                                                                                                                                     OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS: single
                                                                     1 LeuAlaGlnAsnLeuAsnIle***ArgLysGlu 11
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Post-processing: Minimum Match 08
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Listing first 45 summaries
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*
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                                         EP757100-A1
                                                                            Bacillus stearothermophilus
                                                                                                                                                                                Bst DNA polymerase large fragment DNA.
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                                                                                                                 polymerase; Bst Pol I; thermostable enzyme; exonuclease; sequencing; strand displacement amplification; ss.
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ABL17784
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AAT04805
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUMMARIES
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Drosophila melanog
Listeria monocytog
Bacillus lichenifo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Description
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Drosophila melanog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Listeria innocua c
Human secreted pro
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Bacillus caldotena
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        B.stearothermophil
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Enterococcus faeca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plasmid pSE-2 enco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Enterococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA encoding novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA encoding a DNA
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Bacillus stearothe
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pallidus DNA po
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faeca

05-FEB-1997

Searched:

Run on:

Sequence:

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RESULT 2
AAT04802
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                                                                                                                                                                                                                                                                                                                                                                                          Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
                               24-FEB-1995;
01-APR-1994;
16-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A DNA construct (AAT36360) codes for Bacillus stearothermophilus (Bst) DNA polymerase large fragment (AAW10597) which lacks the N-terminal 3'-5' exonuclease domain of the native enzyme. It comprises nucleotides 868-2631 of the full-length Bst polymerase coding sequence, and was obtd. by PCR cloning (see also AAT60826-27) using Bst genomic DNA as template. The DNA construct can be used to produce recombinant Bst polymerase large fragment, pref. as a fusion protein with maltose binding protein, in transformed host cells. The product can be used for nucleic acid sequencing and strand displacement amplification.
                                                                                                                                                                                                                                                                                                                 1294
                                                                           30-MAR-1995;
                                                                                                                   WO9527067-A1
                                                                                                                                         Synthetic.
                                                                                                                                                              amplification; probe; Bacillus caldotenax; exonuclease; recombination; sequencing; polymerase chain reaction; ss.
                                                                                                                                                                                   Bacillus stearothermophilus; thermostable DNA polymerase; PCR; primer;
                                                                                                                                                                                                        B.stearothermophilus DNA polymerase clone Bst2.
                                                                                                                                                                                                                             30-MAY-1996
                                                                                                                                                                                                                                                                       AAT04802 standard; DNA; 1764 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1763 BP; 474 A; 416 C; 486 G; 387 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 3; Page 12-16; 34pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  exonuclease activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1997-111048/11.
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            (GENP-) GEN-PROBE INC
                                                                                               12-OCT-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA encoding recombinant thermophilic Bacillus stearothermophilus DNA polymerase I - substantially free of 3^{\prime}-5^{\prime}, and opt. also 5^{\prime}-3^{\prime}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02-AUG-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     No . .
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                                                                                                                                                                                                                                                                                                                 TTGGCGCAAAACTTGAACATTACGCGCAAAGAA 1326
                                                                                                                                                                                                                                                                                                                             LeuAlaGlnAsnLeuAsnIle***ArgLysGlu 11
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                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kong H,
                               95US-0394232.
94US-0222612.
94US-0307410.
                                                                           95WO-US04080
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48.00
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(ZHAI/)
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AAT90819
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-823-649A-7 (1-11) x AAT04802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alignment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This is the nucleotide sequence of the clone Bst2 encoding a modified Bacillus stearothermophilus thermostable DNA polymerase which lacks the complete 5'-3' exonuclease domain. The gene was constructed by liquting the HindIII-SalI tragment from the clone peemBst2.1Sst. contq. 3' end of the gene with the Sty1-HindIII fragment of the clone peemBst5'end contg. the 5' end of the DNA polymerase gene. The Sty1-HindIII fragment covers the mid-region of the gene up to and including the sequences encoding the 3'-5' exonuclease but not the 5'-3' exonuclease domain. The remainder of the 5' end of the gene was reconstituted by the ligated and extended oligonucleotides AATO4816-17. The modified DNA polymerase can be used in primer extension reactions such as DNA sequencing or polymerase chain reaction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1294 CTGGCGCAAAACTTGAACATTACGCGCAAAGAA 1326
                                                                                                                                                                                                                                                   CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 9; Page 83-85; 135pp; English.
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P-PSDB; AAR81039.
                                                03-MAY-1996;
18-OCT-1995;
                                                                                               17-MAY-1996;
                                                                                                                                26-AUG-1997.
                                                                                                                                                               JP09220087-A
                                                                                                                                                                                                                                                                                                Bacillus stearothermophilus.
                                                                                                                                                                                                                                                                                                                                             Bacillus stearothermophilus; DNA polymerase; DNA amplilication;
                                                                                                                                                                                                                                                                                                                                                                                 Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                  14-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAT90819;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacillus stearothermophilus DNA encoding thermostable polymerase for nucleic acid sequencing and amplification % \left( 1\right) =\left\{ 1\right\} 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Riggs MG,
                                                                                                                                                                                                                                                                                                                             DNA replication; exonuclease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    No.:
               (HONG/)
 (/NAUH)
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               HONG G F.
HUANG W.
                                                                                                                                                                                                                                                                                                                                                                              Stearoth-imophilus DNA polymerase
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                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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                                                95US-0642684
95US-0544643
                                                                                               96JP-0160402
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                                                                                                                                                                                                                                                               Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                             proof reading; ss
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Indels:
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SHANGHAI INST BIOCHEMISTRY CHINESE ACAD

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alignment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  polymerase. This heat stable DNA polymerase has a peptide sequence of 587 amino acids. This DNA polymerase can be used in a method for the replication of a DNA chain. It can also be used in a method for the determination of the sequence of DNA chain. As the DNA polymerase has a proof reading 3'-5' exonuclease activity, possible mismatches of base pairing that occurs in current methods of DNA sequence determination of
Claim 8; Page 93-95; 109pp; English
                                   New DNA polymerase, useful all four dideoxynucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1294 TTGGCGCAAAACTTGAACATTACGCGCAAAGAA 1326
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                                                                          P-PSDB; AAY91930.
                                                                                                                Hong G,
                                                                                                                                                                   21-SEP-1998;
                                                                                                                                                                                                                                                                                   Synthetic.
                                                                                                                                                                                                                                                                                                          Modified DNA polymerase; DNA sequencing; 3' to 5' erandom primer labeling; site-directed mutagenesis;
                                                                                                                                                                                                                                                                                                                                                 B. stearothermophilus 320 modified DNA polymerase coding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This is the DNA sequence of the Bacillus stearothermophilus strain DNA
                                                                                                                                           (SHAN-) SHANGHAI INST BIOCHEMISTRY CHINESE ACAD
                                                                                                                                                                                            14-JAN-1999;
                                                                                                                                                                                                                       30-MAR-2000
                                                                                                                                                                                                                                              WO200017330-A1
                                                                                                                                                                                                                                                                        Bacillus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          No.:
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                                                                                      2000-283563/24
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                                                                                                               Huang W;
                                                                                                                                                                                                                                                                        stearothermophilus.
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                                                                                                                                                                   98US-0157397
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                                    particularly in DNA sequencing, incc
triphosphate terminators with about
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   triphosphates (ddNTP), or their analogs, and reduces the discrimination, observed with the unmodified enzyme, for incorporation of labeled ddCTP and ddATP, is new. The modified DNA polymerase, has proofreading 3'-5' exonuclease activity during DNA sequencing from a template and the polymerase excises mismatched nucleotides from the 3' terminus at a faster rate than it removes correctly matched nucleotides. The polymerase is used particularly for DNA sequencing, also for filling in
                                                                                                                                                                                                                                                                                                                          New DNA polymerase, useful
all four dideoxynucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5'-overhangs, synthesis of DNA probes by random primer labeling and in site-directed mutagenesis, (claimed).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence encodes a modified Bacillus stearothermophilus DNA polymerase (AAY91930) that, during DNA sequencing, effectively incorporates all four fluorescent dye-labeled dideoxynucleotide
                                                                                                                                                                                                                                                                                          efficiency
                                                                                                                                                                                                                                                                                                                                                                                                                        P-PSDB; AAY91931,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Modified DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 B. stearothermophilus 320 wild type DNA polymerase coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAA08545 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1764 BP; 476 A; 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (SHAN-) SHANGHAI INST BIOCHEMISTRY CHINESE ACAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacillus stearothermophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                random primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAA08545;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ر.
و
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTGGCCCAAAACTTGAACATTACGCCCAAAGAA 1329
                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000-283563/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Huang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         polymerase; DNA sequencing; 3' to 5' exonuclease act r labeling; site-directed mutagenesis; wild type; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9805-0157397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99W0-IB00146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0.541
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                                                                                                                                                                                                                                                                                                                       particularly in DNA sequencing, incorporates triphosphate terminators with about equal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           વુષ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; 485 G; 385 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3' to 5' exonuclease activity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1764
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The present sequence encodes a wild type Bacillus Stearothermophilus DNA polymerase (AAY91931) that is modified (see AAY91930) so that during DNA sequencing, it effectively incorporates all four fluorescent dye-labeled dideoxynucleotide triphosphates (ddNTP), or their analogs, and reduces the discrimination, observed with the unmodified enzyme, for incorporation of labeled ddCTP and ddATP, is new. The modified DNA polymerase, has proofreading 3'-5' exonuclease activity during DNA

Example 2; Page 80-82; 109pp; English

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RESULT 6
AAD18459
1D AAD1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
The invention relates to reverse transcription of RNA templates using thermostable DNA polymerase such as Thermoactinomyces vulgaris (Tvu) and Bacillus stearothermophilus (Bst) DNA polymerase. Tvu and Bst DNA polymerase are useful for reverse transcription reactions which allows repetitive heating/cooling cycles without the requirement of fresh enzyme at each cooling step. The invention contemplates single-reaction RT-PCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1294 TTGGCGCAAAACTTGAACATTACGCGCAAAGAA 1326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequencing from a template and the polymerase excises mismatched nucleotides from the 3' terminus at a faster rate than it removes correctly matched nucleotides. The polymerase is used particularly DNA sequencing, also for filling in 5' overhangs, synthesis of DNA
                                                                                                                                                                                                                                                                                                                         Reverse transcription of RNA using Tvu and Bst DNA polymerase, comprises combining the polymerase, RNA containing sample, a primer and reaction buffer having magnesium ions and reacting the mixture to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              02-MAR-2000; 2000US-0517871
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            07-SEP-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAD18459;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAD18459 standard; DNA; 1764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1764 BP; 477 A; 415 C; 486 G; 386 T; 0 other;
                                                                                                                                                                                                                                Claim 9; Fig 9; 118pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P-PSDB; AAE11060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (PROM-) PROMEGA CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-FEB-2001; 2001WO-US06571.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacillus stearothermophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bst; enzyme; amplification; hybridisation; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Reverse transcription;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacillus stearothermophilus (Bst) DNA polymerase 1 fragment DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (claimed).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               l LeuAlaGlnAsnLeuAsnTle***ArgLysGlu ll
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2001-589872/66.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Huang F, Hartnett JR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        by random primer labeling and in site-directed mutagenesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product= "Bacillus stearothermophilus DNA polymerase ]"
/note= "CDS does not include start codes"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /partial
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-823-649A-7 (1-11) x AAD18459 (1-1764)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           wherein reverse transcription and amplification are performed in a single continuous procedure. Primers, template, nucleoside triphosphates, appropriate reaction buffer having magnesium ions, reaction conditions, and polymerase are used in the PCR process, which involves denaturation of target DNA, hybridisation of primers and synthesis of complementary
                          This is the nucleotide sequence of the clone Bst3 encoding a modified Bacillus stearothermophilus thermostable DNA polymerase which contains a deletion in the 5'-3' exonuclease domain. The gene was constructed by digestion and recombination of the full length gene (AAF04801) to remove a 195 bp HinciI-PvulI fragment from the region encoding the 5'-3' exonuclease. The deleted fragment removes 65 amino acids (residues 178-242 of the protein) including 2 Gly residues though to correspond to 2 amino acids in the E.coli DNA polymerase I necessary for 5'-3' exonuclease activity. The modified DNA polymerase can be used in primer exonuclease activity. The modified DNA polymerase can be used in primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1294 TTGGCGCANAACTTGAACATTACGCGCAAAGAA 1326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1764 BP; 477 A; 415 C; 486 G; 386 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        strands. The present DNA sequence is Bacillus stearothermophilus (8st) DNA polymerase 1 fragment which lacks 5' to 3' exonuclease activity.
                                                                                                                                                                                                                            Claim 9; Page 87-90; 135pp; English.
                                                                                                                                                                                                                                                                                                                            P-PSDB; AAR80140.
                                                                                                                                                                                                                                                                                                                                                WPI; 1995-373510/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-APK-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9527067-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequencing; polymerase chain reaction; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amplification; probe; Bacillus caldotenax; exonuclease; recombination;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacillus stearothermophilus; thermostable DNA polymerase; PCR; primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            B.stearothermophilus DNA polymerase clone Bst3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAT04803;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAT04803 standard; DNA; 1767
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                                                                                                                                                                                                                                                                                     Bacillus stearothermophilus DNA encoding thermostable polymerase -
                                                                                                                                                                                                                                                                                                                                                                                                                            (GENP-) GEN-PROBE INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24-FEB-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-MAR-1995;
                                                                                                                                                                                                                                                                   for nucleic acid sequencing and amplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12-0CT-1995
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extension reactions such as DNA sequencing or polymerase chain reaction

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RESULT 8
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             The invention relates to reverse transcription of RNA templates using thermostable DNA polymerase such as Thermoacthomyces vulgaris (Tvu) and Bacillus stearothermophilus (Bst) DNA polymerase Tvu and Bst DNA polymerase are useful for reverse transcription reactions which allows repetitive heating/cooling cycles without the requirement of fresh enzyme at each cooling step. The invention contemplates single-reaction RT-PCR wherein reverse transcription and amplification are performed in a single continuous procedure. Primers, template, nucleoside triphosphates, appropriate reaction buffer having magnesium ions, reaction conditions, and polymerase are used in the PCR process, which involves denaturation
                                                                                                                                                                                                                                                                                                                    Reverse transcription of RNA using Tvu and Bst DNA polymerase, comprises combining the polymerase, RNA containing sample, a primer reaction buffer having magnesium ions and reacting the mixture to
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                                                                                                                                                                                                                                                           Example 11; Fig 5; 118pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (PROM-) PROMEGA CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-MAR-2000; 2000US-0517871
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-FEB-2001; 2001WO-US06571.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Thermoactinomyces vulgaris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       enzyme; amplification; hybridisation; mutant; mutein; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Reverse transcription; DNA polymerase; Thermoactinomyces vulgaris; Tvu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Thermoactinomyces vulgaris DNA polymerase T289M truncated mutant DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Huang F,
                                                                                                                                                                                                                                                                                                        CDNA
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             RESULT 9
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having DNA synthesis activity. It is useful for determining the nucleotide base sequence of a DNA molecule. Twu DNA polymerase can be used for processes of high temperature nucleic acid amplification and sequencing without substantial loss of DNA synthesis activity. The enzean be used to perform high temperature reverse transcription in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of target DNA, hybridisation of primers and synthesis of complementary strands. The present sequence is Thermoactinomyces vulgaris (Tvu) DNA polymerase 7289M truncated mutant DNA. This Tvu T289M mutant DNA is obtained by deleting 864 bases from the 5' end of wild-type Tvu DNA polymerase gone and replacing 'C' at position 866 with 'T' in the wild
                                                                                                          The invention provides compositions comprising thermostable DNA polymerases derived from hyperthermophilic eubacteria, in particular, polymerases derived from hyperthermophilic eubacteria, in particular, polymerases purified and isolated Thermoactinomyces vulgaris (Tvu) DNA polymerase
                                                                                                                                                                                                     Claim 17; Fig 7; 113pp; English
                                                                                                                                                                                                                                           Novel thermostable DNA polymerase derived from Thermoactinomyces vulgaris for us in many recombinant DNA techniques, including amplification, reverse transcription and sequencing reactions -
                                                                                                                                                                                                                                                                                                                                          P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                          Gu T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           02-MAR-2000; 200008-0517439
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Tvu DNA polymerase; nucleic acid amplification; reverse transcription;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         deletion mutant; T289M; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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This DNA sequence of the Bacillus stearothermophilus strain encodes a heat stable DNA polymerase. This DNA polymerase has a peptide sequence of 589 amino acids. This DNA polymerase can be used in a method for the replication of a DNA chain. It can also be used in a method for the determination of the sequence of DNA chain. As the DNA polymerase has a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1297
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  absence of manganese ions and in high throughput robotically-manipulated procedures because greater enzymatic stability is retained at room temperature. Using the Tvu DNA polymerase, reverse transcription reactions can be conducted at increased temperatures so that secondary structure is removed or limited. The present sequence represents the nucleotide sequence encoding a 5′-3′ exonuclease deletion mutant form of Tvu DNA polymerase called T289M.
                                                                                  Claim 13; Pages 27-28; 32pp;
                                                                                                                                                                                WPI; 1997-474304/44
                                                                                                                                                                                                                                                                                                                                                                                                     JP09220087-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacillus stearothermophilus; DNA polymerase; DNA replication; exonuclease; proof reading;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14-APR-1998
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                                                                                                               mismatch
                                                                                                                                                                                                                                                                                                                     03-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacillus stearothermophilus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1767 BP; 427 A; 457 C; 539 G; 344 T; 0 other;
                                                                                                                        DNA polymerase from Bacillus stearothermophilus - used in DNA amplification and sequencing methods having lower frequency of
                                                                                                                                                                    P-PSDB; AAW30094.
                                                                                                                                                                                                          Hong GF,
                                                                                                                                                                                                                                                 (ZHAI/)
                                                                                                                                                                                                                                                                                                          18-OCT-1995;
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                                                                                                                                                                                                                                   ZHAI F. SHANGHAI INST BIOCHEMISTRY CHINESE ACAD
                                                                                                                                                                                                                                                                 HUANG
                                                                                                                                                                                                                                                                              HONG G F.
                                                                                                                                                                                                          Huang W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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                                                                                                                                                                                                                                                                                                        96US-0642684
95US-0544643
                                                                                                                                                                                                                                                                                                                                                 96JP-0160402
                                                                                                                                                                                                                                                                                                                                                                                                                             /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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                                                                                  Japanese
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Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA amplification;
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                               24-FEB-1995;
01-APR-1994;
16-SEP-1994;
                             This is the nucleotide sequence of the clone Bst4 encoding a modified Bacillus stearothermophilus thermostable DNA polymerase. This clone encodes the sequence of a natural degradation product obtained when the DNA polymerase clone Bst3 (AAT04803) is expressed in E.coli. The same sequence is found when the full length clone (AAT04801) is expressed and cleaved with subtilisin to produce a "Klenow-type" DNA polymerase. This sequence starts with the Val residue at pos. 287 of the full length protein. This contrasts with a commercially available B stearothermophilus DNA polymerase subtilisin fragment where the protein sequence starts with the Ala residue corresp. to pos. 290. The modified DNA polymerase can be used in primer extension reactions such a NA segment of the contrasts with the Ala residue corresp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1300 TTGGCGCAAAACTTGAACATTACGCGCAAAGAA 1332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          proof reading 3^{\prime}-5^{\prime} exonuclease activity, possible mismatches of base pairing that occurs in current methods of DNA sequence determination of a DNA clone can be avoided.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacillus stearothermophilus; thermostable DNA polymerase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                B.stearothermophilus DNA polymerase clone Bst4.
                                                                                                                                                                                                    Claim 9;
                                                                                                                                                                                                                                           Bacillus
                                                                                                                                                                                                                                                                     P-PSDB; AAR80141
                                                                                                                                                                                                                                                                                                           Riggs MC
                                                                                                                                                                                                                                                                                                                                                                                                                      30-MAR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             amplification; probe; Bacillus caldotenax; sequencing; polymerase chain reaction; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAT04804;
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                                                                                                                                                                                                                              for nucleic
                                                                                                                                                                                                                                                                                                                                     (GENP-) GEN-PROBE INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                12-OCT-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W09527067-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 LeuAlaGlnAsnLeuAsnIle***ArgLysGlu
                        sequencing or polymerase chain reaction.
                                                                                                                                                                                                                                                                                  1995-373510/48.
                                                                                                                                                                                                                          stearothermophilus eic acid sequencing
                                                                                                                                                                                                Page 92-94; 135pp; English.
                                                                                                                                                                                                                                                                                                             Sivaram M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                               95US-0394232.
94US-0222612.
94US-0307410.
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                                                                                                                                                                                                                           DNA
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                                                                                                                                                                                                                                                                                                           SD;
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                                                                                                                                                                                                                          encoding thermostable polymerase amplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                488
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        exonuclease; recombination;
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Sequence 1773 BP; 433 A; 460 C; 535 G; 345 T; 0 other;

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RESULT 12
AAQ31651
ID AAQ31
Alignment Scores:
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                              03-JUN-1991;
07-NOV-1991;
24-FEB-1992;
25-FEB-1992;
06-APR-1992;
                                                         A gene coding for DNA polymerase I was isolated from B.caldotenax YT-G genomic DNA (see AAQ31650). A series of N-terminal deletions was prepared to eliminate the region responsible for 5′ to 3′ exonuclease activity. Plasmid pUI205 was one of the deletion plasmids which still expressed Poll activity but for which no 5′ to 3′ exonuclease activity was detected. The insert contained in pUI205 is identical to nucleotides 1090 to 2868 of AAQ31650. E.coli HB101 transformed with pUI205 produced a heat-resistant DNA polymerase of mol. wt. 67,000 by SDS-PAGE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1303 CTGGCGCAAAACTTGAACATTACGCGCAAAGAA 1335
                         Sequence 1779 BP;
                                                                                                                                                                                          Claim 2; Page 23-24; 30pp; English.
                                                                                                                                                                                                                Gene for PolI type DNA polymerase and cloning method production of DNA polymerase in high yield.
                                                                                                                                                                                                                                                          P-PSDB; AAR28349
                                                                                                                                                                                                                                                                      WPI; 1992-408872/50.
                                                                                                                                                                                                                                                                                              Fujita K, Ishino Y,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacillus caldotenax truncated DNA PolI gene in plasmid pUI205.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAQ31651 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         polymerase; polymerase chain reaction; strain YT-G; DSM406
to 3' exonuclease activity; ds.
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                                                AAR28340-R28347 and AAQ31648-Q31649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                             91JP-0157368.
91JP-0318685.
92JP-0072090.
92JP-0073161.
92JP-0112400.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
1..1779
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/product% N-terminally_deleted_poll
/note= "5'to 3' exonuclease activity deleted"
                         446 A; 425 C; 529 G; 379 T; 0 other;
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The invention relates to reverse transcription of RNA templates using thermostable DNA polymerase such as Thermoactinomyces vulgaris (Tvu) and Bat DNA polymerase. Tvu and Bat DNA CC polymerase are useful for reverse transcription reactions which allows CC repetitive healing/cooling cycles without the requirement of fresh enzyme CC repetitive healing/cooling cycles without the requirement of fresh enzyme CC wherein reverse transcription and amplification are performed in a single CC continuous procedure. Primers, template, nucleoside triphosphates, CC appropriate reaction buffer having magnesium inons, reaction conditions, CC and polymerase are used in the PCR process, which involves denaturation CC of target DNA, hybridisation of primers and synthesis of complementary CC strands. The present sequence is Thermoactinomyces vulgaris (Tvu) DNA CC polymerase M285 truncated mutant DNA. This Tvu M285 mutant DNA is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       밁
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                                                                                                                                                                                                                                                                                      Reverse transcription of kNA using Tvu and Bst DNA polymerase, comprises combining the polymerase, RNA containing sample, a primer and reaction buffer having magnesium ions and reacting the mixture to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Reverse transcription; DNA polymerase; Thermoa enzyme; amplification; hybridisation; mutant;
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                                                                                                                                                                                                                                               Example 11; Fig 3; 118pp; English.
                                                                                                                                                                                                                                                                                 obtain
                                                                                                                                                                                                                                                                                                                                                           P-PSDB; AAE11057
                                                                                                                                                                                                                                                                                                                                                                           WPI;
                                                                                                                                                                                                                                                                                                                                                                                                      Gu T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                             02-MAR-2000; 2000US-0517871
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Thermoactinomyces vulgaris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Thermoactinomyces vulgaris DNA polymerase M285 truncated mutant DNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 LeuAlaCinAsnLeuAsnIle***ArgLysGlu
                                                                                                                                                                                                                                                                                                                                                                        2001-589872/65
                                                                                                                                                                                                                                                                                                                                                                                                    Huang F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2001WO-US06571.
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/product= "Thermoactinomyces vulgaris DNA polymerase
//285 truncated mutant"
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1..1779
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polymerase gene

Sequence 1779

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AAH47392
ID AAH
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Best Local Similarity:
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                                                                                       The invention provides compositions comprising thermostable DNA polymerases derived from hyperthermophilic cubacteria, in particular, a purified and isolated Thermoactinomyces vulgaris (Tvu) DNA polymerase having DNA synthesis activity. It is useful for determining the nucleotide base sequence of a DNA molecule. Tvu DNA polymerase can be used for processes of high temperature nucleic acid amplification and sequencing without substantial loss of DNA synthesis activity. The enzyme can be used to perform high temperature reverse transcription in the absence of manganese ions and in high throughput robotically manipulated
                               procedures because greater enzymatic stability is retained at room temperature. Using the Tvu DNA polymerase, reverse transcription reactions can be conducted at increased temperatures so that secondary structure is removed or limited. The present sequence represents the
nucleotide sequence encoding a 5'-3' Tvu DNA polymerase called M285.
                                                                                                                                                                                                                                                                                                            Novel thermostable DNA polymerase derived from Thermoactinomyces vulgaris for us in many recombinant DNA techniques, including
                                                                                                                                                                                                                                                             Claim 17; Fig 5; 113pp; English
                                                                                                                                                                                                                                                                                                amplification, reverse transcription and sequencing reactions
                                                                                                                                                                                                                                                                                                                                                                 P-PSDB; AAB85950
                                                                                                                                                                                                                                                                                                                                                                                                                                               (PROM-) PROMEGA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              02-MAR-2000; 2000US-0517439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-FEB-2001; 2001WO-US06436
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Thermoactinomyces vulgaris.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              deletion mutant; M285; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tvu DNA polymerase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Thermostable; DNA polymerase; hyperthermophilic; DNA synthesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tvu DNA polymerase deletion mutint M285 encoding
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                                                                                                                                                                                                                                                                                                                                                                                                              Huang F, Hartnett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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/product= "Tvu DNA polymerase M285"
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               exonuclease deletion mutant form of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity:
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                        This is the sequence of the coding region of the gene encoding the Bacillus stearothermophilus thermostable DNA polymerase. The gene was isolated using the PCR primers and probes AAT04807-15 which were based on sequence similarity with the Bacillus caldotenax DNA polymerase gene. The gene was isolated as two overlapping fragments of 885 and 1143 bp corresp. to the 3' end and the 3'-5' exonuclease region of the protein, resp. Those amplification fragments were used to probe Southern gels and isolate the 3' and 5' ends of the gene as two separate iragments. The complete gene (AAT04801) was subsequently polymerase can be used in primer extension reactions such as DNA sequencing or polymerase chain reaction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1309
  Sequence 2631
                                                                                                                                                                                                      Claim 6; Page 79-82; 135pp; English
                                                                                                                                                                                                                                                                                         WP1; 1995-373510/48
                                                                                                                                                                                                                                                                                                                   Riggs MG,
                                                                                                                                                                                                                                                                                                                                                                                     24-FEB-1995;
01-APR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacillus stearothermophilus; thermostable DNA polymerase; PCR; primer; amplification; probe; Bacillus caldotenax; exonuclease; recombination;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        B.stearothermophilus DNA polymerase coding sequence.
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                                                                                                                                                                                                                                 for nucleic acid sequencing
                                                                                                                                                                                                                                           Bacillus stearothermophilus DNA encoding thermostable polymerase
                                                                                                                                                                                                                                                                            P-PSDB; AAR8ul37
                                                                                                                                                                                                                                                                                                                                                                         16-SEP-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacillus stearothermophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequencing; polymerase chain reaction; ss.
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                                                                                                                                                                                                                                                                                                                                            (GENP-) GEN-PROBE INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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94US-0222612.
94US-0307410.
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 659 A; 676 C;
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48.00
90.91%
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780 G; 516 T;
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Matches:
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Result
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seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Issued_Patents_AA:*
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Listing first 45 summaries
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Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
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 US-08-484-956-90
US-08-520-946-99
US-08-90-946-399-2
US-09-096-399-2
US-09-096-399-14418-5
PCT-USS5-114718-4
PCT-USS5-114718-4
PCT-USS5-114718-7
PCT-USS5-15327-5
PCT-USS5-15327-2
US-09-777-538-2
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US-09-777-538-2
US-09-777-538-2
US-09-777-538-2
US-09-777-538-2
US-08-156-020-6
US-08-156-020-10
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(without alignments)
34.855 Million cell updates/sec
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; Patent No. 5843654
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US-08-484-956-90
                                                                                                                                                                                                            APPLICATION NUMBER: US/08/
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
FILING DATE: US-MAR-1995
PRIOR APPLICATION NUMBER: US 08/
FILING DATE: US-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disj
COMPUTER: BC COMPOTER:
OPERATING SYSTEM: PC-DO'SOFTWARE: Paleulin Relecturement application Data:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: DAHLBERG, APPLICANT: LYAM CHEV, APPLICANT: BROW, MARY APPLICANT: CLDENBURG, APPLICANT: HEISLER, L.TITLE OF INVENTION: D.
                                            FILING DATE: 07-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: CARROOLL J. PETER G.
REGISTRATION UNBER: 32,837
                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/073,384
FILING DATE: 04-JUN-193
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/986,330
FILING DATE: 07-DEC-1992
                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/254,359
FILING DATE: 06-JUN-1994
                         REFERENCE/DOCKET NUMBER: FO TELECOMMUNICATION INFORMATION:
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STREET: 22
CITY: SAN
STATE: CAL
COUNTRY: U
              TELEPHONE:
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E: (415)
(415) 39
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                                                                                                                                                                                                                                                                                                                                                                                                                                 UNITED STATES
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LYAMICHEV, VICTOR I.
BROW, MARY ANN D.
                                                                                                                                                                                                                                                                                                                                                 PaleutIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                            B: Floppy disk
IBM PC compatible
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STREET, SUITE 2200
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US-08-254-559A-8
US-08-483-043-8
US-08-481-238-8
US-08-481-238-8
US-08-484-956-8
US-08-484-956-8
US-08-484-956-8
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US-08-756-386-4
US-08-823-516-4
US-08-682-853A-4
US-08-759-038-4
US-08-759-038-4
US-09-350-309-4
US-08-978-946-4
US-08-978-986-2
PCT-US91-07035-2
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RESULT 3
US-08-520-946-90
; Sequence 90, Application US/08520946
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US-08-757-653-90
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                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: INGOLIA, Diane E.
REGISTRATION NUMBER: 40,027
REFERENCE/POCKET NUMBER: FORS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 90:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patent No. 5843669
GENERAL INFORMATION:
                                                                                                                                                             Matches
                                                                                                                                                                            Query Match 100.0%; Score 54; DB 2; Length 528; Best Local Similarity 100.0%; Pred. No. 0.022;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/757,653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Lyamichev, Victor I.
APPLICANT: Lyamichev, Natasha
TITLE OF INVENTION: Cleavage Of Nucleic Acid Using
TITLE OF INVENTION: Thermostable FEN-1 Endonucleases
NUMBER OF SEQUENCES: 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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                                                                                        374 LSQELAIPYEE 384
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                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 220 Montgomery Street, Suite 2200 CITY: San Francisco. *
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                                                                                                                           1 LSQELAIPYEE 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Application US/08757653
                                                                                                                                                                                                                                                                                                                    528 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ESS: single
linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Medlen & Carroll, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 54; DB 2; 100.0%; Pred. No. 0.022;
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                                                                                                                                                             Mismatches
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                                                                                                                                                             Indels
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                                                                       US-09-096-399-2
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                                                                                                                                         ; SEQ ID NO 2
; LENGTH: 553
; TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application Patent No. 6130045
 Matches
                               Query Match
                                                                                                      FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP:
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; MOLECULE TYPE: protein US-08-520-946-90
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APPLICANT: BROW, MARY ANN D.

APPLICANT: LYAMICHEV, VICTOR I.

APPLICANT: OLIVE, DAVID M.
                                                                                                                                                                                                                                                                                      APPLICANT: WURSL, Helmut
APPLICANT: Qui, ZhI-Hao
TITLE OF INVENTION: Thermostable Polymerase
FILE REFERENCE: CLON-007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 100.0%;
Matches 11; Conservative
                         Best Local Similarity
                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/096,399A
CURRENT FILING DATE: 1998-06-11
NUMBER OF SEQ ID NOS: 4
                                                                                                                                                                                                            SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (415) 397-833 INFORMATION FOR SEQ ID NO:
                                                                                           OTHER INFORMATION: Recombinantly engineered mutant
                                                                                                                            ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 528 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: MEDLEN & CARROLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: RAPID DETECTION AND IDENTIFICATION OF TITLE OF INVENTION: PATHOGENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            374 LSQELAIPYEE 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 220 MONTGOME
CITY: SAN FRANCISCO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 LSQELAIPYEE 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: CARROLL, PETER G. REGISTRATION NUMBER: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: FILING DATE:
         11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                  Application US/09096399A
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397-8338
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53
                     100.0%; Score 54; DB 4; Length 553; 100.0%; Pred. No. 0.023;
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Pred. No. 0.022;
       Mismatches
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     Indels
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Gaps
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                SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 4 LENGTH: 559
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                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                    Sequence 4, Application US/09096399A Patent No. 6130045
                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                CURRENT APPLICATION NUMBER: US/09/096,399A CURRENT FILING DATE: 1998-06-11 NUMBER OF SEQ ID NOS: 4
                                                                                                                              APPLICANT: Wurst, Helmut
APPLICANT: Qui, Zhi-Hao
TITLE OF INVENTION: Thermostable Polymerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                  FILE REFERENCE: CLON-007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
TYPE: PRT
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TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn 1.0, v1.25; EDIX; Wordperfect.
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk, 5
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Blosser, G. Harley
REGISTRATION NUMBER: 33,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
TOPOLOGY: linear
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CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                      1 LSQELAIPYEE 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Barnes Ph.D., Wayne M.
VENTION: Thermostable DNA polymerase with
VENTION: enhanced thermostability and enhanced length and
VENTION: efficiency of primer extension
                                                                                                                                                                                                                                                                                                                                                                        Conservative
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N: 435
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RESULT 8
PCT-US95-15327-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Recombinantly engineered mutant US-09-096-399-4
                                                                                                                           : Sequence 5, Application PC/TUS9515327
: GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                          PCT-US95-14418-5
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APPLICANT:
                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                       Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Artificial Sequence
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Gass, David A.
REGISTRATION NUMBER: 38,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
                                  CORRESPONDENCE ADDRESS:
                                                                       TITLE OF INVENTION:
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                                                       NUMBER OF SEQUENCES:
                                                                                                          APPLICANT:
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                                                                                                                                                                                                                                406 LSQELAIPYEE 416
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         STREET:
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nes 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                            PACK.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Chicago
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                      ADDRESSEE:
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                                                                                                                                                                                                                                                                 1 LSQELAIPYEE 11
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Gass, David A.
                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid
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   6300 Sears Tower,
                                                                                                                                                                                                                                                                                                                                                                                                                                             560 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  312/474-0448
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                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                           linear
                      Marshall,
                                                                                                                                                                                                                                                                                                                 100.0%; Score 54; DB 5; 100.0%; Pred. No. 0.024;
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                                                                     Biologically Active Fragments
Thermus Flavus DNA Polymerase
                                                       51
O'Toole, Gerstein, Murray & Borun
ower, 233 South Wacker Drive
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                                                                                                                                                                                                                                                                                                                                Length 560;
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PCT-US95-14418-4
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                                                     SEQUENCE CHARACTERISTICS:
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                                                                                                                      REFERENCE/DOCKET NUMBER: 28
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Gass, David A.
                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
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MEDIUM TYPE: Floppy disk
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                                                                                          TELEX:
                                                                                                          TELEFAX:
                                                                                                                                                                        NAME: Gass, David A. REGISTRATION NUMBER: 38,153
                                                                                                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                                           APPLICATION NUMBER: PCT/US95/14418
                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: SOFTWARE: Patentl
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                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                   STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                 ClfY: Chicago
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TELEFAX: 312/474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Gass, David A.
REGISTRATION NUMBER: 38,153
REFERENCE/DOCKET NUMBER: 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
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       POPOLOGY:
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                                      ENGTH: 597 amino acids
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     amino acid
GY: linear
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SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
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FILE REFERENCE: WSHU 2009
CURRENT APPLICATION NUMBER: US/09/587,856
CURRENT FILING DATE: 2000-06-06
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                      Sequence 2, Application US/09587856 Patent No. 6214557
                                                                                             APPLICANT: Washingt
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                                                                                               Washington University
VENTION: COLD SENSITIVE MUTANT DNA POLYMERASES
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; MOLECULE TYPE: 'protein PCT-US95-14418-4
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                                                                  Best Local Similarity 100.
Matches 11; Conservative
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                                                                                                                                                                                                                                                 TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION: TELEPHONE: 312/474-6300
                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION: NAME: Gass, David A.
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443 LSQELAIPYEE 453
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                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 28003/31716
                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE:
                                   1 LSQELAIPYEE 11
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                                                                                    100.0%;
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                                                                                    Score 54; DB 5; Length 597 Pred. No. 0.025;
                                                                   Mismatches
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678 LSQELAIPYEE 688

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US-09-777-537-2
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SEQ ID NO 2
LENGTH: 810
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LENGTH: 810
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                                                                                                                                                                                                                                                                                  APPLICANT: Barnes, Wayne M
APPLICANT: Kermekchiev, Milko B
TITLE OF INVENTION: COLD SENSITIVE MUTANT DNA POLYMERASES AND METHODS
TITLE OF INVENTION: USE THEREOF
FILE REFERENCE: WSHU 2009.2
                                                                                                                                                                                                                                                  CURRENT FILING DATE: 2001-02-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/777,537
CURRENT FILING DATE: 2001-02-06
PRIOR APPLICATION NUMBER: 09/587,856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: NUCLEIC ACIDS ENCODING COLD SENSITIVE MUTANT DNA
                                                                                                                                                                                                  PRIOR FILING DATE: 2000-06-06 NUMBER OF SEQ ID NOS: 9
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APPLICANT: Kermekchiev, Milko B
                                                                                                                                                                                    SOFTWARE:
                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 09/587,856
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                                                                                                                 ORGANISM: Thermus aquaticus
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                                                                                                                                    TYPE: PRT
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TYPE: PRT
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                              Local Similarity hes 11; Conserv
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1 LSQELAIPYEE 11
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                               Conservative
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S: 9
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                                            Score 54; DB 4;
Pred. No. 0.036;
                               Mismatches
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                                                             DB 4; Length 810;
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US-07-977-434-2
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                                                                      FILING DATE: 24-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Luann Cserr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: Case NO.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 814-2972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 590,490
FILING DATE: 28-SEP-1990
                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: WO PCT/US90/07641
FILING DATE: 21-DEC-1990
PRIOR APPLICATION DATA:
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THILE OF INVENTION: 5' TO 3' EXONUCLEASE MUTATIONS OF
THILE OF INVENTION: THERMOSTABLE DNA POLYMERASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Celfand, David H
APPLICANT: Abramson, Richard
                                                                                                                                               PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                  PILING DATE: 15-AUG-
PRIOR APPLICATION DATA:
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APPLICATION NUMBER: 1
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                                                                                                                            APPLICATION NUMBER: US 557,517
                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 585,471 FILING DATE: 20-SEP-1990
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15-AUG-1991
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                                    5466591 8753
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; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 832 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-977-434-2
                                                                                                                                                                                                                                                             ; TOPOLOGY: linear; ; MOLECULE TYPE: protein US-08-156-020-2
Search completed: January 15, 2003, 12:38:22 Job time: 9.28571 secs
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US-08-156-020-2
                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Greenfield Ph.D., Michael S.
REGISTRATION NUMBER: 37,142
REFERENCE/DCCKET NUMBER: 93,413
TELECOMMUNICATION INFORMATION:
TELLEPHONE: (312)715-1000
TELLEFAX: (312)715-1234
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 832 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/08156020
Patent No. 5474920
GENERAL INFORMATION:
APPLICANY: Moses M.D., Robb E.
TITLE OF INVENTION: Modified Thermo-Resistant DNA
TITLE OF INVENTION: Polymerases
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
                                                                                                                                                                       Query Match
Best Local Similarity
Matches 11; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 60606

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/156,020
                                                                                  1 LSQELAIPYEE 11
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678 LSQELAIPYEE 688
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CITY: Chicago
STATE: IL
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ZIP: 60606
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Database :
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Maximum DB
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                                                                                                                                                                                                                                                                                                                         Score
      protein search, using sw model
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length: 2000000000
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Listing first 45 summaries
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:/cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
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:: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
:: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
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1: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
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Copyright (c) 1993 - 2003 Compugen Ltd
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.0 US-09-823-649A-3
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.0 US-09-823-649A-11
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.0 US-09-777-430A-15
.0 US-09-777-430A-15
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                            Sequence 3, Appli
Sequence 8, Appli
Sequence 10, Appl
Sequence 11, Appl
Sequence 13, Appl
Sequence 2, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 6, Appli
                                                                                                                                                                                                                                                                                                                       Description
 Sequence 8, A
Sequence 11,
Sequence 15,
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GENERAL INFORMATION:
APPLICANT: Smith, Edward
APPLICANT: Elistrom, Cari
APPLICANT: Gelfand, David
APPLICANT: Higuchi, Russe
APPLICANT: Myers, Thomas

Elfstrom, Carita

Myers, Thomas Higuchi, Russell Gelfand, David US-09-823-649A-3

Sequence 3, Application US/09823649A Patent No. US20020012970A1

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t	. ·		Sequence 10580, A	Sequence 4973, Ap	Sequence 54, Appl	Sequence 10490, A	ш Ш		Sequence 13, Appl	Sequence 2, Appli	Sequence 5, Appli	Sequence 5, Appli	Sequence 9, Appli	2,	.t>	14	Sequence 3, Appli			Sequence 3, Appli	20	14,	Sequence 12, Appl	•	23,	Sequence 20, Appl

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ALIGNMENTS

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RESULT 2
US-09-823-649A-8
: Sequence 8, Application US/09823649A
: Patent No. US20020012970A1
: GENERAL INFORMATION:
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Best Local Similarity
Watches 11; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn version 3.0 SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT FILING DATE: 2001-03-30 PRIOR APPLICATION NUMBER: US 60/198,336 PRIOR FILING DATE: 2000-04-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/823,649A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: HIGH TEMPERATURE REVERSE TRANSCRIPTION USING MUTANT DNA POLYME FILE REFERENCE: REALOG
                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 21
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                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                    FEATURE:
                                                                                                                                                                                                                                                                                                                                                                        LENGTH:
                                                                                                                                                               1 LSQELAIPYEE 11
                                                                                                                                LSQELAIPYEE 11
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                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                 100.0%; Score 54; DB 10;
100.0%; Pred. No. 0.00018;
tive 0; Mismatches 0;
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US-09-823-649A-11
; Sequence 11, Application US/09823649A
; Patent No. US20020012970A1
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                                                                                                                                     RESULT 4
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APPLICANT: Elfstrom, Cari
APPLICANT: Gelfand, Davic
APPLICANT: Higuchi, Russe
APPLICANT: Myers, Thomas
                                                          GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 10
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APPLICANT: Smith, Edward APPLICANT: Elfstrom, Cari APPLICANT: Gelfand, David
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Best Local Similarity
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PRIOR FILING DATE: 2000-04-18
NUMBER OF SEQ JD NOS: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: RPA1006
CURRENT APPLICATION NUMBER: US/09/823,649A
CURRENT FILING DATE: 2001-03-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Schoenbrunner, Nancy
APPLICANT: Wang, Alice
TITLE OF INVENTION: HIGH TEMPERATURE REVERSE TRANSCRIPTION USING MUTANT DNA POLYMERAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Smith, Edward
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FITLE OF INVENTION: HIGH TEMPERATURE REVERSE TRANSCRIPTION USING MUTANT DNA POLYMERAS
                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
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                                                                                                                                                                                                                                                                Score 54; DB 10;
Pred. No. 0.00018;
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US-09-823-649A-13
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US-09-823-649A-11
                                                                                                                                                                 US-10-033-297-4
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                                                                                                         Sequence 4, Application US/10033297
Publication No. US20020187486A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ (b) No 13
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Best Local Similarity
Matches 11; Conserv
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CURRENT FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: US 60/198,336
PRIOR FILING DATE: 2000-04-18
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CURRENT APPLICATION NUMBER: US/09/823,649A
CURRENT FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: US 60/198,336
PRIOR FILING DATE: 2000-04-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Wang, Alice
TITLE OF INVENTION: HIGH TEMPERATURE REVERSE TRANSCRIPTION USING MUTANT DNA POLYME
FILE REFERENCE: RPA1006
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TITLE OF INVENTION: Detection of Nucleic Acids By Multiple Sequential Invasive Cleavages
                                                                      APPLICANT: Hall, Jeff G.
Lyamichev, Victor I.
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Schoenbrunner, Nancy
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                                     Mast, Andrea L.
Brow, Mary Ann D.
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100.0%;
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Pred. No. 0.00018;
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Pred. No. 0.00018;
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                                                                                                                                                                                      Sequence 2, Application US/09972834
Publication No. US20020192663A1
                                                                                                                                                                       GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                        678 LSQELAIPYEE 688
                                                                                                                                                                                                                                                                                                                                                                1 LSQELAIPYEE 11
                    CORRESPONDENCE ADDRESS:
                                            NUMBER OF SEQUENCES:
                                                       TITLE OF INVENTION: Thermostable Polymerases Having Altered Fidelity and Methods of Identifying and Using Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: FORS-02736 TELECOMMUNICATION INFORMATION:
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                                                                                                                                            APPLICANT: Loeb, Lawrence A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
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ADDRESSEE: CAMPBELL & FLORES LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 21-JAN-1997 APPLICATION NUMBER: US 01 FILING DATE: 02-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/823,516 FILING DATE: 24-MAR-1997 APPLICATION NUMBER: PCT/US97/0107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 08/599,491 FILING DATE: 24-JAN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 08/682,853 FILING DATE: 12-JUL-1996
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APPLICATION NUMBER: US 08/756,386
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                                                                                                      Suzuki, Motoshi
                                                                                                                          Hood, Leroy
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; ORGANISM: Thermus aquaticus US-10-071-505-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Publication No.
                                                                                                                                                       SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/10071505
 Best Local Similarity 100 Matches 11; Conservative
                                      Query Match
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TITLE OF INVENTION: E681 and Homologs The
TITLE OF INVENTION: Tolerance
FILE REPERENCE: PB9944
CURRENT APPLICATION NUMBER: US/10/071,505
CURRENT FILING DATE: 2002-02-08
                                                                                                                                                                      SOFTWARE: PatentIn Ver. 2.1
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                                                                                                                  TYPE: PRT
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                                                                                                                                   ENGTH: 832
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Match 100.0%;
Local Similarity 100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/972,834
FILING DATE: 04-Oct-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION: TELEPHONE: (619)535-9001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA: 08/978,806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11;
                                                                                                                                                                                                                                                                                                                                                             Flick, Parke
                                                                                                                                                                                                                                                                                                                                                                                          Kumar, Shiv
Finn, Patrick J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       THLEFAX: (619)535-8949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: P-UW 2873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Campbell, Cathryn A. REGISTRATION NUMBER: 31,815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: San Diego
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 4370 La Jolla Village Drive, Suite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 832 amino acids
                                                                                                                                                                                                                                                                                                                                                                          Nampalli, Satyam
                                                                                                                                                                                                                                                                                                                                                                                                                                   Nelson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0S20020197211A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                     John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   United States
                                                                                                                                                                                                                                                                                                                TAQ DNA Polymerase Having an Amino Acid Substitution
E681 and Homologs Thereof Exhibiting Improved Salt
                   100.0%;
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                   Score 54; DB 9; Length 832; Pred. No. 0.02;
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Pred. No. 0.02;
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   Mismatches
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                                                                                                                                                        RESULT 10
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                                                                                               Sequence 8, Application US/10033297 Publication No. US20020187486A1
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Publication No. US20020197623A1
GENERAL INFORMATION:
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Best Local S
                                                           GENERAL INFORMATION:
APPLICANT: Hall
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                                                                                                                                                                                                                678 LSQELAIPYEE 688
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                                                                                                                                                                                                                                                      1 LSQELAIPYEE 11
                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein SEQUENCE DESCRIPTION: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lyamichev, Victor I.
TITLE OF INVENTION: Invasive Cleavge Of Nucleic Acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Prudent, James R.
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                                                                                                                                                                                                                                                                                             11;
                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 08/682,853
FILIKG DATE: 12-JUL-1996
APPLICATION NUMBER: US 08/599,491
FILING DATE: 24-JAN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/10/081,806 FILING DATE: 22-Feb-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (415) 397-8338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Ingolia, Diane E. REGISTRATION NUMBER: 40,027
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                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 832 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CATION NUMBER: US/08/756,386
                                                             Hall,
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                                      Lyamichev, Victor I.
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, Andrea L.
, Mary Ann D.
                                                           Jeff G
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                                                                                                                                                                                                                                                                                           Score 54; DB 9;
Pred. No. 0.02;
0; Mismatches
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RESULT 11
US-10-033-297-66
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                                                                                                                     Sequence 66, Application US/10033297
Publication No. US20020187486A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 11; Conserv
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                                                                                                                                                                                                                                                                   678 LSQELAIPYEE 688
                                                                                                                                                                                                                                                                                          1 LSQELAIPYEE 11
                           TITLE OF INVENTION:
                                                                                 APPLICANT: Hall, Jeff G.
Lyamichev, Victor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (415) 705-8410
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Detection Of Nucleic Acids By Multiple Sequential Invasive Cleavages
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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FILING DATE: 12-No. US20020187486A1-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DENOTH: 833 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: FORS-02736
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 08/682,853
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/09/350,597 FILING DATE: 09-Jul-1999
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                                                                                                                                                                                                                                                                                                                                               Conservative
                                                            Mast, Andrea L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           220 Montgomery Street, Suite 2200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (415) 397-8338
                                                                                                                                                                                                                                                                                                                                                                  100.0%;
Mary Ann D.
ON: Detection Of Nucleic Acids By Multiple
Sequential Invasive Cleavages
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02-DEC-1996
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Pred. No. 0.02;
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                                                                                                                                                                                             GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                            679 LSQELAIPYEE 689
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                    1 LSQELAIPYEE 11
                      CORRESPONDENCE ADDRESS:
                                          NUMBER OF SEQUENCES:
                                                                                TITLE OF INVENTION: Detection Of Nucleic Acids By Multiple
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APPLICATION NUMBER: US/09/350,597
"ILING DATE: 09-Jul-1999
                                                                                                                                                                       APPLICANT: Hall, Jeff G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein SEQ ID NO: 66:
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ADDRESSEE: Medlen & Carroll, LLF
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APPLICATION NUMBER: US 01
FILING DATE: 02-DEC-1996
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FILING DATE: 12-No. US20020187486A1-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 02-DEC-1996
APPLICATION NUMBER: US 08/756,386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/823,516 FILING DATE: 24-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 833 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (415)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Ingolia, Diane E.
REGISTRATION NUMBER: 40,027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 24-JAN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 08/599,491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 08/682,853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 29-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 08/758,314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: PCT/US97/01072
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: United States Of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Medlen & Carroll, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                        Lyamichev, Victor I.
Mast, Andrea L.
                                                                                                        Brow, Mary Ann D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      220 Montgomery Street, Suite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (415) 705-8410
                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 54; DB 9; Length 833; 100.0%; Pred. No. 0.02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-JUL-1996
                                        Sequential Invasive Cleavages: 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        397-8338
                                                                                                                                                                                                                                                                                                                                                                                                                               0;
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                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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                                                                                                                                                                                                                                                            RESULT 13
US-10-033-297-71
Sequence 71, Application US/100:
Publication No. US20020187486A1
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Best Local Similarity
                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Hall,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 69: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                    679 LSQELAIPYEE 689
                                                                                                                                                                                                                                                                                                                                                                                                                                          1 LSQELAIPYEE 11
                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Medlen & Carroll, LLP
                                                                                                                                          TITLE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                           NUMBER OF SEQUENCES: 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11;
        STREET: 220 Montgomery Street, Suite 2200 CITY: San Francisco
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 833 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (415) 705-8410
TELEPAX: (415) 397-8338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RECISTRATION NUMBER: 40,027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 08/599,491 FILING DATE: 24-JAN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 12-JUL-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 08/756,386
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: <Unknown>
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STATE: California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 08/682,853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 02-DEC-1996
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                                                                                                                                                                                                                                                                                         Application US/10033297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                             INVENTION: Detection Of Nucleic Acids By Multiple
Sequential Invasive Cleavages
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ingolia, Diane E
                                                                                                                                                            Brow,
                                                                                                                                                                              Mast, Andrea L.
                                                                                                                                                                                                  Hall, Jeff G.
Lyamichev, Victor I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    United States Of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 54; DB 9; Length 833; 100.0%; Pred. No. 0.02; Live 0; Mismatches 0; Indels
                                                                                                                                                            Mary Ann D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29-NOV-1996
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; SEQUENCE DESCRIPTION: SEQ ID NO: 71: US-10-033-297-71
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            679 LSQELAIPYEE 689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 LSQELAIPYEE 11
       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                 APPLICANT: Prudent, James R.
Hall, Jeff G.
Lyamichev, Victor I.
TITLE OF INVENTION: Invasive Cleavge Of Nucleic Acids
NUMBER OF SEQUENCES: 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: TELECOMMUNICATION. INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: protein
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SEQUE 'E CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
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                                                                                                  COUNTRY: United States Of America
                                                                                                                       CITY: San Francisco
STATE: California
                                                                                                                                                                 STREET: 220 Montgomery Street, Suite 2200
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TELEFAX: (415) 397-8338
                                                                                                                                                                                         ADDRESSEE: Medlen & Carroll, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Ingolia, Diane E. REGISTRATION NUMBER: 40,027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 08/599,491 FILING DATE: 24-JAN-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 08/758,314 FILING DATE: 02-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 08/759,038 FILING DATE: 02-DEC-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/10/033,297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 09-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 54; DH 9; Length 833; 100.0%; Pred. No. 0.02;
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US-10-033-297-6
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Publication No. US20020187486A1
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TELEFAX: (415) 397-8338
INFORMATION FOR SEQ 1D NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 LSQULAIPYEE 11
                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/033,297
APLICATION NUMBER: US20020187486A1-2001
CIASSIFICATION: <Unknown>
                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/350,597
FILING DATE: 09-Jul-1999
                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: peptide SEQUENCE DESCRIPTION: SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 24-JAN-1996 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Detection Of Nucleic Acids By Multiple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 163
APPLICATION NUMBER: PCT/US97/01072
                         APPLICATION NUMBER: US/08/823,516 FILING DATE: 24-MAR-1997
                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                         STATE:
                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 220 Montgomery Street, Suite 2200 CITY: San Francisco
                                                                                                                                                                                                                              SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                             COUNTRY: United States Of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Ingolia, Diane E. REGISTRATION NUMBER: 40,027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 08/682,853 FILING DATE: 12-JUL-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Medlen & Carroll, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: FORS-02564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 08/599,491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 22-Feb-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/10/081,806
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mast, Audrea L.
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                                                                                                                                                                                                                                                                                                                                                                                         California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lyamichev, Victor I.
                                                                                                                                                                                                                          PatentIn Release #1.0, Version #1.30
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Pred. No. 0.02;
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FILING DATE: 21-JAN-1997
APPLICATION NUMBER: US 08/759,038
FILING DATE: 02-DEC-1996
APPLICATION NUMBER: US 08/756,346
FILING DATE: 02-DEC-1996
APPLICATION NUMBER: US 08/756,386
FILING DATE: 12-UL-1996
APPLICATION NUMBER: US 08/682,853
FILING DATE: 12-UL-1996
APPLICATION NUMBER: US 08/682,853
FILING DATE: 12-UL-1996
APPLICATION NUMBER: US 08/599,491
FILING DATE: 13-UL-1996
APPLICATION NUMBER: US 08/599,491
FILING DATE: 10-08/59/599,491
FILING DATE: 10-08/599,491
FILING DATE: 10-08/5
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Result
No.
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Maximum DB
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re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
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length: 2000000000
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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47
1 LSXELXIPYEE 11
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Match Length
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                                                                                                                                                                                                                                                                                                                                                                                        Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GenCore version 5.1.3 Coppright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                   /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/backfiles1.seq:*
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  US-08-073-384C-12

US-08-254-359A-12

US-08-483-043-12

US-08-481-238-12

US-08-471-066B-12

US-08-471-066B-12

US-08-756-12

US-08-756-386-12

US-08-756-386-12

US-08-756-386-12

US-08-756-386-12

US-08-682-853A-12

US-08-759-038-12
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TELEPHONE:
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415/705-8410
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US-09-350-309-12
US-08-520-946-12
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RESULT 1 SEQUENCE 12, APPLICANT SEQUENCE 12, APPLICANT DATA APPLICANT: DATA APPLICANT: LYANN TITLE OF INVENTI TO STATE: COMPUTER: DATE: CURRENT APPLICATION NU APPLICATION NU APPLICATION NU FILING DATE: CLASSIFICATION NU APPLICATION APPLIC	111111111111111111111111111111111111
12. 12. 12. 12. 12. 12. 12. 12. 12. 12.	化亚代亚亚 化双氯化二甲甲甲甲甲甲甲甲甲甲甲甲甲甲甲甲甲甲甲甲甲甲甲甲甲甲甲甲甲甲甲甲甲甲甲
IT 1 IT 1 IT 1 IT 1 IT 1 IT 2 IT 2 IT 3	\$\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\
ICATION US/080733 ITON: htberg, James E. amichev, Victor I OW, Mary Ann D. WION: SYNTHESIS- WION: SYNTHESIS- WION: SYNTHESIS- WION: SYNTHESIS- WION: SYNTHESIS- WIONESS: 29 ENCES: 29 ENCES: 29 ENCES: 29 ENCES: 29 ENCES: 29 ENCYMERASE HAVERSTOCK, MEDLE MANUGOMETY Street MANUGOMETY Street MANUGOMETY Street MANUGOMETY Street Floppy disk MANUGOMETY ENCYMENTALINE BLE FORM: Floppy disk MANUGOMETY FLOOK/MATION BLE FORM ATION DATA: NUMBER: US/08/07 04-JUN-1993 ON: 536 ION DATA: NUMBER: US 07/98 O7-DEC-1992 INFORMATION: 11, Peter G. NUMBER: 32,837 INFORMATION: 11, PETERMATION:	11600 11600
NATIONAL SERVICE SERVI	⊗ 4 4 € C C C C C C C C C C C C C C C C C
DB073384C ps E. thor I. D. D. MEDILEN & CARROLL Street, Suite 2200 of America of America of America of America 101016 10208/073,384C 1030986,330 1008.	US-08-758-314-12 US-08-520-390-12 US-08-648-657-1 US-08-648-657-1 US-08-648-657-1 US-08-648-657-1 US-08-648-657-2 US-09-096-399-3 PCT-US95-14418-3 PCT-US95-14318-3 PCT-US95-14318-3 PCT-US95-14318-3 PCT-US95-14318-3 PCT-US95-14318-3 US-08-481-238-2 US-08-481-238-2 US-08-481-238-2 US-08-481-238-2 US-08-481-238-2 US-08-853-62-2 US-08-853-63-2 US-08-853-63-2 US-08-853-63-2 US-08-853-2 US-08-853-11-2 US-08-88-88-853-2 US-08-757-633-2 US-08-758-314-2 US-08-758-858-1 US-09-858-819-1 US-09-858-819-1 US-09-858-819-1 US-09-777-537-1
JE DNA	Sequence 12, Appl Sequence 12, Appl Sequence 12, Appl Sequence 1, Appli Sequence 1, Appli Sequence 2, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 5, Appli Sequence 5, Appli Sequence 6, Appli Sequence 7, Appli Sequence 2, Appli Sequence 1, Appli

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; TOPOLOGY: 1:
; MOLECULE TYPE:
US-08-254-359A-12
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                                                                                                                             APPLICATION NUMBER: US 07/986,330
FILING DATE: 07-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: CARROLL, PETER G.
REGISTRATION NUMBER: 32,837
REFERENCE/DOCAET NUMBER: FORS-01000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415, 397-8338
INFORMATION FOR SEQ ID NO: 12:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-823-649A-2 (1-11) x US-08-073-384C-12 (1-1600)
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; MOLECULE TYPE: US-08-073-384C-12
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Patent No. 5614402
GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1600 base pair
                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 1600 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: LYAMICHEY, VICTOR I.

APPLICANT: BROW, MARY ANN D.

TITLE OF INVENTION: 54 MCCLEASES DERIVED FROM THERMOSTABLE

TITLE OF INVENTION: DNA POLYMERASE

NUMBER OF SEQUENCES: 40

CORRESPONDENCE ADDRESS:

ADDRESSEE: HAVERSTOCK, MEDIEN & CARROLL
STREET: 220 MONTGOMERY STREET, SUITE 2200

CITY: SAN FRANCISCO

STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1133 CTCTCCCAGGAGCTAGCCATCCCTTACGAGGAG 1165
                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 08 FILING DATE: 06-JUN-1993 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/254,359A FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: U
ZIP: 94104
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STRANDEDNESS: double
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                                     linear
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                 DNA (genomic)
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81.82%
81.82%
93.62%
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Matches:
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220 Montgomery Street, Suite 2200

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US-08-471-066B-12
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Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; MOLECULE TYPE: US-08-481-238-12
                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-481-238-12
                                                                                                                                                            Sequence 12, Application US/084710668 Patent No. 5837450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 12, Application US/08481238 Patent No. 5795763
                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: FOI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 12:
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                                                                                                                                                                                                                                                         TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                   APPLICANT: Dahlberg, James E.
APPLICANT: Lyamichev, Victor I.
APPLICANT: Brow, Mary Ann D.
TITLE OF INVENTION: 5' Nucleases Derived From Thermostable
                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 94104
COMPUTER READABLE FORM:
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APPLICANT: BROW, MARY ANN D.
TITLE OF INVENTION: SYNTHESIS-DEFICIENT THERMOSTABLE DNA
TITLE OF INVENTION: POLYMERASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 220 MONTGOMERY STREET, SUITE 2200 CITY: SAN FRANCISCO STATE: CALIFORNIA
ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: CARROLL, PETER G. REGISTRATION NUMBER: 32,837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/481,238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
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Medlen & Carroll, LLP
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                                                  DNA Polyermase
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RESULT 6
US-08-484-956-12
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alignment Scores:
                                                                                                                                                                                                                                                                                                           Patent No.
                                                                                                                                                                                                                                                                                                           Sequence 12, Application US/08484956 Patent No. 5843654
                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/073,384
FILING DATE: 04-JUN-1993
FRIOR APPLICATION DATA: US 07/986,330
APPLICATION NUMBER: US 07/986,330
FILING DATH: 07-DEC-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                               APPLICANT: DAHLBERG, JAMES E.
APPLICANT: LYAMICHEV, VICTOR I.
APPLICANT: BROW, MARY ANN D.
APPLICANT: OLLEWBURG, MARY C.
APPLICANT: HEISLER, LAURA
TITLE OF INVENTION: DETECTION OF p53 MUTATIONS
COMPUTER READABLE FORM:
                                                                                                           NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSE: HAVERSTOC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: FO
TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER: US,
FILING DATE: 06-JUN-199
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/254,359
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ZIP: 941
                                                                        ADDRESSEE: HAVERSTOCK, MEDLEN & CARROLL STREET: 220 MONTGOMERY STREET, SUITE 2200 CITY: SAN FRANCISCO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 220 Montgome
CITY: San Francisco
STATE: California
                                      COUNTRY:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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STRANDEDNESS: double
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                    94104
                                  CALIFORNIA
: UNITED STATES OF AMERICA
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Matches:
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RESULT 7
US-08-757-653-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent No. 5
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Kaiser, niculo.

APPLICANT: Lyamichev, Victor I.

APPLICANT: Lyamichev, Natasha

A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: 07
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Cleavage Of Nucleic Acid Using TITLE OF INVENTION: Thermostable FEN-1 Endonucleases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 09-NOV-
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APPLICATION NUMBER: US,
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APPLICATION NUMBER: US 08/402,601
FILING DATE: 09-MAR-1995
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                                                                                                                                                     STATE:
                                                                                                                                                                 ADDRESSEE: Medlen & Carroll, LLF
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 1600 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 0 FILING DATE: 06-JUN-1994
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                                                                                    94104
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                                                                                                                                                     California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Application US/08757653
                                                                                                               United States Of America
Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Floppy disk
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US-09-823-649A-2 (1-11) x US-08-757-653-12 (1-1600)
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Best Local Similarity:
Query Match:
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                                                                  APPLICATION NUMBER: US/08/599,491
FILING DATE: 23-JAM-1996
CLASSIFICATION: 435
ATTORNEY_AGENT IMPORTATION:
NAME: INGOLIA, DIANE E.
REGISTRATION NUMBER: P-40,027
                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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ATTORNEY/AGENT INFORMATION:
NAME: ingolia, Dianc E.
TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 705-8410 TELEFAX: (415) 397-8338
                                                                                                                                                                                     CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: MEDIEN & CARROLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: PRUDKNY, JAMES R.
TITLE OF INVENTION: DETECTION OF NUCLEIC ACID SEQUENCES BY
TITLE OF INVENTION: INVADER-DIRECTED CLEAVAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: GROTELUESCHEN HALL, JEFF S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: BROW, MARY ANN D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                   COMPUTER: IBM PC COmpatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                        REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                              CITY: SAN FRANCISCO
STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                    STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 40,027 REFERENCE/DOCKET NUMBER: FO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/757,653
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE:
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5. 5846717
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                                                                                                                                                                                                                                                                                                           94104
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                                                                                                                                                                                                                                                                                                                            UNITED STATES OF AMERICA
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                                                        FORS-01802
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Matches:
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; MOLECULE TYPE: US-08-756-386-12
Pred. No.:
                 Alignment Scores:
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Best Local Similarity:
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                                                                                                                                                  TELEFAX: (415) 397-833 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                            AFFULCATION NUMBER: US 08/599,491
FILING DATE: 24-JAN-1996
ATTORNEY/AGENT INFORMATION:
NAMP: TACATION
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No..
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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APPLICATION NUMBER:
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APPLICATION NUMBER: US
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ZIP: 94
                                                                                    STRANDEDNESS:
TOPOLOGY: li
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 08/682,853 FILING DATE: 12-JUL-1996
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STRANDEDNESS: double
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                                                                                                                  nucleic acid
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San Francisco
                                                                                                                                                                                                                                                                     Ingolia, Diane E
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                                                                                                                                  1600 base pairs
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Hall, Jeff G
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                                                                 DNA (genomic)
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 Length:
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Percent Similarity:
Best Local Similarity:
Query Match:
US-08-823-516-12
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Patent No. 5>>>...
Patent No. 5>>
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                                                                                                                                                                                                                         TELEFAX: (415) 397-83
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 21-JAN-PRIOR APPLICATION NUMBER:
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                            MOLECULE TYPE:
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                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                             TELEPHONE: (415) 705-8410
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ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Mast, Andrea I..

APPLICANT: Brow, Mary Ann D.
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OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                TOPOLOGY:
                                                                                         STRANDEDNESS:
                                                                                                                                    TYPE:
                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                          NAME: Ingolia, Diane E. REGISTRATION NUMBER: 40,027
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San Francisco
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                     DNA (genomic)
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US-09-823-649A-2 (1-11) x US-08-682-853A-12 (1-1600)
                                                     Percent Similarity:
Best Local Similarity:
                                            Query Match:
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                                                                                                                        Alignment Scores:
                                                                                                                                                       US-08-682-853A-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 12,
                                                                                                                                                                                                                                                             TELEFAX: (415) 397-83
INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 08/599,491 FILING DATE: 24-JAN-1996 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 12-JUL-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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                                                                                                                                                                      MOLECULE TYPE:
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TITLE OF INVENTION: DETECTION OF NUCLEIC ACID SEQUENCES BY TITLE OF INVENTION: INVADER-DIRECTED CLEAVAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                  STRANDEDNESS:
                                                                                                                                                                                                                    TYPE:
                                                                                                                                                                                                                                                                                                                                           NAME: Ingolia, Diane E. REGISTRATION NUMBER: 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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STATE: California...
                                                                                                                                                                                     TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/682,853A
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                                                                                                                                                                                                                               1600 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              United States Of America
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                                                                                                                                                                                     linear
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US-08-758-314-12
                   RESULT 13
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Best Local Similarity:
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US-08-759-038-12
                                                                                                                                                                    Query Match:
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                                            1133 CTCTCCCAGGAGCTAGCCATCCCTTACGAGGAG 1165
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APPLICATION NUMBER:
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APPLICATION NUMBER:
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APPLICANT Dahlberg, James E.
Cleavage Of Nucleic Acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Ingolia, Diane E. REGISTRATION NUMBER: 40,027 REFERENCE/DOCKET NUMBER: FO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 24-JAN-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
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CITY: San Francisco
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                                                                            1 LeuSer***GluLeu***IleProTyrGluGlu 11
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nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                             (415) 705-8410
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                                                                                                                                                                                  Conservative: Mismatches:
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US-09-350-309-12
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                                                                                           Sequence 12, Application US/09350309 Patent No. 6348314 GENERAL INFORMATION:
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                                                                                                                                                                                                          1133 CTCTCCCAGGAGCTAGCCATCCCTTACGAGGAG 1165
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
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LENGTH: 1600 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: FO.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
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APPLICATION NUMBER: US 0
FILING DATE: 24-JAN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 29-NOV-1996
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US 08/682,853
FILING DATE: 12-JUL-1996
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PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US/01
FILING DATE: 02-DEC-1996
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                               1 LeuSer***GluLeu***IleProTyrGluGlu 11
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TOPOLOGY: lin
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Lyamichev, Victor I.
TITLE OF INVENTION: Invasive Cleavge Of Nucleic Acids NUMBER OF SEQUENCES: 69
                                                                         APPLICANT: Prudent,
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Ingolia, Piane E.

Ingolia, Piane E.
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220 Montgomery Street, Su
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                                                                           James R.
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US-09-823-649A-2 (1-11) x US-09-350-309-12 (1-1600)
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Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score:
                                                                                                                                                                                                                                                                                                                                                                      Patent No.
                                                                                                                                                                                                                                                                                                                                                                        Sequence 12, Application US/08520946 Patent No. 6372424
                                                                                                                                                                                                                               GENERAL INFORMATION:

APPLICANT: BROW, MARY ANN D.

APPLICANT: LYAMICHEY, VICTOR I.

APPLICANT: OLIVE, DAVID M.

TITLE OF INVENTION: RAPID DETECTION AND IDENTIFICATION OF

TITLE OF INVENTION: PATHOGENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (415) 705-84:
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 12:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1133 CTCTCCCAGGAGCTAGCCATCCCTTACGAGGAG 1165
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ADDRESSEE: MEDLEN & CARROLL
                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           No.:
                                                                                                                       STREET: 220 MONIGUME
CITY: SAN FRANCISCO
                                                                                       COUNTRY:
                                                                                                              STATE:
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MOLECULE TYPE: DNA (genomic)
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPIJCATION NUMBER: US 08/599,491
FILING DATE: 24-JAN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Ingolia, Diane E.
REGISTRATION NUMBER: 40,027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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ADDRESSEE: Medlen & Carroll, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE DESCRIPTION: SEQ ID NO: 12:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
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TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARK: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 08/756,386 FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: United States Of America
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                                                                                                            CALIFORNIA
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                                                                                                                                                  220 MONTGOMERY STREET, SUITE 2200
                                                                                       UNITED STATES OF AMERICA
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOUTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NATA:
APPLICATION NATA:
APPLICATION USATA:
CLASSIFICATION UNBER: US/08/520,946
FILING DATE:
CLASSIFICATION UNBER: US/08/520,946
FILING DATE:
CLASSIFICATION UNBER: 32,837
REFIRENCE/DOCKET NUMBER: 9RS-01756
FELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEPHONE: (415) 705-8410
TELEPHONE: (415) 397-8338
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 1600 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-520-946-12
Alignment Scores:
Pred. No.:
OSCORE:
Pred. No.:
OSCORE:
Pred. No.:
OSCORE:
Percent Similarity: 81.828
Best Local Similarity: 81.828
Ouery Match: 44.00
Percent Similarity: 81.828
Best Local Similarity: 81.828
Ouery Match: 0
DB:
US-09-823-649A-2 (1-11) x US-08-520-946-12 (1-1600)
OY
ILBUST***GluLeu******TeperoTyrGluClu 11
IDD 1133 CTCTCCCAGGAGCTAGCCATCCCTTACGAGGAG 1165
Search completed: January 15, 2003, 12:58:39
Job time: 29 secs
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Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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Copyright (c) 1993 - 2003 Compugen Ltd
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AAR80140
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B.stearothermophil
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B. stearothermophi
Bacillus stearothe
B.stearothermophil
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3561 3561 3568 3764 9758	AAU35075 AAU34824 AAW71203 ABB55496 ABB90587 AAW73523	AAW72752 AAB47797 ABB48886 AAW59032 AAW59033 AAW59034	AAE11059 AAB85949 AAR28348 AAR2845 AAW22845 AAW22847	AAB85951 AAW30094 AAR80141 AAB11057 AAB85950 AAR28349 AAR28349 AAR80143 AAR80143 AAR80143 AAR80143 AAR80143 AAR80143
1 a C C C D a	s fae lular oded oded lact	DNA polymerase I e Native DNA polymer Listeria monocytog B. pallidus DNA po B. pallidus DNA po B. pallidus DNA po	Bacillus stearothe Amino acid sequenc Bacillus caldotena Bacillus caldotena Bacillus caldotena	Tvu DNA polymerase Bacillus stearothe B. stearothermophil Thermoactinomyces Tvu DNA polymerase Bacillus caldotena B. stearothermophil B. stearothermophil B. stearothermophil B. stearothermophil B. stearothermophil B. stearothermophil Bacillus stearothe Thermoactinomyces

ALIGNMENTS

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Reverse transcribing an RNA, comprises performing a reverse transcriptase polymerase chain reaction amplification of a mixture
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacillus caldotenax.
                                                                                  WPI; 2002-076891/11.
                                                                                                                                Schoenbrunner NJ, Wang AM;
                                                                                                                                                          Smith ES, Elfstrom CM,
                                                                                                                                                                                                                                                         18-APR-2000; 2000US-198336P
                                                                                                                                                                                                                                                                                                  12-APR-2001; 2001EP-0109341.
                                                                                                                                                                                                        (HOFF ) HOFFMANN LA ROCHE & CO AG F.
                                                                                                                                                          Gelfand DH,
                                                                                                                                                          Higuchi RG,
                                                                                                                                                          Myers TW;
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dye; amplification.

Native DNA polymerase motif #18 25-MAR-2002 (first entry) AAM48269;

AAM48269 standard; Peptide;

11

DNA polymerase; reverse transcription; primer; divalent cation; mutant; transverse transcription reaction; fluorescein; cyanine; thermoactive;

Disclosure; Page 7; 23pp; English.

sequences given in AAB47791-97 and AAM48259-AAM48270

using a mutant thermoactive DNA polymerase

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RESULT 2
AAM48270
ID AAM4
XX
AC AAM4
XX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local
The sequences given in AAB47791-97 and AAM48279-AAM48270 represent the native forms of motifs derived from DNA polymerases used in the method of the invention. The method for reverse transcribing an RNA, comprises treating a transverse transcription reaction mixture which comprises that, a primer, a divalent cation, and a mutant thermoactive DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                       Disclosure; Page 7; 23pp; English.
                                                                                                              Reverse transcribing an RNA, comprises performing a reverse transcriptase polymerase chain reaction amplification of a mixture using a mutant thermoactive DNA polymerase
                                                                                                                                                                                    WPI; 2002-076891/11.
                                                                                                                                                                                                              Schoenbrunner NJ,
                                                                                                                                                                                                                                                                              18-APR-2000; 2000US-198336P
                                                                                                                                                                                                                                                    (HOFF ) HOFFMANN LA ROCHE & CO AG F.
                                                                                                                                                                                                                                                                                                            12-APR-2001; 2001EP-0109341
                                                                                                                                                                                                                                                                                                                                             07-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                        EP1152062-A2
                                                                                                                                                                                                                                                                                                                                                                                                Bacillus stearothermophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                            DNA polymerase; reverse transcription; primer; divalent cation; mutant; transverse transcription reaction; fluorescein; cyanine; thermoactive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Native DNA polymerase motif #19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAM48270;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAM48270 standard; Peptide; 11 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    fluorescein and cyanine family dyes. The method of the invention is useful in reverse transcription/amplification reactions. The method conventrations relative to previous high temperature reverse transcription methods, and provide a wider range of usable salt concentrations. The use of the mutant DNA polymerase provides faster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          reverse transcription extension rates, and consequently less time
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RNA, a primer, a divalent cation, and a mutant thermoactive DNA polymerase. These motifs represent a conserved region which affects the DNA polymerase's ability to incorporate dideoxynucleotides labelled with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                native forms of motifs derived from DNA polymerases used in the method of the invention. The method for reverse transcribing an RNA, comprises treating a transverse transcription reaction mixture which comprises the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 LAQNLNISRKE 11
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                                                                                                                                                                                                                            Elfstrom CM,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA;
                                                                                                                                                                                                           Wang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98.0%;
                                                                                                                                                                                                             ΑM;
                                                                                                                                                                                                                         Gelfand DH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 48;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                    Higuchi RG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0.0025;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 11;
                                                                                                                                                                                                                    Myers TW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8
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Best Local S
              stearothermophilus thermostable DNA polymerase clone 8st2 which lacks the complete 5'-3' exonuclease domain. The corresp. gene was constructed by ligating the HindIII-SalI fragment from the clone pdemBst2.1Sst contg send of the gene with the Styl-HindIII fragment of the clone pdemBst2.1Sst contg pdemBst5'end contg. the 5' end of the DNA polymerase gene. The Styl-HindIII fragment covers the mid-region of the gene up to and exonuclease domain. The remainder of the 5'-5' exonuclease but not the 5'-3' reconstituted by the ligated and extended oligonucleotides AAT04816-17. The modified DNA polymerase can be seed in primer extension reactions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                  Claim
                                                                                                                                                                                                                                                                                                             This is the amino acid sequence of the modified Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                    Bacillus stearothermophilus DNA encoding thermostable polymerase for nucleic acid sequencing and amplification  \begin{tabular}{ll} \hline \end{tabular} \begin{tabular}{ll} \hline \e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAT04802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1995-373510/48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Riggs MG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24-FEB-1995;
01-APR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (GENP-) GEN-PROBE INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-MAR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              W09527067-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacillus stearothermophilus; thermostable DNA polymerase; PCR; primer; amplification; probe; Bacillus caldotenax; exonuclease; recombination;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 B.stearothermophilus DNA polymerase variant Bst2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-0CT-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-MAY-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR80139 standard; Protein; 587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR80139;
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                                                                                                                                                                                                                                                                                                                                                                                                     9,
DNA sequencing or polymerase chain reaction
                                                                                                                                                                                                                                                                                                                                                                              Page 83-85; 135pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sivaram M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      polymerase chain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94US-0222612.
94US-0307410.
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90.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SD;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ΑA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 11;
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                                                                                                                                                                                                                 gene was constructed pGemBst2.1Sst contg.
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RESULT 5
AAW10597
ID AAW1
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AAW30093
ID AAW3
                                                                                                                           Query Match
Best Local Similarity
Thes 10; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                 can be used in a method for the replication of a DNA chain. It can also be used in a method for the determination of the sequence of DNA chain. As the DNA polymerase has a proof reading 3'-5' exonuclease activity, possible mismatches of base pairing that occurs in current methods of DNA sequence determination of a DNA clone can be avoided.
       AAW10597 standard; Protein; 587 AA
                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                              stearothermophilus strain DNA polymerase. The heat stable DNA polymerase can be used in a method for the replication of a DNA chain. It can also
                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 2; 32pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                     DNA polymerase from Bacillus stearothermophilus - used in DNA amplification and sequencing methods having lower frequency of
                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAT90819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hong GF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                            This is the peptide sequence (587 amino acids) of the Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1997-474304/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JP09220087-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HUAN/)
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18-oct-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA replication; exonuclease; proof reading.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacillus stearothermophilus; DNA polymerase; DNA amplification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacillus stearothermophilus DNA polymerase (peptides 1-587).
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                                                                                  432 LAQNLNITRKE 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (SHAN-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HONG/) HONG G F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        432 LAQNLNITRKE 442
                                                                                                               1 LAQNLNIXRKE 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZHAI F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HUANG W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Huang W,
                                                                                                                                                                                                        587 AA;
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                                                                                                                                           Conservative
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950S-0544643
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                                                                                                                                                          98.0%;
90.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98.0%;
90.9%;
                                                                                                                                           Score 48; DB Pred. No. 0.2; 0; Mismatches
                                                                                                                                             0;
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Pred. No.
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       RESULT 6
AAY91931
                                                                                                                                                                                                                                                                                                                             Вb
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                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacillus stearothermophilus DNA polymerase (Bst Pol 1) large fragment (AAW10597) lacks the N-terminal 3'-5' exonuclease domain of native Bst Pol I. It is encoded by a DNA construct (AAT36360) obtd. by PCR cloning of genomic DNA using a primer (AAT60826) based on the large fragment N-terminal sequence (AAW10599). Recombinant Bst Pol I large fragment can be produced in transformed host cells, esp. as a fusion protein with maltose binding protein. It is thermophilic, retaining its activity at 65 deg, and is useful for nucleic acid
/note= "modified to Thr-Pro-Leu in AAY91930" Misc-difference 421
                               rey Location/Qualifiers Misc-difference 341..343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA encoding recombinant thermophilic Bacillus stearothermophilus DNA polymerase I - substantially free of 3'-5', and opt. also 5'-3' exonuclease activity
                                                                                                                                                     B. stearothermophilus 320 wild type DNA polymerase.
                                                                                                                                                                                        19-JUL-2000
                                                                                 Bacillus
                                                                                                        Modified DNA polymerase; DNA sequencing; 3′ to 5′ exonuclease activity; random primer labeling; site-directed mutagenesis; wild type.
                                                                                                                                                                                                                     AAY91931;
                                                                                                                                                                                                                                                AAY91931 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-AUG-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacillus stearothermophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bst DNA polymerase large fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequencing and strand displacement amplification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 12-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (NEWE ) NEW ENGLAND BIOLABS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW10597;
                                                                                                                                                                                                                                                                                                                            432 LAQNLNITRKE 442
                                                                                                                                                                                                                                                                                                                                                          1 LAQNLNIXRKE 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequencing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   polymerase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1997-111048/11.
                                                                                                                                                                                                                                                                                                                                                                                        10;
                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                             stearothermophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                587 AA;
                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95US-0510215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96EP-0202169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bst Pol I; thermostable enzyme; exonuclease; strand displacement amplification.
                                                                                                                                                                                                                                                                                                                                                                                                   98.0%;
90.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pelletier JJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                34pp; English.
                                                                                                                                                                                                                                                 587
                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                  Score 48; DB
Pred. No. 0.2;
                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                  DH 18;
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Length 587; Indels

0;

Gaps

0;

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RESULT 4
AAT76647
                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alignment Scores:
            02-DEC-1996;
24-JAN-1996;
12-JUL-1996;
29-NOV-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    . No. :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence, clone 4F encodes a Taq DNA polymerase enzyme that has normal 5' nuclease activity, but reduced synthetic ability. This sequence was derived from the mulTaq construct described in AAT70343. The entire mutTaq gene was cut from the plasmid, and cloned into pET-3c. This clone was digested with BstXI and BamHI, at unique sites. The 3' overhang of BstXI was trimmed to a blunt end, while the overhang of BamHI was filled in. The blunt ends were ligated together. This resulted in an in-frame deletion of 903 nucleotides. The enzyme encoded by the present protein is also referred to as Cleavase BB.
  02-DEC-1996;
                                                                        22-JAN-1997;
                                                                                                 31-JUL-1997
                                                                                                                         W09727214-A1
                                                                                                                                                                                                                                                                                               AAT76647 standard; DNA; 1600
                                                                                                                                                                                                                                                                                                                                              1133 CTCTCCCAGGAGCTAGCCATCCCTTACGAGGAG
                                                                                                                                                          Thermus aquaticus YT-1.
                                                                                                                                                                                              Nucleic acid
                                                                                                                                                                                                                      Taq gene 5'
                                                                                                                                                                                                                                                14-APR-1998
                                                                                                                                                                                                                                                                        AAT76647;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1600 BP; 286 A; 519 C; 553 G; 242 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Thermostable 5' nuclease derived from thermostable polymerase - has reduced synthetic activity useful in nucleic acid detection assays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1997-201481/18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Brow MAD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-DEC-1992;
04-JUN-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 2A; Columns 79-82; 93pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (THIR-) THIRD WAVE TECHNOLOGIES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-JUN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                      <u>بـــا</u>
                                                                                                                                                                                                                                                                                                                                                            DNA polymerase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dahlberg JE,
                                                                                                                                                                                                                      nuclease clone 3F (Cleavase BB).
                                                                                                                                                                                  cleavage; DNA cleavage; RNA cleavage; 5' nuclease;
ymerase; Cleavase BB; ds.
                                                                                                                                                                                                                                             (first entry)
 96US-0599491.
96US-0682853.
96US-0756386.
96US-0758314.
                                                 96US-0759038
                                                                        97WO-US01072
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        92US-0986330
93US-0073384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9408-0254359
                                                                                                                                                                                                                                                                                                                                                                                                                                 0.0649
54.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lyamichev VI;
                                                                                                                                                                                                                                                                                               82
                                                                                                                                                                                                                                                                                                                                                                                             (1-1600)
                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative: Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches:
                                                                                                                                                                                                                                                                                                                                               1165
                                                                                                                                                                                                                                                                                                                                                                                                                    1600
11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 5
AAV65786
В
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                                                                                                                                                                                                                                                                                                                                                                                            Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                             Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Brow MAD,
Olive DM,
                                             24-MAR-1998;
                                                                      01-OCT-1998
                                                                                                                                                                                                                     02-РЕВ-1999
                                                                                                                                                                                                                                              AAV65786;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        No . .
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g Qγ 踞:

Score: Pred.

(THIR-) THIRD WAVE TECHNOLOGIES INC

Dahlberg JE, Hall JG, Kaiser MW, Lyamichev VI;

WPI; 1997-393613/36

Thermostable structure-specific nuclease(s) characterisation of nucleic acid sequences acid sequences)'- used for detection and and variations in nucleic

Example 2; Page 245; 457pp; English

NA. It relates to methods for forming a NA cleavage structure on a target sequence and cleaving the NA cleavage structure in a site-specific manner. The 5' nuclease activity of various enzymes (see AAW24210-13) is used to cleave the target-dependent cleavage structure, thereby indicating the presence of specific NA sequences or specific variations of them. structure-specific nuclease preferred for use in nucleic acid cleavage methods of the invention. Mutant genes (AAT76644-47) were constructed in order to determine which portions of the Tag polymerase domain can be altered without eliminating 5' nuclease altered Thermus aquaticus DNA polymerase (Taq) gene in which nucleotides 875-1778 of the wild-type gene coding sequence are deleted. Mutant gene mutTag (see AAT76643) was used as the starting material for the construct. Cleavase BB is a thermostable activity. The invention relates to means for the detection and characterisation of nucleic acid (NA) sequences and variations This DNA sequence, denoted clone 3F or Cleavase BB, comprises an

Sequence 1600 BP; 286 A; 519 C; 553 G; 242 T; 0 other;

US-09-823-649A-3 (1-11) x AAT76647 (1 1600) Best Local Similarity: Alignment Scores: Percent Similarity: 0.0649 54.00 100.00% 100.00% 100.00% Conservative: Mismatches: Indels: Gaps: Matches: 1600 11 0 0 0

AAV65786 Standard; DNA; 1600 49

(first entry)

Thermus aquaticus nuclease clone 3F (Cleavase BB) DNA

Nucleic acid detection; multiple sequential invasive cleavage; DNA polymerase; nuclease; Cleavase 88;

Thermus aquaticus strain YT-1 Synthetic.

ID XXX ACC XXX

98WO-US05809

24-MAR-1997; 97US-0823516

(THIR-) THIRD WAVE TECHNOLOGIES INC

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RESULT 6
AAV53855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                          this structure in a site-specific manner, preferably using a thermostable structure-specific nuclease such as a modified Tag DNAP that has reduced synthetic activity (see AAV65783-86). Cleavage of the cleavage structure by the nuclease indicates the presence of specific nucleic acid sequences or specific variants. The invention further relates to methods for the separation of nucleic acid molecules based on charge, methods for the detection of nor target cleavage products via the formation of a complete and activated protein binding region, and methods for the detection of nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Brow MAD,
Mast AL,
                                                          04-JUN-1998
                                                                                              WO9823774-A1
                                                                                                                                                                      Clone 4D; Taq mutant gene; thermostable; structure-specific nuclease; mutant DNA polymerase; bacteria; fungi; protozoa; RNA virus; hepatitis C virus; HCV; ds.
                                                                                                                                                                                                                                                                                                                                AAV53855;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1600 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      acid from various viruses (e.g. human cytomegalovirus) in a sample. The method amplifies the detection molecule rather than the target itself, is less subject to contamination than exponential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        characterisation of nucleic acid sequences, and variations in nucleic acid sequences. It also relates to methods for forming a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This nucleotide sequence (clone 3F) codes for a thermostable nuclease (Cleavase BB) derived from the DNA polymerase (DNAP) of Thermus aquaticus (Taq). In comparison to the wild-type Taq DNAP sequence (see AAV65779), it contains an in-frame deletion of 903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Detecting target nucleic acid by sequence-specific cleavage of complex with two specific oligonucleotides - used to detect
                      26-NOV-1997;
                                                                                                                                      Thermus
                                                                                                                                                                                                                                                Nucleotide sequence of clone 4F of the Taq gene mutant.
                                                                                                                                                                                                                                                                                          21-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                  AAV53855 standard; DNA; 1600 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      a single reaction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amplification processes, and allows many targets to be analysed in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nucleic acid cleavage structure on a target sequence and cleaving
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nucleotices.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 2; Page 278; 524pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cytomegalovirus DNA
                                                                                                                                    sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hall JG,
Vavra SH;
                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to means for the detection and
                      97WO-US21783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.00%
100.00%
100.00%
19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              286 A; 519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0.0649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kwiatkowski RW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ç
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              553 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lyamichev VI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                242 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1600
11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 7
AAV63407
Db
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alignment Scores:
                  Brow MAD,
                                                                                                            07-DEC-1992;
04-JUN-1993;
                                                                                                                                                                                                                                                                  US5837450-A
                                                                                          06-JUN-1995;
                                                                                                                                                  06-JUN-1994;
                                                                                                                                                                                        06-JUN-1995;
                                                                                                                                                                                                                              17-NOV-1998
                                                                                                                                                                                                                                                                                                                                                              thermostable
                                                                                                                                                                                                                                                                                                                                                                                  Thermostable
                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAV63407;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kaiser MW,
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US-09-823-649A-3 (1-11) x AAV53855 (1-1600)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This is the nucleotide sequence of a clone of a mutant Tag gene, used in the method of the invention. In this process thermostable structure-specific nucleases are derived from mutant DNA polymerases, which can be used for detecting mutant alleles or strains of microorganisms. The structure-specific nucleases can be used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mixtures, compositions and kits to treat nucleic acid, e.g. for detection of wild type and mutant alleles of genes, for detection and/or identification of strains of microorganisms such as bacteria, fungi, protozoa, especially for detection of RNA viruses such as the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-DEC-1996;
29-NOV-1996;
                                                                                                                                                                                                                                           Synthetic.
Thermus aquaticus.
                                                                                                                                                                                                                                                                                                                                    DNA sequence of a thermostable 5' nuclease derived from Taq polymerase.
                                                                                                                                                                                                                                                                                                                                                                                                                                         AAV63407 standard; DNA; 1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1600 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 2; Page 238; 472pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1998-322748/28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hepatitis C virus (HCV).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  microorganisms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Thermostable structure-specific nuclease(s) derived from mutant DNA polymerase(s) - useful for detecting mutant allele(s) or strains of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (THIR-) THIRD WAVE TECHNOLOGIES INC
                            (THIR-) THIRD WAVE TECHNOLOGIES INC
Dahlberg JE, Lyamichev VI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lyamichev VI,
                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                           DNA polymerase; nucleic acid detection; Cleavase BB; 5' nuclease; ds.
                                                                              92US-0986330.
93US-0073384.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96US-0758314.
96US-0757653.
                                                              95US-0471066
                                                                                                                94US-0254359
                                                                                                                                              95US-0471066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   286 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0.0649
54.00
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100.00%
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                                                                                                                                                                                                                                                                                                                                                                                                                                         ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ç;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   553 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches: Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches:
Conservative;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  z
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0 other;
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В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-823-649A-3 (1-11)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence represents a thermostable 5' nuclease derived from a thermostable polymerase modified to have reduced synthetic activity, where the 5' nuclease is capable of cleaving a linear nucleic acid duplex structure to create a single, single-stranded cleavage product. The nuclease, designated Cleavase BB, is used in a mothod for detecting the presence of a nucleic acid molecule. The method is used for the specific detection of nucleic acid sequences, via a cleavage-based procedure, but without the need for amplification of target sequences. Thermostable polymerases, altered to have nuclease, but not polymerase activity are preferably used due to their specificity. The cleavage product specifically formed is detected, preferably by the use of radioactively labelled oligonucleotides. These can be used in c.g. forensic testing or paternity determination.
                                                             28-SEP-1990;
28-SEP-1990;
28-SEP-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Detection of target nucleic acid molecules - uses modified thermostable enzymes with specific cleavage activity to create specific detection products from oligo:nucleotide(s) and target
            Abramson RD,
                                                                                                                 30-SEP-1991;
                                                                                                                                                                                                                                  old_sequence
                                                                                                                                                                                                                                                                       Thermus aquaticus.
                                                                                                                                                                                                                                                                                                5'-3'; exonuclease; PCR; amplification; SSR; sequencing; PLCR;
                                                                                                                                                                                                                                                                                                                         Mutant thermostable DNA polymerase pLSG8
                                                                                                                                                                                                                                                                                                                                                   22-OCT-1992 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 10; Columns 79-82; 91pp; English.
                                    (CETU ) CETUS
                                                                                                                                           16-APR-1992
                                                                                                                                                                    WO9206200-A
                                                                                                                                                                                                                                                                                                                                                                             AAQ23998;
                                                                                                                                                                                                                                                                                                                                                                                                    AAQ23998 standard; DNA; 1635 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hybridisation
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                                      CORP.
            Gelfand DH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BP;
                                                             90US-0590213.
90US-0590466.
90US-0590490.
                                                                                                                  91WO-US07035
                                                                                                                                                                                                                                  Location/Qualifiers 1..2
                                                                                                                                                                                                                    /*tag=
                                                                                                                                                                                                        /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       286 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          x AAV63407
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0.0649
                                                                                                                                                                                                           "nucleotides
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels:
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                                                                                                                                                                                                         4-867 deleted from native
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DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No.:
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                          28-SEP-1990;
28-SEP-1990;
28-SEP-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        polymerases are useful in many recombinant DNA techniques, esp. nucleic acid amplification by PCR, self-sustained sequence replication (SSR) and high temp. DNA sequencing. The absence of 5'-3' nuclease activity may facilitate higher sensitivity alielic discrimination in a combined polymerase ligase chain reaction (PLCR) assay. An enhanced amt. of 5'-3' exonuclease activity may be desirable in enzymes used in homogeneous assays for the amplification and detection of a target nucleic acid sequence. Mulation of the DNA encoding particular regions of the enzymes can be used to prepare a range of recombinant proteins having 5'-3' exonuclease activity to a scenario AAQ23993-Q24013, AAQ24320-36 and AAQ24343-60.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Thermostable DNA polymerases with altered 5'-3' exo nuclease activity - having conserved regions mutated or deleted, for use in e.g. PCR, sequencing and detection assays
                                                                                                                                                                                                           old_sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                  1168 CTCTCCCAGGAGCTAGCCATCCCTTACGAGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the polymerase enzyme produced to exhibit a different amt. of exonuclease activity than the native enzyme. Thermostable DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 11; Page 59;
                                                                                   30-SEP-1991;
                                                                                                                                        W09206200-A
                                                                                                                                                                                                                                                      Thermus
                                                                                                                                                                                                                                                                             5'-3'; exonuclease; PCR; amplification; SSR; sequencing; PLCR; ss
                                                                                                                                                                                                                                                                                                        Mutant thermostable DNA polymerase p205A292
                                                                                                                                                                                                                                                                                                                                       22-0CT-1992
                                                                                                                                                                                                                                                                                                                                                                 AAQ24322;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The sequence is that of Thermus aquaticus polymerase DNA which has been mutated. The mutation, resulting in mutant pLSG8, causes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P-PSDB; AAR23145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1992-150885/18.
                                                                                                               16-APR-1992
                                                                                                                                                                                                                                                                                                                                                                                            AAQ24322 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1635
                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 LeuSerGlnGluLeuAlaIleProTyrGluGlu
                                                                                                                                                                                                                                                      species
                                                                                                                                                                                                                                                                                                                                     (first entry)
                        90US-0590213.
90US-0590466.
90US-0590490.
                                                                                  91WO-US07035
                                                                                                                                                                                                                                                      205.
                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                /note= "nucleotides 4-873 deleted from the native
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 274 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.00%
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                            DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   185pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0.0666
54.00
                                                                                                                                                                                                                                                                                                                                                                                            1635
                                                                                                                                                                  sequence."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 551 C;
                                                                                                                                                                                                                                                                                                                                                                                            ΒP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 564 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length:
Matches:
Conservative:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   1200
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RESULT 10
AAQ24328
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nucleic acid amplification by PCR, self-sustained sequence replication (SSR) and high temp. DNA sequencing. The absence of solution (SSR) and high temp. DNA sequencing. The absence of solution in a combined polymerase ligher sensitivity allelic discrimination in a combined polymerase ligher sensitivity may be desirable assay. An enhanced amt. of 5'-3' exonuclease activity may be desirable in enzymes used in homogeneous assays on the amplification and detection of a target nuclear acid sequence. Mutation of the DNA encoding particular regions of the enzymes can be used to prepare
28-SEP-1990;
28-SEP-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                1168 CTCTCCCAGGAGCTTGCCATCCCCTACGAGGAG 1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   a range of recombinant proteins having 5'-3' exonuclease activity to a complete lack of activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The sequence is that of Thermus species 205 polymerase DNA which has been mutated. The mutation designated p205A292 causes the polymerase enzyme produced to exhibit a different amt. of 5'-3'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Thermostable DNA polymerases with altered 5'-3' exo nuclease activity - having conserved regions mutated or deleted, for use
                                         30-SEP-1991;
                                                                       16-APR-1992
                                                                                                   W09206200-A
                                                                                                                                                                           old_sequence
                                                                                                                                                                                                                     Thermus thermophilus.
                                                                                                                                                                                                                                                  5'-3'; exonuclease; PCR; amplification; SSR; sequencing; PLCR; ss
                                                                                                                                                                                                                                                                                Mutant thermostable DNA polymerase pTTHA292
                                                                                                                                                                                                                                                                                                                                                                       AAQ24?28 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  exonuclease activity than the native enzyme. Thermostable DNA polymerases are useful in many recombinant DNA techniques, esp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 11; Page 59; 185pp; English.
                                                                                                                                                                                                                                                                                                             22-OCT-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     See also AAQ23993-Q24013, AAQ24320-36 and AAQ24343-60.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        in e.g. PCR, sequencing and detection assays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P-PSDB; AAR23163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 LeuSerGlnGluLeuAlaIleProTyrGluGlu 11
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                                                                                                                                                                                                                                                                                                          (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BP;
900S-0590213
900S-0590466
                                           91WO-US07035
                                                                                                                               /*tag=
                                                                                                                                                                                         Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       291 A; 577
                                                                                                                                                                                                                                                                                                                                                                       DNA; 1635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0.0566°
54.00
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                                                                                                                                                                                                                                                                                                                                                                       ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; 529 G; 238 T; 0 other;
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The sequence is that of Thormus thermophilus polymerase DNA which has been mutated. The mutation designated prHAA92 causes the polymerase enzyme produced to exhibit a different amt. of 5'.3' exonuclease activity than the native enzyme. Thermostable DNA polymerases are useful in many recombinant DNA techniques, esp. nucleic acid amplification by PCR, self-sustained sequence replication (SSR) and high temp. DNA sequencing. The absence of 5'.3' nuclease activity may facilitate higher sensitivity allelic discrimination in a combined polymerase ligase chain reaction (PLCR) assay. An enhanced amt. of 5'.3' exonuclease activity may be desirable in enzymes used in homogeneous assays for the amplification and forter through the second content of t
                                                                                                                                                                                                                                          Thermostable DNA dependent polymerase; nuclease activity; "aq polymerase; mutant: Polymerase Chain Reaction, PCR, N-terminal domain, protectlytic; thermal stability; bydrophilic solution; sequencing; labeling; diagnosis; genetic disorder; primer driven mutagenesis; identification of pathogen; mutational analysis; forensic identification; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              detection of a target nucleic acid sequence. Mutation of the DNA encoding particular regions of the enzymes can be used to prepare a range of recombinant proteins having 5'-3' exonuclease activity to a complete lack of activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Thermostable DNA polymerases with altered 5'-3' exo nuclease activity - having conserved regions mutated or deleted, for u in e.g. PCR, sequencing and detection assays
                                                                                                                                                                             Synthetic.
                                                                                                                                                                                                      Thermus aquaticus.
                                                                                                                                                                                                                                                                                                                                                                                                             Thermostable DNA dependent mutant Tag polymerase-1 encoding DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 11; Page 59; 185pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAZ29460;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAZ29460 Standard; DNA; 1682 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P-PSDB; AAR23168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAQ23993-Q24013, AAQ24320-36 and AAQ24343-60.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (lirst entry)
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        /*tag= a
/product= "Thermostable mutant Tag
/note= "Identical at C-terminus to
                                                                                             Location/Qualifiers
8..1669
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Taq polymerase
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from Thermus aquaticus"

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RESULT 12
AAT47959
ID AAT47
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Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                     Score:
                                                                                                                                                                                                                                                                                                                                                                                               Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                        Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence is the DNA encoding a novel, thermostable DNA dependent, mutant Tag polymerase-1 enzyme. The N-terminal domain of the polymerase includes a sequence of 9 amino acids, that has 40-50% sequence identity with residues 280-288 of native Thermus aquaticus polymerase, Tag. The residues 10-553 of encoded by this sequence is identical to residues 289-832 of Tag polymerase. This sequence has no significant nuclease activity, but good proteolytic and thermal stabilities and improved solubility in hydrophilic solutions. This sequence is used for synthesis of polynuclectides, particularly in polymerase chain reaction (PCR) based processes, like sequencing, labeling, primer-driven mutagenesis, diagnosis of genetic disorders, identification of pathogens, mutational analysis and forensic
                                                                                                                                                                                                                                                                       1202 CTCTCCCAGGAGCTAGCCATCCCTTACGAGGAG 1234
           31-MAY-1995;
                                                       04-DEC-1996
                                                                            EP745676-A1
                                                                                                 Thermus aquaticus.
                                                                                                                    Taq; polymerase; FY2; FY3; FY4; thermostable; Thermus; enzyme; DNA sequencing; PCR; ss.
                                                                                                                                                       Mutant Taq polymerase FY2
                                                                                                                                                                                                      AAT47959;
                                                                                                                                                                                                                          AAT47959 standard; DNA; 1686
                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1682 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 22; Fig 1; 32pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel enzyme, particularly useful in polymerase chain reaction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-DEC-1999
                                30-MAY-1996;
                                                                                                                                                                                11-MAY-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11-JUN-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      identification.
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           95US-0455686
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                                96EP-0303880
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RESULT 13
AAT47961
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 New enzymatically active Thermus DNA polymerase(s) - having a tyrosine at a position equivalent to 667 of Taq DNA polymerase and lacking 5' to 3' exonuclease activity
                                                                                     ;IdM
                                                                                                                                                                                                                                                                                                                                                                      Taq; polymerase; FY2; FY3; FY4; Thermostable; Thermus; enzyme; DNA sequencina; FCR; ss
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                                                                       P-PSDB; AAW09317
                                                                                                                         Davis
                                                                                                                                                                                             31-MAY-1995;
                                                                                                                                                                                                                              30-MAY-1996;
                                                                                                                                                                                                                                                                04-DEC-1996
                                                                                                                                                                                                                                                                                                   HP745676-A1
                                                                                                                                                                                                                                                                                                                                    Thermus thermophilus
                                                                                                                                                                                                                                                                                                                                                                                                                       Mutant Tag polymerase FY4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 5; Page 10-13; 36pp; English.
                                                                                                                                                        (AMSH ) AMERSHAM LIFE SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAT47961;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAT47961 standard; DNA; 1686
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                                                                                                                                                                                                                                                                                                                                                                    sequencing; PCR; ss
                                                                                   1997-013699/02.
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                                                                                                                      Fuller C,
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exonuclease activity
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                                                                                                                      Fuller CW,
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                          This sequence encodes a thermostable DNA polymerase of the invention. The thermostable polymerases of the invention are variants of Taq DNA polymerase having a Tyr residue at a position corresponding to Taq DNA polymerase residue 667 in its dNNP binding site, and lacking 5′ to 3′ exonuclease activity as a result of an N-terminal deletion. The polymerases can be used for the sequencing of DNA, either by manual or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1219 CTCTCCCAGGAGCTAGCCATCCCCTACGAAGAA 1251
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automated means
                                                                                                                                                                                                                                                                                                                                            Claim
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31-MAY-1995;
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95US-0455686.
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US-09-823-649A-3 (1-11) x AAX27132 (1-1686)
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                                                                                                                             thermostable polymerases of the invention are variants of Taq DNA polymerase having a Tyr residue at a position corresponding to Taq DNA polymerase residue 667 in its dNMP binding site, and lacking 5′ to 3′ exonuclease activity as a result of an N-terminal deletion. The polymerases can be used for the sequencing of DNA, either by manual or
                                                                                                                                                                                                                        New thermostable DNA polymerases - having and lacking 5' to 3' exonuclease activity
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                                                                                                     Sequence 1686
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                                                                                                                                                                                  This sequence encodes a thermostable DNA polymerase of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                          polymerase;
sequencing;
                                                                                                                                                                                                                                                                                                           AMERSHAM LIFE SCI INC
                                                                                                                        means
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                       Davis M,
                                                                                                     BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         B₽;
                                                                                                                                                                                                                                                                                                                             96US-0648657.
95US-0455686.
                                                                                                                                                                                                                                                                                                                                                            96US-0648657
                                                                                                                                                                                                                                                                                                                                                                                                                                           SS
                                                                                                                                                                                                                                                                                                                                                                                                                                                  FY3 polymerase; FY4 polymerase; Taq polymerase variant;
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                                                                                                                                                                                                    27pp; English.
                                                                                                                                                                                                                                                                                      Fuller CW,
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                                                                                                                                                                                                                                   having 540 to 582 amino acids
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Search completed: January 15, 2003, 12:55:28 Job time: 133.143 secs

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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Run on:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Perfect score:
                                                                                                                                                                                                                                                                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,
                                                                                                                                                                                                                                                                                                                                                   and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                          Score
    Query
Match
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1: /SIDS2/gcgd=+-/
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/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1985.DAT: *
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Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /SIDS2/gc@data/geneseq/geneseqp-emb1/AA1982.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1984.DAT:*
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/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1981.
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AAM48259
AAM48261
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810	810	\vdash	789	789	787	758	758	757	680	680	680	654	634	632	632	632	631	604	604	597	597	562	562	562	562	561	561	561	561	560	560	559	554	553
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ABB08340	ABB08339	AAB62314	AAR23164	AAR23159	AAR23142	AAR23165	AAR23160	AAR23141	AAR23166	AAR23161	AAR23143	AAE15569	AAE15568	AAE15565	AAR23167	AAR23162	AAR23144	AAU00575	AAU00574	AAR96204	AAR99543	AAE09310	AAE09305	AAY00887	AAW09316	AAY00888	AAY00886	AAW09317	AAW09315	AAR96205	AAR99544	AAY44353	AAR66209	AAY44352
-sensi	ld type Tac	þ	Mutant thermostabl	Mutant thermostabl	Mutant thermostabl	thermostab	thermostab	Mutant thermostabl			7		aci	0			ermosta	CauTaq	eric CauTaq	DNA polymerase I e		aquaticus	rmus thermo		ant Taq polyme	polymerase.) ymei	Tag.	<;	merase	IS DI	Thermostable DNA d	stabl	Thermostable DNA d

ALIGNMENTS

AAB47793 standard; peptide;

<u>⊢</u>

AAB47793;

DNA polymerase; reverse transcription; primer; divalent cation; mutant; transverse transcription reaction; fluorescein; cyanine; thermoactive; dye; amplification. Reverse transcribing an RNA, comprises performing a reverse transcriptase polymerase chain reaction amplification of a mixture Smith ES, Elfstrom CM, Schoenbrunner NJ, Wang 07-NOV-2001 EP1152062-A2 Thermus sp. 18-APR-2000; 2000US-198336P 12-APR-2001; 2001EP-0109341. Native DNA polymerase motif #3. 25-MAR-2002 (first entry) (HOFF) HOFFMANN LA ROCHE & CO AG F. 2002-076891/11 Wang AM; Gelfand DH, Higuchi RG, Myers TW;

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RESULT 2
AAM48259
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Matches
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The sequences given in AAB47791-97 and AAM48259-AAM48270 represent the native forms of motifs derived from DAA polymerases used in the method of the invention. The method for reverse transcribing an RAA, comprises treating a transverse transcription reaction mixture which comprises the
                                                                                                                       Reverse transcribing an RNA, comprises performing a reverse transcriptase polymerase chain reaction amplification of a mixture using a mutant thermoactive DNA polymerase
                                                                                    Disclosure; Page 7; 23pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         concentrations relative to previous high temperature reverse transcription methods, and provide a wider range of usable salt concentrations. The use of the mutant DNA polymerase provides faster reverse transcription extension rates, and consequently less time is needed for the reaction. This motif is derived from DNA polymerases from Thermus species aquaticus, thermophilus, ZO5 and caldophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              polymerase. These motifs represent a conserved region which affects the DNA polymerase's ability to incorporate dideaxynucleotides labelled with fluorescein and cyanine family dyes. The method of the invention is useful in reverse transcription/amplification reactions. The method provides improved reverse transcription efficiency at lower enzyme
                                                                                                                                                                                               WPI; 2002-076891/11.
                                                                                                                                                                                                                                Schoenbrunner NJ,
                                                                                                                                                                                                                                                                                                                      18-APR-2000; 2000US-198336P.
                                                                                                                                                                                                                                                                                                                                                         12-APR-2001; 2001EP-0109341
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA polymerase; reverse transcription; primer; divalent cation; mutant; transverse transcription reaction; fluorescein; cyanine; thermoactive;
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                                                                                                                                                                                                                                                                                   (HOFF ) HOFFMANN LA ROCHE & CO AG F.
                                                                                                                                                                                                                                                                                                                                                                                                                             EP1152062-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Thermus aquaticus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  dye; amplification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Native DNA polymerase motif #8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 4; Page 3; 23pp; English.
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les 11; Conserv
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                                                                                                                                                                                                                              m CM, Gelfand DH,
Wang AM;
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Pred. No. 0.00096;
; Mismatches 0;
                                                                                                                                                                                                                                                 Higuchi RG,
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                                                                                                                                                                                                                                                 Myers TW;
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Best Local Similarity
               RNA, a primer, a divalent cation, and a mutant thermoactive DNA polymerase. These motifs represent a conserved region which affects the DNA polymerase's ability to incorporate dideoxynuclectides labelled with fluorescein and cyanine family dyes. The method of the invention is useful in reverse transcription/amplification reactions. The method provides improved reverse transcription efficiency at lower enzyme concentrations relative to previous high temperature reverse transcription methods, and provide a wider range of usable salt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     polymerase. These motifs represent a conserved region which affects the DNA polymerase's ability to incorporate dideoxynucleolides labelled with fluorescein and cyanine family dyes. The method of the invention is useful in reverse transcription/amplification reactions. The method provides improved reverse transcription efficiency at lower enzyme concentrations relative to previous high temperature reverse transcription methods, and provide a wider range of usable salt concentrations. The use of the mutant DNA polymerase provides itsister.
transcription methods, and provide a wider range of usable salt concentrations. The use of the mutant DNA polymerase provides faster
                                                                                                                                                                                    The sequences given in AAB47791-97 and AAM48259-AAM48270 represent the native forms of motifs derived from DNA polymerases used in the method of the invention. The method for reverse transcribing an RNA, comprises
                                                                                                                                                                                                                                                                   Disclosure; Page 7; 23pp; English.
                                                                                                                                                                                                                                                                                                         using a mutant thermoactive DNA polymerase
                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-076891/11.
                                                                                                                                                                                                                                                                                                                                                                                                                        Schoenbrunner NJ, Wang AM:
                                                                                                                                                                                                                                                                                                                                                                                                                                          Smith ES, Elistrom CM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-APR-2000; 20000S-198336P
                                                                                                                                                                                                                                                                                                                         Reverse transcribing an RNA, comprises performing a reverse transcriptase polymerase chain reaction amplification of a mixture
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HOFF ) HOFFMANN LA ROCHE & CO AC F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-APR-2001; 2001EP-0109341
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               dye; amplification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAM48261 standard; Peptide; 11 AA
                                                                                                                                                                    treating a transverse transcription reaction mixture which comprises
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA polymerase; reverse transcription; primer; divalent cation; mulunt; transverse transcription reaction; iluorescein; cyanine; thermoactive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Native DNA polymerase motif #10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-MAR-2002 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RNA, a primer, a divalent cation, and a mutant thermoactive DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Gelfand DH, Higuchi RG,

 Mismatches

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Pred. No.
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RESULT 4
AAM48262
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Matches 11; Conserv
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                                                                                                      Sequence
                                                                                                                                                                             provides improved reverse transcription efficiency at lower enzyme concentrations relative to previous high temperature reverse transcription methods, and provide a wider range of usable salt concentrations. The use of the mutant DNA polymerase provides faster
                                                                                                                                                                                                                                                 DNA polymerase's ability to incorporate dideoxynucleotides labelled with fluorescein and cyanine family dyes. The method of the invention is useful in reverse transcription/amplification reactions. The method
                                                                                                                                                                                                                                                                                                                              of the invention. The method for reverse transcribing an RNA, comprises treating a transverse transcription reaction mixture which comprises the RNA, a primer, a divalent cation, and a mutant thermoactive DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 7; 23pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-NOV-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Thermus species Z05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 dye; amplification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA polymerase; reverse transcription; primer; divalent cation; mutant; transverse transcription reaction; fluorescein; cyanine; thermoactive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Native DNA polymerase motif #11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAM48262 standard; Peptide; 11 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                           reverse transcription extension rates, and consequently less time is
                                                                                                                                                                                                                                                                                                                                                                                     The sequences given in AAB47791-97 and AAM48259-AAM48270 native forms of motifs derived from DNA polymerases used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  using a mutant thermoactive DNA polymerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Reverse transcribing an RNA, comprises performing a reverse transcriptase polymerase chain reaction amplification {}_{\circ}\mathsf{f} a mixture
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-076891/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Schoenbrunner NJ, Wang AM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18-APR-2000; 2000US-198336P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12-APR-2001; 2001EP-0109341.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-MAR-2002 (first entry)
                                                                                                                                                                                                                                                                                                             polymerase. These motifs represent a conserved region which affects the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HOFF') HER'EMANN LA ROCHE & CO AG F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              reverse transcription extension rates, and consequently less time
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Elfstrom CM,
                                                                                                      11
                                                                                                                                           the reaction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1
                           Conservative
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                                                                                                      AA;
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                                         100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gelfand DH,
                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                         Score 54; DB 23;
Pred. No. 0.00096;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 54; DB 23;
Pred. No. 0.00096;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Higuchi RG,
                           0;
                                                            Length 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 11;
                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , W.J.
                         0,
                                                                                                                                                                                                                                                                                                                                                                                     the method
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                         Gaps
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AAR96267
ID AAR962
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AAM48264
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                                                                                                                                                                                              Matches
                                                                                                                                                                                                                  Best
                                                                                                                                                                                                                                  Query Match
                     AAR96267 standard; Protein; 528 AA.
                                                                                                                                                                                                                                                                                                                      provides improved reverse transcription efficiency at lower enzyme concentrations relative to previous high temperature reverse transcription methods, and provide a wider range of usable salt concentrations. The use of the mutant DNA polymerase provides faster reverse transcription extension rates, and consequently less time is
                                                                                                                                                                                                                                                                                                                                                                                                                                                    The sequences given in AAB47791-97 and AAM48259-AAM48270 represent the native forms of motifs derived from DNA polymerases used in the method of the invention. The method for reverse transcribing an RNA, comprises treating a transverse transcription reaction mixture which comprises the RNA, a primer, a divalent cation, and a mutant thermoactive DNA polymerase. These motifs represent a conserved region which affects the DNA polymerase's abilly to incorporate dideoxynucleotides labelled with
                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Smith
                                                                                                                                                                                                                                                                                                                                                                                                                             useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 7; 23pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               using a mutant thermoactive DNA polymerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12-APR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Thermus caldophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   dye; amplification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA polymerase; reverse transcription; primer; divalent cation; mutant; transverse transcription reaction; fluorescein; cyanine; thermoactive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Native DNA polymerase motif #13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAM48264;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAM48264 standard; Peptide; 11 AA
                                                                                                                                                                                                                                                                                                                                                                                                                     fluorescein and cyanine family dyes. The method of the invention is useful in reverse transcription/amplification reactions. The method
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Reverse transcribing an RNA, comprises performing a reverse transcriptase polymerase chain reaction amplification of a mixture
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-076891/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Schoenbrunner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EP1152062-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (HOFF ) HOFFMANN LA ROCHE & CO AG
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                                                                                                                                                                                                                Local Similarity
                                                                                                                        <u>س</u>
                                                                                                                                         1 LSQELAIPYEE 11
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                                                                                                                      LSQELAIPYEE 11
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                                                                                                                                                                                          11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Elfstrom CM,
                                                                                                                                                                                                                                                                       11 AA;
                                                                                                                                                                                                                                                                                                             the reaction.
                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2001EP-0109341.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wang AM;
                                                                                                                                                                                                                100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gelfand DH,
                                                                                                                                                                                            0;
                                                                                                                                                                                                            Score 54; DB 23;
Pred. No. 0.00096;
                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Higuchi RG,
                                                                                                                                                                                                                              Length 11;
                                                                                                                                                                                            Indels
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0;

Gaps

0;

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Query Match
Best Local Similarity
                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                   oligonucleotide containing a human p53 gene sequence or alternatively, microbial gene sequences. Cleavage products are compared to the cleavage products of reference gene sequences. The method is used for detecting mutation in the human p53 gene; for identifying strains of microorganisms, especially bacteria selected from the the group of members of the genera Campylobacter, Escherichia, Mycobacterium, Salmonella, Shigella and Staphylococcus. The method may also be used for the identification of viruses, especially hepatitis C virus and simian immunodeficiency virus.
                                                                                                                                                                                                                      then treated with the Klenow fragment of DNAPBC1 to trim both 3' overhangs to blunt ends which were then ligated together, result in an in frame deletion of 903 nucleotides. This mutant Tag polymerase is also referred to as the Cleavase BB enzyme.
                                                                                                                                                                                                                                                                                                                                        Thermus aquaticus (Taq) DNA polymerase was amplified using two primers (AAT27679, AAT27680). The Taq polymerase DNA was inserted into the BamHI restriction site of the expression vector pET-3c and mutant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cleavage of nucleic acids using an enzyme, especially a nucleas selected from the group consisting of Cleavase (RTM) BN enzyme, Thermus aquaticus DNA polymerase, Thermus thermophilus DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Brow MAD, Dahlberg Oldenburg MC, Olive
                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                       genes were created from that construct. This mutant was created after the vector was digested with BstXI and BamHI. The DNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rad1/Rad10 complex.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 2A; Page 287-288; 433pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cleavage of nucleic acids to detect mutation(s) - allows detection esp. in human p53 gene, to identify strains of microorganisms and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAT27686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1996-259862/26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-JUN-1995;
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09-MAR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09-NOV-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-MAY-19' 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Thermus aquaticus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Staphylococcus; identification; detection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          p53; mutant; mutation; cleavage; nuclease; cleavase; Thermus;
Escherichia; Saccharomyces; Campylobacter; Mycobacterium; Shigella;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mutant Thermus aquaticus DNA polymerase (Clone 4F).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (THIR-) THIRD WAVE TECHNOLOGIES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-AUG-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-NOV-1996
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                       374 LSQELAIPYEE 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            polymerase, Escherichia coli ExoIII and the Saccharomyces cerevisiae
                                                             1 LSQELAIPYEE 11
                                                                                                                                                                                   528
                                                                                                     Conservative
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                                                                                                                                                                                 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94US-0337164.
95US-0402601.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JE,
                                                                                                                   100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The nucleic acid substrate is preferably an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fors L,
                                                                                                     0
                                                                                                                   Score 54; DB 17;
Pred. No. 0.074;
                                                                                                     Mismatches
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                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lyamichev VI;
                                                                                                                                         Length 528;
                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nuclease
                                                                                                                                                                                                                                                               resulting
                                                                                                0;
                                                                                                   Gaps
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                                                                                                                                                                                                                                                               RESULT 8
AAR23163
ID AAR2
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                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                 Matches
                                                                                                                                                                                                      Best
                                                                                                                                                                                                                                                                                                                   sequence replication (SSR) and high temp. DNA sequencing. The absence of 5'-3' nuclease activity may tacilitate higher sensitivity allelic discrimination in a combined polymerase ligase chain reaction (PLCR) assay. An enhanced ann. of 5'-3' exonuclease activity may be desirable in enzymes used in homogeneous assays for the amplification and detection of a target nucleic acid sequence. Mutation of the DNA encoding particular regions of the enzymes can be used to prepare a range of recombinant proteins having 5'-3' exonuclease activity to a complete lack of activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-SEP-1990;
28-SEP-1990;
28-SEP-1990;
                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The sequence is that of a mutant of Thermus aquaticus polymerase mutant MET-SER 290 Taq (the Stoffel fragment) having a different amt. of 5'-3' exonuclease activity than the native enzyme. Thermostable DNA polymerases are useful in many recombinant DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 11; Page 59; 185pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Thermostable DNA polymerases with altered 5'-3' exo nuclease activity - having conserved regions mutated or deleted, for use in e.g. PCR, sequencing and detection assays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Abramson RD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5'-3'; exonuclease; PCR; amplification; SSR; sequencing; PLCR
AAR23163 standard; Protein; 544 AA.
                                                                                                                                                                                                                                                                                                  See also AAR23140-79 and AAR23722.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                techniques, esp. nucleic acid amplification by PCR, self-sustained
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (CETU ) CETUS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-SEP-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       W09206200-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Thermus aquaticus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mutant thermostable DNA polymerase enzyme MET-SER 290 Tag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-OCT-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR23145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR23145 standard; Protein; 544 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-APR-1992
                                                                                                390 LSQELAIPYEE 400
                                                                                                                                                                                                    Local
                                                                                                                                      1 LSQELAIPYEE 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1992-150885/18.
                                                                                                                                                                              11;
                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAQ23998
                                                                                                                                                                                                                                                            544 AA;
                                                                                                                                                                            100.0%;
ilarity 100.0%;
Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gelfand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       900S-0590466.
900S-0590490.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 90US-0590213.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       91WO-US07035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "deletion of residues 2-289 of native segmence."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DH;
                                                                                                                                                                            0;
                                                                                                                                                                                               Score 54;
Pred. No.
                                                                                                                                                                              Mismatches
                                                                                                                                                                                             0.076;
                                                                                                                                                                                                                DB 13;
                                                                                                                                                                          0;
                                                                                                                                                                                                                  Length 544;
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Dβ 9

RESULT 7

AAR23163

Indels

0; Gaps

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RESULT 9
AARZ33168
AID AARZ
XX
AC AAR2
XX
DT 22-C
DT 22-C
DX
XX
DE Muta
XX
XX
5'-3
XX
Ther
XX
                                                                                                                                                                                                                                                  В
                                                                                                                                                                                                                                                                             δÃ
                                                                                                                                                                                                                                                                                                                                                                        PF PF XX
                                                                                                                                                                                                                                                                                                           Best Local Similarity
Matches 11; Conser
                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                          The sequence is that of a mutant of Thermus species 205 polymerase mutant MET-ALA 292 TRO5, having a different ant. of 5'-3' exonuclease activity than the native enzyme. Thermostable DNA polymerases are useful in many recombinant DNA techniques, esp. nucleic acid amplification by PCR, self-sustained sequence replication (SSR) and high temp. DNA sequencing. The absence of 5'-3' nuclease activity may facilitate higher sensitivity allelic discrimination in a combined polymerase ligase chain reaction (PLCR) assay. An enhanced ant. of 5'-3' exonuclease activity may be desirable in enzymes used in homogeneous assays for the amplification and detection of a target nucleace activity may be desirable in enzymes used in homogeneous assays for the amplification and detection of a target nucleace activity may be desirable in enzymes used in homogeneous assays for the amplification and detection of a target nucleace of the new models are the second of the polymerase contacts.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-SEP-1990;
28-SEP-1990;
28-SEP-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Thermostable DNA polymerases with altered 5'-3' exo nuclease activity - having conserved regions mutated or deleted, for use in e.g. PCR, sequencing and detection assays
                 Thermus thermophilus
                                            5'-3'; exonuclease; PCR; amplification; SSR; sequencing; PLCR
                                                                        Mutant thermostable DNA polymerase enzyme MET-ALA 292 Tth.
                                                                                                         22-0CT-1992
                                                                                                                                        AAR23168;
                                                                                                                                                                     AAR23168 standard; Protein; 544 AA
                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 11; Page 59; 185pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Thermus species Z05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5'-3'; exonuclease; PCR; amplification; SSR; sequencing; PLCR
                                                                                                                                                                                                                                                                                                                                                                                                                                  proteins having 5'-3' exonuclease activity to a complete lack of
                                                                                                                                                                                                                                                                                                                                                                                                                                                regions of the enzymes can be used to prepare a range of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (CETU ) CETUS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-APR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9206200-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mutant thermostable DNA polymerase enzyme MET-ALA 292 TZ05.
                                                                                                                                                                                                                                                                                                                                                                                                       See also AAR23140-79 and AAR23722.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Abramson RD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-SEP-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22-OCT-1992 (first entry)
                                                                                                                                                                                                                                                390 LSQELAIPYEE 400
                                                                                                                                                                                                                                                                1 LSQELAIPYEE 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1992-150885/18.
                                                                                                                                                                                                                                                                                                                                                                        544
                                                                                                                                                                                                                                                                                                          100.0%; ilarity 100.0%; Conservative 0;
                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gelfand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90US-0590213.
90US-0590466.
90US-0590490.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DH
                                                                                                                                                                                                                                                                                                          Score 54; DB 13;
Pred. No. 0.076;
0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                        DB 13; Length 544;
                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                  recombinant
                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                           0;
 PD XXX
                                                                                                                                                                                                                                                                                                           Дb
                                                                                                                                                                                                                                                                                                                                      27
23-AUG-2001
                            WO200161015-A2
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RESULT 10
AAE09304
                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                           Best
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28-SEP-1990;
28-SEP-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The sequence is that of a mutant of Thermus thermophilus polymerase mutant MET-ALA 292 Tth. having a different amt. of 5'-3' exonuclease activity than the native enzyme. Thermostable DNA polymerases are useful in many recombinant DNA techniques, esp. nucleic acid amplification by PCR, self-sustained sequence replication (SSR) and high temp. DNA sequencing. The absence of 5'-3' nuclease activity may facilitate higher sensitivity allelic discrimination in a combined polymerase ligase chain reaction (PCCR) assay. An enhanced amt. of 5'-3' exonuclease activity may be desirable in enzymes used in homogeneous assays for the amplification and detection of a target
                            Thermus aquaticus; Taq; DNA polymerase; polymerisation; PCR protocol; genetic engineering.
                                                                                                                                                                                                                                                                                                                                                                                                              nucleic acid sequence. Mutation of the DNA encoding particular regions of the enzymes can be used to prepare a range of recombing proteins having 5'-3' exonuclease activity to a complete lack of activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Thermostable DNA polymerases with altered 5'-3' exo nuclease activity - having conserved regions mutated or deleted, for use in e.g. PCR, sequencing and detection assays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Key Location/Qualifiers Misc-difference 1..2
                                                                       Thermus aquaticus (Taq) DNA polymerase #1.
                                                                                                       22-NOV-2001 (first entry)
                                                                                                                                        AAE09304;
                                                                                                                                                                 AAE09304 standard; Protein; 552 AA
                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 11; Page 59; 185pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDH; AAQ24328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Idm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-SEP-1991;
Thermus aquaticus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Abramson RD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-APR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    W09206200-A
                                                                                                                                                                                                                                                                                                                                                                                                   See also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CETU ) CETUS CORP.
                                                                                                                                                                                                                                              390 LSQELAIPYEE 400
                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                          1 LSQELAIPYEE 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1992-150885/18.
                                                                                                                                                                                                                                                                                                          11;
                                                                                                                                                                                                                                                                                                                                                                                                AAR23140-79 and AAR23722.
                                                                                                                                                                                                                                                                                                                                                                     544 AA;
                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gelland DH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              90US-0590490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           90US-0590213
90US-0590466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         91WO-US07035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%;
                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                    Score 54; DB 13
Pred. No. 0.076;
                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                   DB 13;
                                                                                                                                                                                                                                                                                                        9
                                                                                                                                                                                                                                                                                                                                   Length 544;
                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                            recombinant
                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                       Gaps
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RESULT 11
AAY44352
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                       Thermostable DNA dependent polymerase; nuclease activity; "aq polymerase; mutant; Polymerase Chain Reaction, PCR; N-terminal domain; proteolytic; thermal stability, hydrophilic solution; sequencing; labeling; diagnosis; genetic disorder; primer driven mutagenesis; identification of pathogen; mutational analysis; forensic identification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       associated. The polymerase is thermostable and possesses new or improved catalytic properties compared to known nucleic acid polymerases. The polymerase eliminates the need to specifically develop multi-enzyme reaction mixtures, which are often difficult to optimise and expensive to use. The polymerase facilitates rapid, efficient and accurate generation of nucleic acid molecules, particularly in regard to PCR protocols. The polymerase is also useful for nucleic acid polymerisation which is useful in genetic engineering techniques and molecular biology.
       11-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 12; Page 46-49; 93pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chimeric nucleic acid polymerase for nucleic acid polymerization and generation of nucleic acids, comprises two enzymatically active domains
                                  16-DEC-1999
                                                               W09964438-A1
                                                                                                                                                                                                                             Synthetic
                                                                                                                                                                                                                                           Thermus aquaticus.
                                                                                                                                                                                                                                                                                                                                                              Thermostable DNA dependent mutant Taq polymerase-1.
                                                                                                                                                                                                                                                                                                                                                                                             14-MAR- 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY44352 standard; Protein; 553 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-536571/59.
                                                                                                                         Region
                                                                                                                                                                                   Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a chimeric nucleic acid polymerase comprising at least two enzymatically active domains which are non-naturally
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present protein sequence is Thermus aquaticus (Taq) DNA polymerase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      which are non-naturally associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Loeffert D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (QIAG-) QIAGEN GMBH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-FEB-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 LSQELAIPYEE 11
|||||||||
398 LSQELAIPYEE 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   552 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Missel A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2001WO-EP01790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2000US-0506153
                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
       99WO-US13305
                                                                                                                                    Thermus aquaticus"
                                                                                                                                                   /label= Nine_residue_domain
/note= "40-50% identical to
                                                                                                                                                                                               Location/Qualifiers
                                                                                          /note= "Identical to residues 289\text{-}832 of native Thermus aquaticus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ۲.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 0.078;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 54; DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                     residues 280-288 of native
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 552;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QУ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local

    1 LSQELAIPYEE 11

Claim 3; Page 39-44; 79pp; English
                                                                                        WPI; 1995-006692/01.
N-PSDB; AAQ79545.
                                                                                                                                     Barnes WM;
                                                                                                                                                                                             19-FEB-1993;
22-FEB-1994;
                                                                                                                                                                                                                                         22-FEB-1994;
                                                                                                                                                                                                                                                                                                    W09426766-A
                                                                                                                                                                                                                                                                                                                                Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                      10-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAZ29460
                                                                                                                                                                (BARN/) BARNES
                                                                                                                                                                                                                                                                       24-NOV-1994.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR66209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-105869/09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          399 LSQELAIPYEE 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Qui Z;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             553 AA;
                                                                                                                                                                W M
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The present amino acid sequence is a novel, thermostable DNA dependent mutant Taq polymerase-! enzyme. The N-terminal domain, includes a sequence of 9 amino acids, that has 40-50% sequence identity with residues 280-280 of native Thermus aquaticus polymerase, Taq. The residues 10-53 of this polymerase sequence is identical to residues 289-832 of Taq polymerase. This sequence has no significant nuclease activity, but good proteolytic and thermal stabilities and improved solubility in hydrophilic solutions. This sequence is used for synthesis of polymucleotides, particularly in polymerase chain reaction (PCR) hased processes, like sequencing, labeling, primer-driven mutagenesis, diagnosis of genetic disorders, identification of pathogens, mutational analysis and forensic identification.
DNA polymerase and formulations comprising it - allowing the amplification of sequences up to 35 kilobases and reducing the mutagenicity generated by the PCR process.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Thermostable polymerase; Klentay 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel thermostable DNA polymerase Klentaq-278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 16; Fig 2; 32pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR66209 standard; Protein; 554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel enzyme, particularly useful in polymerase chain reaction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (CLON-) CLONTECH LAB INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98US-0096399.
                                                                                                                                                                                                                                                                                                                                                            93US-0021623
94US-0021623
                                                                                                                                                                                                                                                                                                                                                                                                                                                     94WO-US01867
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 54;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ΑA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.078;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 553;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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AAX44353
ID AAY444353
XX AAY444353
AC AAY44
AC AAY44
AC Thern
Thern
Thern
KW Thern
KW Thern
KW Thern
KW Genet
KW Genet
KW Thern
OS Synth
XX Synth
FT Domai
FT Domai
FT Domai
FT Regic
  맑
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          X00000000000000000XX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CC Kientaq-278 is a thermostable polymerase lacking 3'-exonuclease activity. The AA sequence is substantially the same AA sequence as CC Thermus aquaticus DNA polymerase but lacks the N-terminal 280 AAS. A CC DNA encoding such a polymerase is claimed, as is the polymerase CC itself. The polymerase also has substantially the same AA sequence CC as that of Thermus flavus, but excludes the N-terminal 279 AAs. Primers AAO79543, AAO79553 and AAO79554 can be used for the CC amplification of the gene for KlemTaq-278. Essentially the same CC primers can be used for the amplification of the analagous gene from CC Thermus flavus (see AAO79543, AAO79556, AAO7957). An intiator Met and a CC Gly occupy the first two N-terminal posns of Klentaq-278, CC praviously occupied by residues 279 and 280 of T. aquaticus CC DNA polymerase, followed by the AA sequence of wt T. aquaticus CC DNA polymerase, followed by the AA sequence of Roman advance CC Plasmid pw854b contains the sequence in AAO79545.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
  WPI; 2000-105869/09
                           Wurst H,
                                                                             11-JUN-1998;
                                                                                                       11-JUN-1999;
                                                                                                                                                         WO9964438-A1
                                                                                                                                                                                                                                                              Domain
                                                                                                                                                                                                                                                                                                                                                       Thermus aquaticus Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                             mutational analysis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY44353;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY44353 standard; Protein; 559 AA.
                                                   (CLON-) CLONTECH LAB INC
                                                                                                                                 16-DEC-1999
                                                                                                                                                                                                          Region
                                                                                                                                                                                                                                                                                                                  Domain
                                                                                                                                                                                                                                                                                                                                                                                                                       tnermal
                                                                                                                                                                                                                                                                                                                                                                                                                                    mutant;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Thermostable DNA dependent polymerase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Thermostable DNA dependent mutant Taq polymerase-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       400 LSQELAIPYEE 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 LSQELAIPYEE 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        l Similarity
11; Conser
                                                                                                                                                                                                                                                                                                                                                                                          table DNA dependent polymerase; nuclease activity; Tag polymerase; Polymerase Chain Reaction; PCR; N-terminal domain; proteolytic; stability; hydrophilic solution; sequencing; labeling; diagnosis; disorder; primer-driven mutagenesis; identification of pathogen; nal analysis; forensic identification.
                         Qui Z;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA;
                                                                             98US-0096399
                                                                                                       99WO-US13305
                                                                                                                                                                                                                     /label= Nine_residue_domain
/note= "40-50% identical with
Thermus aquaticus"
                                                                                                                                                                                                                                                                         Thermus aquaticus"
                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                     /note= "40-50% identical to N-terminal
                                                                                                                                                                               /note= "Identical to residues 289-832 of native
                                                                                                                                                                                                                                                                                                   /label- Leader_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 54; DB 16
Pred. No. 0.078;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
                                                                                                                                                                                                                                    residues 280-288 of native
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 554;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                        domain of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
RESULT 14
AAR99544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                     03-NOV-1995;
                                                                                                                                                                                           Swaminathan
                                                                                                                                                                                                                                                           04-NOV-1994;
                                                                                                                                                                                                                                                                                                                                         W09614417-A
                                                                                                                                                                                                                                                                                                                                                                  Thermus flavus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                   WPI; 1996-251767/25
                                                                                                                                                                                                         Mueller RD,
                                                                                                                                                                                                                                                                                                               17 - MAY - 1996
                                                                                                                                                                                                                                                                                                                                                                                                      polymerase chain reaction;
                                                                                                                                                                                                                                                                                                                                                                                                                   DNA polymerase; thermostable;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR99544;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          405 I.SQELAIPYEE 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 LSQELAIPYEE 11
                                                                                                                                                                                                                                                                                                                                                                                          ligase chain reaction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20; Fig 4; 32pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             559 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                        Nickerson DA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                           9408-0334640
                                                                                                                                                                                                                                                                                     95WU-US14418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ).0%;
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SXCCCCCCCCCCX PX PX X R
polymerase enzyme retrieved from the culture supernatant. Such recombinantly produced polymerase can be used in applications such as DNA sequencing, DNA amplification, thermal cycle labelling (TCL)
                                                                                DNA encoding a thermostable polymerase can be inserted into expression vector which in turn can be used to transform cel transformed cells can then be cultured and the thermostable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The residues 16-559 of this polymerase sequence is identical to residues 289-832 of Tag polymerase. This sequence has no significant nuclease activity, but good proteolytic and thermal stabilities and improved solubility in hydrophilic solutions. This sequence is used for synthesis of polymucleotides, particularly in polymerase chain reaction (PCR) based processes, like sequencing, labeling, primer-driven mutagenesis, diagnosis of genetic disorders, identification of pathogens, mutational
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present amino acid sequence is a novel, thermostable DNA dependent mutant Taq polymerase-2 enzyme. The N-terminal domain, includes a sequence of 15 amino acids, that has 40-50% sequence to dentity with N-terminal residues of native Thermus aquaticus polymerase, Taq.
                                                                                                                                                                                               Disclosure; Page 93-95; 139pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR99544 standard; Protein; 560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    analysis and forensic identification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel enzyme, particularly useful in polymerase chain reaction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAZ29461
                                                                                                                                                                                                                                                                                                         DNA encoding thermostable Thermus flavus DNA polymerase - useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (MOLE-) MOLECULAR BIOLOGY RESOURCES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Thermus flavus DNA polymerase I exonuclease free fragment.
                                                                                                                                                                                                                                                      sequencing, polymerase chain reaction, thermal cycle labelling ligase chain reaction, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   universal thermal cycle labelling; UTCL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Piehl RF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 54; DB 21
Pred. No. 0.079;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequencing; amplification; PCR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ã
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Skowron PM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 559;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                               nto an
cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
     (TCL),
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RESULT 15
AAR96-205
XX AAR96-
XX DNA |
XW DNA |
XX DNA |
XX
Ъ
                                                    δÃ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        32 X 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local S
Matches 11
                                                                                                               Query Match 100.0%; Score 54; DB 17; Length 560; Best Local Similarity 100.0%; Pred. No. 0.079; Matches 11; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                              The present sequence is that of a truncated Thermus flavus DNA polymerase I, which is exonuclease-free, and corresponds to amino acids 275 to 834 of AAR96203. A vector lacking the 5' one-third of the T. flavus DNA polymerase I was generated. The ATC startcodon of lack was brought in frame with the DNA encoding amino acids 239 to 834 of the Tfl DNA pol I holoenzyme using site-directed mutagenesis. This was used to generate the present sequence. This recombinant polymerase is thermostable and can be used in applications such as DNA sequencing, polymerase chain reaction, (universal) thermal cycle labelling and ligase chain reaction.
                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04-NOV-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA polymerase I; truncated; exonuclease free; holocnzyme; universal; DNA sequencing; amplification; polymerase chain reaction; ligase chain reaction; thermal cycle labelling.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA polymerase I exonuclease-free fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR96205;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR96205 standard; Protein; 560 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          universal thermal cycle labelling (UTCL) and ligase chain reaction (LCR). This fragment of the exonuclease free fragment of DNA polymerase I retains its polymerase activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 93-95; 139pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 useful for DNA sequencing, polymerase chain reaction, thermal cycle labelling and ligase chain reaction, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Biologically active fragments of Thermus Flavus DNA polymerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1996-251756/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mueller RD, Piehl RF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 03-NOV-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-MAY-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             W09614405-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Thermus flavus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29-NOV '995 (first entry)
                                                                                                                                                                                                                                                                                                             chain reaction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAT27255.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (MOLE-) MOLECULAR BIOLOGY RESOURCES INC.
406 LSQELAIPYEE 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               406 LSQELAIPYEE 416
                                                           ш
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 LSQELAIPYEE 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 100. es 11; Conservative
                             LSQELAIPYEE 11
                                                                                                                                                                                                                                               560 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        560 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94US-0334645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95WO-US15327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Skowron PM, Swaminathan N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 54; DB 17; Length 560; Pred. No. 0.079; Mismatches 0; Indels
                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
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Search completed: January 15, 2003, 11:20:14 Job time: 28.2857 secs

4. Appli 2. Appli 2. Appli 2. Appli 2. Appli 3. Appli 4. Appli 6. A. Appli 6. Appli 6.

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Minimum DB
Maximum DB
                                                                                                                                                                                                                                                                                                                                  Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Total number
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Title:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OM protein -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Database :
                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                    Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq length: 0
seq length: 2000000000
of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein search, using sw model
                                                                                                                                                                                                                                                                                                                                    Query
Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-823-649A-4
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         Issued_Patents_AA:*
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
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                                US-07-977-434-6
US-08-458-6119-6
PCT-US-10-10705-6
PCT-US-10-73-384C-5
US-08-254-359A-5
US-08-481-238-5
US-08-481-956-5
US-08-481-956-5
US-08-757-653-5
US-08-759-491-5
US-08-753-516-5
US-08-759-038-5
US-08-90-359-96-90
US-08-90-946-90
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; Patent No. 5466591
; GENERAL INFORMATION:
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US-07-977-434-6
                                                                                                   APPLICATION NUMBER: US 590
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 523
FILING DATE: 15-MAY-1990
PRIOR APPLICATION UNDER: US 143
APPLICATION UNDER: US 143
FILING DATE: 12-JAN-1988
PRIOR APPLICATION DATA:
APPLICATION UNDER: US 143
FILING DATE: 12-JAN-1988
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Gelfand, Do APPLICANT: Abramson, I TITLE OF INVENTION: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 28-SEP-PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA: US 590,490
                                                                                                                                                                                                                                                                                                                                    SOFTWARE: WordPerfect 2.1 CURRENT APPLICATION DATA:
 PRIOR APPLICATION DATA
                                 PRIOR APPLICATION DATA:
                                                                    FILING DATE: 17-JUN-
PRIOR APPLICATION DATA:
                                                                                                                                                                                                              FILING DATE: 28-SEP-1990 PRIOR APPLICATION DATA:
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STREET: 34
CITY: Nutl
STATE: New
ZIP: 07110
           APPLICATION NUMBER: US 746,121 FILING DATE: 15-AUG-1991
                                            APPLICATION NUMBER: US 8 FILING DATE: 22-AUG-1986
                                                                              APPLICATION NUMBER: US 0: FILING DATE: 17-JUN-1987
                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/07/977,434
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                                                                                                                                                                                                                                                                                                                                                                                                                                           340 Kingsland Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gelfand, David
                                                                                                                                                                                                                                                                                                                                                                     Macintosh
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5' TO 3' EXONUCLEASE MUTATIONS
THERMOSTABLE DNA POLYMERASES
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                                                                                                                                                                                                                                       US 590,466
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                                                                                            US 063,509
                                                                                                                                                                                                   US 590,213
                                                         US 899,241
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US-09-777-538-2
US-09-777-538-2
US-07-977-434-2
US-08-156-020-6
US-08-156-020-6
US-08-156-020-10
US-08-156-020-10
US-08-156-020-10
US-08-156-020-10
US-08-156-020-10
US-08-156-020-10
US-08-156-020-10
US-08-158-020-10
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US-08-458-819-6
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Patent No. 5795762
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            FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 590,213
                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/977,434
FILING DATE: 23-FEB-1993
                                                                                                                                                                                                                                                             SOFTWARE: WordPerfect 2.1
CURRENT APPLICATION DATA:
                                                                                          FILING DATE: 28-SEP-1990 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:

ADDRESSEE: Hoffmann-La Roche inc.
STREET: 340 Kingsland Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Gelfand, David H.
APPLICANT: Abramson, Richard D.
TITLE OF INVENTION: 5' TO 3' EXONUCLEASE MUTATIONS OF
TITLE OF INVENTION: THERMOSTABLE DNA POLYMERASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION: TELEPHONE: (510) 814-2972
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                                                                                                                                                                                                                                                                                                                                                                                        STATE: Notley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
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APPLICATION NUMBER: US 609, 157
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CLASSIFICATION: 435
                                                                                                                                APPLICATION NUMBER: US 590,490
FILING DATE:
                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/458,819
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SOFTWARE: WordPer
                                                                                                                                                                                                                                                                                                                              COMPUTER:
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Local Similarity 90.9%;
Les 10; Conservative
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                                                    UMBER: US 590,466
28-SEP-1990
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28-SEP-1990
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Pred. No. 0.
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// TOPOLOGY: linear
// MOLECULE TYPE: protein
US-08-458-819-6

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Best Local Similarity 90.9
Matches 10; conservative
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FILING DATE: 22-AUG ...
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 746,123
APPLICATION NUMBER: 15-AUG-1991
                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                            NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                              APPLICANT: Abramson, Richard D.
TITLE OF INVENTION: 5' TO 3' EXONUCLEASE MUTATIONS OF
TITLE OF INVENTION: THERMOSTABLE DNA POLYMERASES
                                                                                                                                                                                                                                                     APPLICANT: Gelfand, David H. APPLICANT: Abramson, Richard
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LENGTH: 830 amino acids
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APPLICATION NUMBER:
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APPLICATION NUMBER: WO PCT/US90/07641
FILLING DATE: 21-DEC-1990
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APPLICATION NUMBER:
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                                                                              STATE: Ca.
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                                                                                                                             CITY:
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                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                        SSEE: Cetus Corporation
T: 1400 Fifty-third Street
Emeryville
: California
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WordPerfect 5.0
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20-SEP-1990
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RESULT 4
US-08-073-384C-5
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                                   Sequence 5, Application US/08073384C Patent No. 5541311 GENERAL INFORMATION:
                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                       Best Local Similarity
                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 6:
APPLICANT: Dahlberg, James E. APPLICANT: Lyamichev, Victor 1.
                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE_TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: Ca. TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 143,441 FILING DATE: 12-JAN-1988 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 24-JUL-1990 ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER:
FILING DATE: 21-DEC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 89 FILING DATE: 22-AUG-1986 PRIOR APPLICATION DATA:
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APPLICATION NUMBER: PC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 585,471 FILING DATE: 20-SEP-1990
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AMINO ACID
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                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                       Score 48; DB 5
Pred. No. 0.34;
                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                       DB 5;
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US-08-254-359A-5
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Best Local Simi
Thes 10;
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                                                                                                                                                                                                                                                                     APPLICANT: DAHLBERG, JAMES E.
APPLICANT: LYAMICHEV, VICTOR I.
APPLICANT: HROW, MARY ANN D.
TITLE OF INVENTION: 5' NUCLEASES DERIVED FROM THERMOSTABLE
TITLE OF INVENTION: DNA POLYMERASE
NUMBER OF SEQUENCES: 40
SOFTWARE: PALLULIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/254,359A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 07/986,330 FILING DATE: 07-DEC-1992 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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TITLE OF INVENTION: SYNTHESIS-D
TITLE OF INVENTION: POLYMERASE
TOTAL OF SPONENCES: 29
                                                                                                                    COMPUTER READABLE FORM:
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                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                        ADDRESSEE: HAVEKSTOCK, MADDLESSEE: 220 MONTGOMERY STREET, SUITE 2200 CITY: SAN FRANCISCO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                  MEDIUM TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 94104
                                                                                                                                                        COUNTRY:
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220 Montgomery Street, Suite 2200
                                                                                                                                                        UNITED STATES OF AMERICA
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                                                                                                Floppy disk
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INFORMATION FOR SEQ ID NO:
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APPLICANT: Dahlbe
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                               REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: FORS-00613
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/705-8410
                                                                                                               PRIOR APPLICATION NUMBER: US 08/073,384
FILING DATE: 04-UN-1993
APPLICATION NUMBER: US 07/986,330
AFILING DATE: 07-DEC-1992
ATTORNEY/AGENT INFORMATION:
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APPLICANT: Brow, Mary Ann D.
TITLE OF INVENTION: SYNTHESIS-DI
TITLE OF INVENTION: POLYMERASE
                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
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ADDRESSEE: HAVERSTOCK, MEDLEN & CARROLL
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APPLICATION NUMBER: 1
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                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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Local Similarity 90.98;
es 10; Conservative
                                                                                                                                                                                                                                            APPLICATION NUMBER: US/OFILING DATE: 06-JUN-1995
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                                                                                                                                                                                                                               CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE:
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STRANDEDNESS: si
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                                                                                                                                                                                                                                                                                                                                                                                           94104
                                                                                                      Carroll,
                                                                                                                                                                                                                                                                                                                                                                                                                             California
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                  415/397-833
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                                                                                                    Peter G.
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Pred. No. 0.34;
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                                                            Matches
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Best Local Similarity
Matches 10; Conserv
                                                                            Best
                                                                                        Query Match
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                                                                                                                                                                                                                         TELEFAX: (415) 397-83 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 831 amino acids
                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patenlin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
                                                                                                                                MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION: NAME: CARROLL, PETER G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: DAHLBERG, JAMES E.
APPLICANN: LYAM (CHEY, VICTOR I.
APPLICANN: BROW, MARY ANN D.
TITLE OF INVENTION: SYNTHESIS-DEFICIENT THERMOSTABLE DNA
TITLE OF INVENTION: POLYMERASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 831 amino acids
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677 LSGELSIPYEE 687
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                                                         Local Similarity hes 10; Conserv
                                                                                                                                                         STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                          FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                 TYPE:
                                                                                                                                                                                                                                                      TELEPHONE:
                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER:
                             1 LSXELSIPYEE 11
                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94104
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                                                                                                                                                                            amino acid
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                                                           Conservative
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 Mismatches

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                                                                     Score 48; DB 1
Pred. No. 0.34;
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Pred. No. 0.34;
                                                                                   DB 1;
                                                                                   Length 831;
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; Sequence 5, Application US/08471066B
; Patent No. 5837450

RESULT 8 US-08-471-066B-5

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                                                                                                                                                                                                    Sequence 5, Application US/08484956 Patent No. 5843654
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Best Local Similarity
                                                                                                                                                                                     GENERAL INFORMATION:
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                                                                                                                                   APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC comparible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                   NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: FORS-01800
TELECOMMUNICATION INFORMATION:
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                                                                                      TITLE OF INVENTION: DETECTION OF p53 MUTATIONS
                                                                                                       APPLICANT:
                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 08/073,384
FILING DATE: 04-JUN-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08
FILING DATE: 06-JUN-1994
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                     677 LSGELSIPYEE 687
      STREET: 220 MONTGOMERY STREET, SUITE 2200 CITY: SAN FRANCISCO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/471,066B FILING DATE: 06-JUN-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 07/986,330 FILING DATE: 07-DEC-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
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                                       ADDRESSEE:
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Brow, Mary Ann D.
WENTION: 5' Nucleases Derived From Thermostable
                                                                                                                                   BROW, MARY ANN D.
                                                                                                    HEISLER,
                                                                                                                                                                     DAHLBERG, JAMES E.
                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                     OLDENBURG, MARY C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dahlberg, James E.
                                     HAVERSTOCK, MEDLEN & CARROLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (415) 705-8410
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Pred. No. 0.34;
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US-08-757-653-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE:
   COMPUTER:
                                                                                                                                   ADDRESSEE:
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E: Floppy disk
IBM PC compatible
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Sequence 5, Application US/08757653
Patent No. 5843669
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STREET: 220 ACC. CITY: San Francisco STATE: California
                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                          APPLICANT: Lyamichev, Victor I.

APPLICANT: Lyamichev, Natasha
TITLE OF INVENTION: Cleavage Of Nucleic Acid Using
TITLE OF INVENTION: Thermostable FEN-1 Endonucleases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
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PRIOR APPLICATION NUMBER: US 08/402,601
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                                                                                                               NUMBER OF SEQUENCES:
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APPLICATION NUMBER: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: FORS-01801
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                                                      220 Montgomery Street, Suite 2200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   831 amino acids
 United States Of America
                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                          Kaiser, Michael W.
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                                                                          Medlen & Carroll, LLP
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Pred. No. 0.34;
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US-08-599-491-5
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                                                                                                TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: BROW, MARY ANN D.
APPLICANT: GROTELUESCHEN HALL,
APPLICANT: LYANICHEW, VICTOR
APPLICANT: OLIVE, DAVID M.
                                                                                                                   TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 705-8410 TELEFAX: (415) 397-8338
                                                                                                                                                                                             FILING DATE: 23-JAN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: INGOLIA, DIANE E
REGISTRATION NUMBER: P-40,027
                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORREST JNDENCE ADDRESS:
ADDRESSEE: MEDLEN & CARROLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: DETECTION OF NUCLEIC ACID SEQUENCES BY TITLE OF INVENTION: INVADER-DIRECTED CLEAVAGE NUMBER OF SEQUENCES: 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 831 amino acid
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                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                REFERENCE/DOCKET NUMBER: FORS-01802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Ingolia, Diane E. REGISTRATION NUMBER: 40,027
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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STREET: 220 MONTGOMERY STREET, SUITE 2200
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                        STRANDEDNESS:
                                         TYPE: amino acid
                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/599,491
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                                                           ENGTH:
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                                                         831 amino acids
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Pred. No. 0.34;
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; Sequence 5, Application US/08823516
; Patent No. 5994069
                                         US-08-823-516-5
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us-08-756-386-5
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; Patent No. 5985557
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Best Local Similarity
Matches 10; Conserv
                                                                                      Query Match
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                                                         Best Local Similarity Matches 10; Conserv
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                                                                                                                                 MOLECULE TYPE: protein
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COMPUTER READABLE FORM:
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LENGTH: 831 amino acids
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CURRENT APPLICATION DATA:
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PRIOR APPLICATION DATA:
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677 LSGELSIPYEE 687
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                                                                                                                                                                                                                                                                                                                NAME:
                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 08/599,491 FILING DATE: 24-JAN-1996
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CITY: San Francisco
                             1 LSXELSIPYEE 11
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Lyamichev, Victor I.
NVENTION: Invasive Cleavge Of Nucleic Acids
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                                                                                                                                                                                                                                       (415)
                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IBM PC compatible
                                                                                                                                                 linear
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                                                                       96.0%;
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Pred. No. 0.34;
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Pred. No. 0.34;
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Jeff S

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RESULT 14
US-08-682-853A-5
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Sequence 5, Application US/08682853A Patent No. 6001567
GENERAL INFORMATION:
APPLICANT: Brow, Mary Ann D.
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SEQUENCE CHARACTERISTICS:
LENGTH: 831 amino acids
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                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
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PRIOR APPLICATION NUMBER: US 08/756,386
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APPLICATION NUMBER: US 08/759,038
FILING DATE: 02-DEC-1996
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APPLICATION NUMBER: I
FILING DATE: 21-JAN-1
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ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: 0
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                                                                                                                                           677 LSGELSIPYEE 687
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OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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02-DEC-1996
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90.9%;
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; Patent No. 6090543
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Best Local Similarity 90.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (415) 397-83 INFORMATION FOR SEQ ID NO:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                     APPLICANT: Prudent, James R.
APPLICANT: Hall, Jeff G.
APPLICANT: Lyamichev, Victor I.
APPLICANT: Erow, Mary Ann D.
APPLICANT: Dahlberg, James E.
TITLE OF INVENTION: Cleavage Of Nucleic Acids
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APPLICANT:
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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APPLICANT:
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APPLICATION NUMBER: 1
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                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                        677 LSGELSIPYEE 687
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COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 220 Montgome
CITY: San Francisco
                                                                       COUNTRY:
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                                                                                                           CITY:
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                                                                                                          T: 220 Montgomery Street, Suite 2200
San Francisco
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220 Montgomery Street, Suite 2200
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Lyamichev, Victor
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COPERATING SYSTEM: PC-DOS/MS-DOS

SOUTWARE: Patentin Release #1.0, Version #1.30

LORERNY APPLICATION DATA:

APPLICATION NUMBER: US/08/759,038

FILING DATE: 02-DEC-1996

FILING DATE: 29-NOV-1996

FILING DATE: 12-UIL-1996

FILING DATE: 29-NOV-1996

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Minimum DB
Maximum DB
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Sequence:
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Listing first 45 summaries
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seq length: 2000000000
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Gapop 10.0 , Gapext 0.5
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6,	373	Sequence 585, App	58,	2	` '	13,	'n	Sequence 13, Appl	2	Sequence 14, Appl	Sequence 3, Appli	Sequence 14, Appl	Sequence 3, Appli	Sequence 3, Appli	2, ,	2, 4	Sequence 26, Appl	23,	20,	15,	Sequence 11, Appl	0	Sequence 6, Appli	`	Sequence 8, Appli

ALIGNMENTS

; Sequence 4, Application US/09823649A; Patent No. US20020012970A1; GENERAL INFORMATION:

Smith, Edward Elfstrom, Carita Gelfand, David

APPLICANT: Smith,
APPLICANT: Elfst
APPLICANT: Gelfar
APPLICANT: Higuel

US-09-823-649A-4

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; NAME/KEY: VARIANT
; LOCATION: (3)...(3)
; OTHER INFORMATION: X is Q or G
US-09-823-649A-4
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                                                            Query Match 96.0
Best Local Similarity 100.
Matches 11; Conservative
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                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US 60/198,336 PRIOR FILING DATE: 2000-04-18
                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Wang, Alice
TITLE OF INVENTION: HIGH TEMPERATURE REVERSE TRANSCRIPTION USING MUTANT DNA POLYM
                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 21
                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: RPA1006
                                                                                                                                                                                             FEATURE:
OTHER INFORMATION: sequence motif
                                                                                                                                                                                                                                ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                 LENGTH: 11
1 LSXELSIPYEE
                   1 LSXELSIPYEE 11
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Myers, Thomas
Schoenbrunner, Nancy
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RESULT 2 US-09-823-649A-9

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US-09-823-649A-14
Sequence 14, Application US/09823649A
Fatent No. US20020012970Al
GENERAL INFORMATION:
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Best Local Similarity
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Best Local Similarity
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CURRENT FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: US 60/198,336
PRIOR FILING DATE: 2000-04-18
NUMBER OF SEQ ID NOS: 21
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PRIOR FILING DATE: 2000-04-18
NUMBER OF SEQ ID NOS: 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: HIGH TEMPERATURE REVERSE TRANSCRIPTION USING MUTANT DNA POLYMERA: FILE REFERENCE: RPA1006
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TYPE: PRT
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TYPE: PFT
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Gelfand, David
Higuchi, Russell
Myers, Thomas
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Schoenbrunner, Nancy
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Gelfand, David
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90.9%;
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Pred. No. 0.00
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US-10-033-297-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Thermus filiformis US-09-823-649A-14
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LENGTH: 11
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Best Local Similarity 90.9%;
Matches 10; Conservative
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                   PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/350,597

FILING DATE: 09-Jul-1999

APPLICATION NUMBER: US/08/823,516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Medlen & Carroll,
                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Detection Of Nucleic Acids By Multiple Sequential Invasive Cleavages
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Hall, Jeff G.
                                                                 APPLICATION NUMBER: PCT/US97/01072
FILING DATE: 21-JAN-1997
APPLICATION NUMBER: US 08/759,038
FILING DATE: 02-DEC-1996
APPLICATION NUMBER: US 08/758,314
FILING DATE: 02-DEC-1996
                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/10/033,297
FILING DATE: 12-No. US20020187486A1-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: San Francisco
APPLICATION NUMBER: US 08/756,386
FILLING DATE: 29-NOV-1996
APPLICATION NUMBER: US 08/682,853
FILLING DATE: 12-JUL-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: United States Of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 220 Montgomery Street, Suite 2200
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Higuchi, Russell
Myers, Thomas
                                                                                                                                                                                    FILING DATE: 24-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wang, Alice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Elfstrom, Carita
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mast, Andrea L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Brow, Mary Ann D.
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FILE REFERENCE: RPA1006
CURRENT APPLICATION NUMBER: US/09/823,649A
CURRENT FILING DATE: 2001-03-30
                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US 60/198,336 PRIOR FILING DAVE: 2000-04-18 NUMBER OF SEQ (I) NOS: 21 SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: HIGH TEMPERATURE REVERSE TRANSCRIPTION USING MUTANT DNA POLYMI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Smith, Edward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Schoenbrunner, Nancy
  0,
                      Score 48; DB 10
Pred. No. 0.001;
                                                 DB 10; Length 11;
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SEQUENCE DESCRIPTION: SEQ ID NO: 5: US-10-033-297-5
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Best Local Similarity 90.9%;
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                                                                         INFORMATION FOR SEQ ID NO: 5:
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                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/081,806
FILING DATE: 22-Feb-2002
                                   SEQUENCE CHARACTERISTICS:
LENGTH: 831 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 94104
COMPUTER READABLE FORM:
                                                                                                               TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 705-8410
                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION: Invasive Cleavge Of Nucleic Acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Prudent, James R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10; Conservative
                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/756,386 FILING DATE: <UIDKNOWD>
APPLICATION NUMBER: US 08/682,853 FILING DATE: 12-UUL-1996
APPLICATION NUMBER: US 08/599,491 FILING DATE: 24-JAN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: San Francisco
STATE: California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 08/599,491 FILING DATE: 24-JAN-1996
   STRANDEDNESS: single
                                                                                             TELEFAX: (415)
                                                                                                                                                    REFERENCE/DOCKET NUMBER: FORS-02564
                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 220 Montgomery Street, Suite 2200
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                                                                                                                                                                        REGISTRATION NUMBER: 40,027
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                                                                                                                                                                                            NAME:
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                     amino acid
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                                                                                               397-8338
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Pred. No. 0.13;
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SEQ ID NO 8
LENGTH: 11
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LENGTH: 11
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Query Match
Best Local Similarity
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CURRENT APPLICATION NUMBER: US/09/823,649A CURRENT FILING DATE: 2001-03-30 PRIOR APPLICATION NUMBER: US 60/198,336 PRIOR FILING DATE: 2000-04-18 NUMBER OF SEQ ID NOS: 21 SOFTMARE: Patentin version 3.0
                                                                                                                                                                                                                                              APPLICANT: Smith, Edward APPLICANT: Elfstrom, Car APPLICANT: Gelfand, Dav.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/823,649A CURRENT FILING DATE: 2001-03-30 PRIOR APPLICATION NUMBER: US 60/198,336
                                                                                                                        TITLE OF INVENTION: HIGH TEMPERATURE REVERSE TRANSCRIPTION USING MUTANT DNA POLYME FILE REFERENCE: RPA1006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE: 2000-
NUMBER OF SEQ ID NOS: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: HIGH TEMPERATURE REVERSE TRANSCRIPTION USING MUTANT DNA POLYME FILE REFERENCE: RPA1006
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: sequence motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Artificial Sequence
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SEQUENCE DESCRIPTION: SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Schoenbrunner, Nancy
Wang, Alice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
                                                                                                                                                                                                                                                              Elfstrom, Carita
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                                                                                                                                                             Wang, Alice
                                                                                                                                                                                                        Myers, Thomas
                                                                                                                                                                                                                                            Gelfand, David
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                                                                                                                                                                                Schoenbrunner, Nancy
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81.8%;
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Pred. No. 0.0039;
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US-09-823-649A-11
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Best Local Similarity 81.0
Conservative
                                                          SOFTWARE: PatentIn version 3.0 SEQ ID NO 11
                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                           Sequence 11, Application US/09823649A Patent No. US20020012970A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 21
SOFTWARE: PatentIn version*3.0
SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION
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                                                                                                          CURRENT APPLICATION NUMBER: US/09/823,649A
CURRENT FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: US 60/198,336
PRIOR FILING DATE: 2000-04-18
                                                                                                                                                                           TITLE OF INVENTION: HIGH TEMPERATURE REVERSE TRANSCRIPTION USING MUTANT DNA POLYMERAS FILE REFERENCE: RPA1006
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APPLICANT: Elfstrom, Carita
APPLICANT: Gelfand, David
                                                                                           NUMBER OF SEQ ID NOS: 21
                                                                                                                                                                                                                                                                                             APPLICANT: Smith, Edward APPLICANT: Elfstrom, Ca
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            ORGANISM: Thermus sp. 205
                             TYPE: PRT
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                                            LENGTH: 11
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Gelfand, David
Higuchi, Russell
Myers, Thomas
Schoenbrunner, Nancy
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Schoenbrunner, Nancy
Wang, Alice
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Pred. No. 0.0039;
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Pred. No. 0.0039;
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US-10-033-297-4
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Publication No. US20020187486A1
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APPLICANT:
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Best Local Similarity
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Best Local
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                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Detection Of Nucleic Acids By Multiple
Sequential Invasive Cleavages
                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
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APPLICATION NUMBER: US/10/033,297
FILING DATE: 12-No. US20020187486A1-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                         STREET: 220 Montgomery Street, Suite 2200 CITY: San Francisco
                                                                                                                                                                                      COUNTRY: United States Of America
                                                                                                                                                                                                          STATE: California
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Lyamichev, Victor I.
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81.8%;
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Pred. No. 0.00
1; Mismatches
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Pred. No. 0.0039;
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US-09-972-834-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   678 LSQELAIPYEE 688
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                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/972,834
FILING DATE: 04-Oct-2001
CLASSIFICATION: CUnknown>
PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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NAME: Ingolia, Diane E.
REGISTRATION NUMBER: 40,027
                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: CAMPBELL & FLORES LLP
STREET: 4370 La Jolla Village Drive,
                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Thermostable Polymerases Having Altered Fidelity and Methods of Identifying and Using Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS: NO. US20020187486A1 Relevant
TOPOLOGY: NO. US20020187486A1 Relevant
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
3-297-4
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                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 11
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                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                     STATE: California
                                                                                                                                                                                                                                                                                                             CITY: San Diego
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APPLICATION NUMBER: US 08/599,491
FILING DATE: 24-JAN-1996
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                   APPLICATION NUMBER: 08/978,806
                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                              ZIP: 92121
                                                                                                                                                                                                                                                                 COUNTRY: United States
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APPLICATION NUMBER: US 08/682,853
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FILING DATE: <Unknown>
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81.8%;
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TYPE: PRT
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; ORGANISM: Thermus equations 0s\text{-}10\text{-}071\text{-}505\text{-}1
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Publication No. US20020197211A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90.0%;
Best Local Similarity 81.8%;
Matches 9; Conservative
                                                                                                                                                             Sequence 4, Application US/10081806 Publication No. US20020197623A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: TAQ DNA Polymerase Having an Amino Acid Substitution at TITLE OF INVENTION: E681 and Homologs Thereof Exhibiting improved Sait TITLE OF INVENTION: Tolerance FILE REFERENCE: pB9944

CURRENT APPLICATION NUMBER: US/10/071,505

CURRENT FILINC DATE: 2002-02-08

PRIOR APPLICATION UNMER: 607/148,012

PRIOR FILING DATE: 1999-08-10

NUMBER OF SEQ ID NOS: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Davis, Maria APPLICANT: Nelson, Joh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                              Hall, Jeff G. ...

Lyamichev, Victor I.

TITLE OF INVENTION: Invasive Cleavge Of Nucleic Acids NUMBER OF SEQUENCES: 69

CORRECEDENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REPERRICE_/DOCKET WIMBER: P-UW 2873
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619)535-9001
TELEPHAX: (619)535-8949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Finn, Patrick J.
Nampalli, Satyam
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kumar, Shiv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 31,815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Flick, Parke
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nelson, John
ADDRESSEE: Medlen & Carroll, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 832 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                           90.0%; Score 45; DB 9
81.8%; Pred. No. 0.48;
tive 1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 832;
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CITY: Sentaciseo
STATE: California
COMPUTE: California
COMPUTE: Colifornia
COMPUTE: Toliced States Of America
COMPUTE: Toliced States
COMPUTE: Toli
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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence:
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                                                                                                                                                                                                                                                                                                                                                                                                                                    DB DB
                                                                                                                                                                                                                                                                 Score
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   protein search, using sw model
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Match
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pir4:*
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F87631
$50809
T30452
T27289
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JQ0494
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AE3130
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S74356
A97735
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JC7337
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C70133
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A33530
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S25321
AC1580
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endo-1,4-beta-gluc
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glutathione S-tran
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glutathione S-tran
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ALIGNMENTS

C;Species: Thermus aquaticus
C;Date: 03-May-1994 #sequence_revision 20-Feb-1995 #text_change 18-Jun-1999
C;Accession: \$26675; \$24929
R;Akhmetzjanov, A.A.; Vakhitov, V.A.
Nucleic Acids Res. 20, 5839, 1992
A;Title: Molecular cloning and nucleotide sequence of the DNA polymerase gone from Tb A; Reference number: \$26675; MUID:93087201; PMID:1454544
A;Accession: \$26675

DNA-directed DNA polymerase (EC 2.7.7.7) I - Thermus aquaticus

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DNA-directed DNA polymerase (EC 2.7.7.7) - Thermus aquaticus C:Species: Thermus aquaticus C:Date: 04-Sep-1998 #sequence_revision 04-Sep-1998 #text_change 07-May-1999 C:Accession: JX0359 R:Ishino, Y: Ueno, T: Miyagi, M.; Uemori, T.; Imamura, M.; Tsunasawa, S.; Kato, I. J. Biochem. 116, 1019-1024, 1994 A:Title: Overproduction of Thermus aquaticus DNA polymerase and its structural analys A; Reference number: JX0359; MUID:95204371; PMID:7896728 A; Accession: JX0359
                                                                            A;Molecule type: DNA
A;Residues: 1-831 <ISH>
C;Superfamily: DNA-directed DNA polymerase
C;Keywords: nucleotidyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Gene: polI
C;Superfamily: DNA-directed DNA polymerase I
C;Keywords: DNA binding; nucleotidyltransferase
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A; Residues: 1-831 < AKII>
                                                                                                                                                                        A; Status: preliminary
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A;Note: the source is designated as Thermus flavus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Status: translation not shown
  Query Match
Best Local S
Matches 9
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Best Local :
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    Local Similarity
nes 9; Conserv
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10; Conserv
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    Conservative
90.0%; Score 45; DB 2
81.8%; Pred. No. 0.75;
ative 1; Mismatches
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Pred. No. 0.19;
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                                          DB 2;
                                          Length 831;
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    Indels
  0;
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  Gaps
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δÃ

1 LSXELSIPYEE 11

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C;Accession: S46696
R;Latreille, P.
                                          N;Alternate names: hypothetical protein H8025.1
C;Species: Saccharomyces cerevisiae
C;Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 29-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; C.A.; Li, J.H.; Li, Y; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Ma Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H. A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; T. Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis. A;Reference number: A86141; MUID:21016719; PMID:11130712
                                                                                                                                                                                                                                              β
                                                                                                                                                                                                                                                                                      γ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Qy
                                                                                                                   hypothetical protein YHR071w - yeast (Saccharomyces cerevisiae)
                                                                                                                                                      S46696
                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Map position: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Date: 29-Jan-1990 #sequence_revision 29-Jan-1990 #text_change 18-Jun-1999
C;Accession: A33530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ansen, N.F.; Hughes, B.; Huizar, L. Nature 408, 816-820, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R; Theologis, A.; Ecker, J.R.; Palm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-832 <LAW>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R; Lawyer, F.C.; Stoffel, S.; Saiki, R.K.; Myambo, K.; Dr
J. Biol. Chem. 264, 6427-6437, 1989
A; Title: Isolation, characterization, and expression in
A; Reference number: A33530; MUID:89197950; PMID:2649500
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                                                                                                                                                                                                                                                                                                                                        Best Local Similarity Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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Matches 9; Conserv
                                                                                                                                                                                                                                              491 LSNELSVPYDK 501
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                                                                                                                                                                                                                                                                                           1 LSXELSIPYEE 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1451 <STO>
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L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,
                                                                                                                                                                                                                                                                                                                                           ω,
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Pred. No. 15;
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                                                                                                                                                                                                                                                                                                                                           Mismatches
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                                                                                                                                                                                                                                                                                                                                      Caps
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A; Molecule type: DNA
A; Residues: 1-850 <AOF>
A; Cross-references: GB:AE000686; NID:g2983038; PIDN:AAC06656.1; PID:g2983047; GB:AE00
                                                                                                                                                                   A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus A;Reference number: A70300; MUID:98196666; PMID:9537320 A;Accession: G70332
                                               A; Experimental source: strain VF5
                                                                                                                                                                                                                                                                                                                           conserved hypothetical protein aq_367 - Aquifex aeolicus
C:Species: Aquifex aeolicus
C:Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 05-Nov-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Authors: Smith, H.O.; Venter, J.C.
A;Title: Genomic sequence of a Lyme disease spirochaete,
A;Reference number: A70100; MUID:98065943; PMID:9403685
A;Accession: C70133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    conserved hypothetical protein BB0267 - Lyme disease spirochete C;Species: Borrella burgdorferi (Lyme disease spirochete) C;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 08-Oct-1999 C;Accession: C70133
A; Gene: aq_367
                         C; Genetics:
                                                                                                                                     A; Status: preliminary; nucleic acid sequence not
                                                                                                                                                                                                                                                                                R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.;
                                                                                                                                                                                                                                                                                                              C; Accession: G70332
                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 7
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A; Residues: 1-634 <KLE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    son, D.; Peterson, J.; Kerlavage,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Gene: SGD:PCL5
A;Cross-references: SGD:S0001113; MIPS:YHR071w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-229 <LAT>
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A;Description: The sequence of S. cerevisiae
A;Reference number: S46696
                                                                                                                                                                                                                                            Nature 392, 353-358, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Experimental source: strain B31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: GB:AE001137; GB:AE000783; NID:g2688160; PIDN:AAC66681.1; PID:g268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Status: preliminary; nucleic acid sequence not shown; translation not shown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R; Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             78.0%;
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63.6%;
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Similarity

78.0%; 54.5%;

Score 39; Pred. No.

DB 2;

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Conservative

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genome polyprotein - Ornithogalum mosaic virus (fragment)
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                        JQ0494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Science 294, 2323-2328, 2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alpha-galactosidase melA [imported] - Agrobacterium tumefaciens (strain C58, Dupont) C;Species: Agrobacterium tumefaciens C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 17-May-2002
                                                                                                                                                                                                                                                                                                                          A; Gene: AGR_L_436
                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: GB:AE007870; PIDN:AAK88782.1; PID:g15158531; GSPDB:GN00170
                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-474 < KUR>
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A; Residues: 1-457 < KUR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
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63.6%;
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                                                                                                                                                                                                              Pred. No.
                                                                                                                                                                                                                                     Score 38;
                                                                                                                                                                                                                                                                                alpha-galactosidase
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2; Mismatches
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kelz, B.
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Best Local :
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C;Comment: This protein may be involved in the oncogenic C;Superfamily: papillomavirus E6 protein c;Keywords: DNA binding; early protein; zinc finger
                                                                       A;Molecule type: DNA
A;Residues: 1-149 <GOL>
A;Cross-references: GB:J04353; NID:g333048; PIDN:AAA46950.1; PID:g459916
                                                                                                                                                                                                                                                       R;Goldsborough, M.D.; Disilvestre, D.; Temple, G.F.; Lorincz, A.T Virology 171, 306-311, 1989
                                                                                                                                                                                                                                                                               C:Accession: A32444
R:Goldsborough, M.D
                                                                                                                                                                                                                                                                                                                    A;Note: host Homo sapiens (man)
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                         E6 protein - human papillomavirus type 31 C; Species: human papillomavirus type 31 A; Note: host Homo sapiens (man)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Map position: 3
C;Superfamily: Saccharomyces probable membrane protein YLR106c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Murphy, L.; Harris, D.; Wood, V.; submitted to the EMBL Data Library,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F;884-1136/Product: coat protein #status predicted <CTP>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N;Contains: coat protein; nuclear inclusion protein NI6; nuclear inclusion protein C;Species: Ornithogalum mosaic virus, OrMV C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 17-Nov-2000
                                                                                                                                                        A; Status: translation not shown
                                                                                                                                                                                   A; Accession: A32444
                                                                                                                                                                                                     A; Title: Nucleotide sequence of human papillomavirus type 31: A; Reference number: A94398; MUID:89299478; PMID:2545036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Residues: 1-4717 <MUR>
A;Cross-references: RMHL:AL031546; PIDN:CAA20864.1; GSPDB:GN00068; SPDH:SPCC737.08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Reference number: 222002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical coiled-coil protein C; Species: Schizosaccharomyces po
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F;1-365/Product: nuclear inclusion protein NIa (fragment) #status predicted <NIA>F;366-883/Product: nuclear inclusion protein NIb #status predicted <NIB>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Reference number: A; Accession: JQ0494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            submitted to JIPID, May 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Gene: SPDB:SPCC737.08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Experimental source: strain 972h.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Status: translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Accession: T41581
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Superfamily: tobacco etch virus genome polyprotein
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Matches 7; Conserv
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7; Conserv
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87.5%;
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Library, September 1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             fission yeast (Schizosaccharomyces pombe)
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A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-111,'F',113-116,'P',118-121,'T',123-127,'H',129-281,'K',283-731,'E',733-75
A;Cross-references: EMBL:X57088; NID:g50054; PIDN:CAA40368.1; PID:g50055
A;Cross-ruftences: EMBL:X57088; NID:g50054; PIDN:CAA40368.1; PID:g50055
R;Korner, J.; Chun, J.; Harter, D.; Axel, R.
Proc. Natl. Acad. Sci. U.S.A. 88, 6834-6838, 1991
A;Title: Isolation and functional expression of a mammalian prohormone processing enzyme
A;Reference number: A39604; MUID:g1319778; PMID:1862107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1992 *Sequence_revision 31-Dec-1992 *text_change 19-May-2000
C;Accession: Jx0171; S19165; A39604; A35571; A39002; A37951; A46622
R;Nakayama, K.; Hosaka, M.; Hatsuzawa, K.; Murakami, K.
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                                                       A; Residues: 1-609 < KOR>
                                                                                                  A; Accession: A39604
                                                                                                                                                                                                                                                                                                            A; Reference number: A; Accession: S19165
                                                                                                                                                                                                                                                                                                                               submitted to the EMBL Data Library, December 1990 A; Reference number: S19165
                                                                                                                                                                                                                                                                                                                                                                                       R; Nakayama,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Title: Cloning and functional expression of a novel endoprocease involved in A; Reference number: JX0171; MUID:92041727; PMID:1657897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           proprotein convertase 1 (EC 3.4.21.93) precursor - mouse
N;Alternate names: furin homolog PC1; kexin homolog PC1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R; Kubodera, T.; Yamashita, N.; Nishimura, A. Biosci. Biotechnol. Biochem. 64, 1416-1421,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Date: 08-Sep-2000 #sequence_revision 08-Sep-2000 #text_change 03-Aug-2001
C;Accession: JC7337
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                       A; Cross-references: GB:M69196
                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1-753 < NAK>
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A; Accession: JX0171
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Pyrithiamin resistance gene (ptrA) of Aspergillus
nce number: JC7337; MUID:20399355; PMID:10945258
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Pred. No.
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Pred. No. 6.9;
P.; Marcinkiewicz,
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     M.; Chretien,
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A; Map position: 13C
C; Superfamily: kexin; subtilisin homology
C; Keywords: glycoprotein; hydrolase; serine proteinase
F; 1-24/Domain: signal sequence *status predicted <SIG>F; 25-110/Domain: propeptide *status predicted <PRO>F; 25-110/Domain: propeptide *status propeptide *stat
                              A; Experimental source: cultivar Columbia; BAC clone F28J12 R; Bevan, M.; Mueller, M.W.; Muendlein, A.; Felber, R.; Band submitted to the Protein Sequence Database, February 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein F28J12.260 - Arabidopsis thaliana N;Alternate names: hypothetical protein F28A21.10 C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-Jun-1999 C;Accession: T04556; T04852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F;167,208,382/Active site: Asp, His, F;173,401,645/Binding site: carbohyd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Residues: 214-478 <SBI>
A;Residues: 214-478 <SBI>
A;Rote: the authors gave the codon for residue 330-Ser as CTC
A;Note: the authors gave the codon for residue 330-Ser as CTC
R;Smeekens, S.P.; Avruch, A.S.; LaMendola, J.; Chan, S.J.; Steiner, D.F.
Proc. Natl. Acad. Sci. U.S.A. 88, 340-344, 1991
A;Title: Identification of a cDNA encoding a second putative prohormone convertase
A;Reference number: A39002; MUID:91110525; PMID:1988934
                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-1890 <BEV>
A; Cross references: EMBL: AL021710
                                                                                                                                                                                                                                                                                                                                                                                                                            R; Bevan, M.; Hilbert, H.; Braun, M.; Holzer, E.; Brandt, submitted to the Protein Sequence Database, February 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Comment: This protein is a member of a family of subtilisin-like proteinases respon C;Comment: This protein lacks a classical hydrophobic transmembrane segment but may a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: protein A; Residues: 111-120 < ZHO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              J. Biol. Chem. 268, 5615-5623, 1993
A;Tittle: Purification and characterization
A;Reference number: A46622; MUID:93194858;
A;Accession: A46622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F;158-396/Domain: subtilisin homology <SBT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Zhou, Y.; Jindberg, I.
J. Biol. Chem. 268, 5615-5623, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 1-360, 'S', 362-363, 'P', 365-753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pituitary compared to PC2. A; Reference number: A37951; MUID:91203919;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Title: cDNA sequence of two distinct pituitary proteins homologous to Kex2 and furi A; Reference number: A35571; MUID:91000356; PMID:2169760
A; Reference number: 215387
                                                                                                                                                                                                                                                                                                                                      A; Accession: T04556
                                                                                                                                                                                                                                                                                                                                                                                    A; Reference number: Z15377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        F;111-753/Product: prohormone-processing proteinase PC1 #status
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A; Title: cDNA sequence of two d
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Best Local
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7; Conserv
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l; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ser #status predicted
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                                                                                     Bancroft,
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                                                                                     Mewes, H.W.; May
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T04852

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A; Molecule type: DNA
A; Rosidues: 1-1560 <BEW>
A; Residues: 1-150/2; 194/3; 324/3; 1470/1; 1785/1
A; Experimental source: cultivar Columbia; BAC clone F28A21
C; Genetics:
A; Map position: 4
A; Introns: 54/2; 109/1; 150/2; 194/3; 324/3; 1470/1; 1785/1
A; Introns: 54/2; 109/1; 150/2; 194/3; 324/3; 1470/1; 1785/1
A; Introns: 54/2; 109/1; 150/2; 194/3; 324/3; 1470/1; 1785/1
A; Introns: 54/2; 109/1; 109/1; 109/1; 109/1; 1785/1
A; Introns: 54/2; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109
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Result
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**MODEL=frame+_p2n.model -DBY=Xlh
-Q=/cgn2_1/USPTQ_spool/US09823649/runat_14012003_151002_29127/app_query.fasta_1.1393
-DB=Iasued_patents_NA -QFMT=fastap -SUFFIX=rni -MINMARCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXIEN=200000000
-USER=-US09823649_@cGN_1_1_35_@runat_14012003_151002_29127 -NCPU=6 -ICPU=3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
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Maximum DB
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Perfect score:
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Maximum Match 100%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein
       Score
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         greater
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Ygapop 10.0 , 1
Fgapop 6.0 , I
Delop 6.0 , I
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54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/Dackfiles1.seq:*
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Ygapext
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US-08-073-384C-12

US-08-254-359A-12

US-08-483-043-12

US-08-481-328-12

US-08-471-056B-12

US-08-471-056B-12

US-08-491-156-12

US-08-757-653-12

US-08-756-316-12

US-08-756-316-12

US-08-756-316-12

US-08-823-516-12

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US-08-759-038-12
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    ; Sequence 12, Application US/08073384C
; Patent No. 5541311
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US-08-073-384C-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/073,384C
TELECOMMUNICATION INFORMATION: TELEPHONE: 415/705-8410
                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/986,330
FILING DATE: 07-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: CAITOL!, Peter G.
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: FORS-00613
                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 220 Montgomer CITY: San Francisco STATE: California COUNTRY: United State ZIP: 94104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: SYNTHESIS-DEFICIENT THERMOSTABLE TITLE OF INVENTION: POLYMERASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Dahlberg, James E APPLICANT: Lyamichev, Victor APPLICANT: Brow, Mary Ann D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                 FILING DATE: 04-JUN-1993 CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
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Lyamichev, Victor I.
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US-09-350-309-12
US-08-520-946-12
US-08-548-657-1
US-08-648-657-1
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US-08-648-657-1
US-08-448-657-1
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PCT-US95-14418-3
PCT-US95-14418-3
PCT-US95-15327-3
US-07-977-434-1
US-08-458-819-1
US-09-777-537-1
US-09-777-537-1
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PCT-US91-07035-1
US-08-073-384C-21
US-08-073-384C-21
US-08-254-359A-7
US-08-483-043-7
US-08-483-043-21
US-08-481-238-7
US-08-481-238-21
US-08-481-238-21
US-08-481-256-7
US-08-481-256-7
US-08-481-956-7
US-08-484-956-7
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US-08-757-653-7
US-08-757-653-7
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US-08-254-359A-12
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-254-359A-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patent No. 5614402
GENERAL INFORMATION:
                                                                                                                       TELEFAX: (415) 397-83:
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 415/397-8338
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
TOPOLOGY: line
MOLECULE TYPE: I
             MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                          TELEPHONE: (415) 705-8410]
                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 07/986,330 FILING DATE: 07-DEC-1992 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: LYAMICHEV, VICTOR I.
APPLICANT: BROW, MARY ANN D.
TITLE OF INVENTION: 5'. NUCLEASES DERIVED FROM THERMOSTABLE
TITLE OF INVENTION: DNA POLYMERASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1133 CTCTCCCAGGAGCTAGCCATCCCTTACGAGGAG 1165
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                                                  STRANDEDNESS:
                                                                                                                                                                                                 REGISTRATION NUMBER: 32, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 08/073,384 FILING DATE: 06-JUN-1993
                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 LeuSerGlnGluLeuAlaIleProTyrGluGlu 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/254,359A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                     LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
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                                                                 nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SSEE: HAVERSTOCK, MEDLEN & CARROLL
1: 220 MONTGOMERY STREET, SUITE 2200
SAN FRANCISCO
                                                                                                                                                                                                                                       CARROLL, PETER G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CALIFORNIA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      UNITED STATES OF AMERICA
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                                  linear
             DNA (genomic)
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US-09-823-649A-3 (1-11) x US-08-483-043-12 (1-1600)
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Best Local Similarity:
Query Match:
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Best Local Similarity:
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                                                                                                          Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRION AFFEL
APPLICATION NUMBER: US 07-986,330
APPLICATION NUMBER: US 07/986,330
FILING DATE: 07-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Carroll, Peter G.
**Corroll, Peter G.**
**Corroll, Peter G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 415/397-8338
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Dahlberg, James E. APPLICANT: Lyamichev, Victor I. APPLICANT: Brow, Mary Ann D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: FO TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 LeuSerGlnGluLeuAlaIleProTyrGluGlu 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 06-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
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415/397-8338
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                double
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                                                                                                                                               Mismatches:
                                                                                                                                                                                Conservative:
                                                                                                          Indels:
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1 LeuSerGlnGluLeuAlaIleProTyrGluGlu 11

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Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                             US-08-471-066B-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; MOLECULE TYPE: US-08-481-238-12
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                                                                                                                                                                                                                                    RESULT 5
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                                                                                                                                              Patent No. 5837450
GENERAL INFORMATION:
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                                                                                                                                                                      Sequence 12, Application US/08471066B Patent No. 5837450
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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APPLICANT: LYAMICHEV, VICTOR I.
APPLICANT: BROW, MARY ANN D.
TITLE OF INVENTION: SYNTHESIS-DEFICIENT THERMOSTABLE DNA
TITLE OF INVENTION: POLYMERASE
                                   TITLE OF INVENTION: 5' Nucleases De TITLE OF INVENTION: DNA Polyermase NUMBER OF SEQUENCES: 40
                                                                                                             APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                       1133 CTCTCCCAGGAGCTAGCCATCCCTTACGAGGAG 1165
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                  CORRESPONDENCE ADDRESS:
                                                                                            APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     No . .
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ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/481,238
                                                                                                                                                                                                                                                                                                          1 LeuSerGlnGluLeuAlaIleProTyrGluGlu 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1600 base pairs
                                                                   Dahlberg, James E.
Lyamichev, Victor I.
Brow, Mary Ann D.
WENTION: 5' Nucleases Derived From Thermostable
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Medlen & Carroll, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (415) 705-8410
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Query Match:
| DB:
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                                                                                                                                                                                                                                                                                                                                   US-08-484-956-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                     RESULT 6
                                                                                                                                                                                                                                                                                      Sequence 12, Applia
Sequence 10, 5843654
                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 12:
                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: FO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                          NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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APPLICATION NUMBER: US 08/254,359
FILING DATE: 06-JUN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
COMPUTER READABLE FORM:
                                                                                                                                                         APPLICANT: HEISLER, LAURA TITLE OF INVENTION: DETECTION OF p53 MUTATIONS
                                                                                                                                                                                                    APPLICANT: OLDENBURG, MARY C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                           APPLICANT: DAHLBERG, JAMES E.
                                                                    ADDRESSEE: HAVERSTOCK, MEDLEN & CARROLL STREET: 220 MONTGOMERY STREET, SUITE 2200 CITY: SAN FRANCISCO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 0: FILING DATE: 04-JUN-1993
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                   COUNTRY: U
ZIP: 94104
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CITY: San Francisco
                                                      STATE:
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STRANDEDNESS: double
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                                                                                                           ADDRESSEE:
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                                                      CALLFORNIA
                                                                                                                                                                                                                                                                                                                Application US/08484956
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                                                                                                                                                                                                                    LYAMICHEV, VICTOR I. BROW, MARY ANN D.
                                   UNITED STATES OF AMERICA
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MEDIUM TYPE:

Floppy disk

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US-08-757-653-12
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alignment Scores:
                                                                                                                                                                                                                                                                                 Sequence 12, Application US/08757653 Patent No. 5843669
                                                                                                                                                                                                                                                                GENERAL INFORMATION:
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                COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                       1133 CTCTCCCAGGAGCTAGCCATCCCTTACGAGGAG 1165
                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                       TITLE OF INVENTION: Cleavage Of Nucleic Acid Using TITLE OF INVENTION: Thermostable FEN-1 Endonucleases
                                                                                                                                                                                                              APPLICANT: Lyamichev, Victor I. APPLICANT: Lyamichev, Natasha
                                                                                                                                                                                                                                            APPLICANT:
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MEDIUM TYPE: Floppy disk
                                     ZIP: 94104
                                                                                                      STREET:
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                                                                                                        220 Montgomery Street, Suite 2200
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                                                                                                                       Medlen & Carroll, LLP
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INFORMATION FOR SEQ ID NO: 12:
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                                                                              ATTORNEY/AGENT INFORMATION:
NAME: INGOLIA, DIANE E.
                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
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                                TELECOMMUNICATION INFORMATION:
                                                                                                                                                                    CURRENT APPLICATION DATA:
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APPLICANT: PRODENT, JAMES R.
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REFERENCE/DOCKET NUMBER: FORS
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CITY: SAN FRANCISCO
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(415) 397-8310
                                                                                                                                                                                                                                                                                     UNITED STATES OF AMERICA
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: (415) 705-8410
(415) 397-8338
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                                          ; MOLECULE TYPE: US-08-756-386-12
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Lyamichev, Victor I.
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SYSTEM: PC-DOS/MS-DOS
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; MOLECULE TYPE: DNA (genomic) US-08-823-516-12
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Sequence 12, Apprix
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                                                                                                                  TELEFAX: (415) 397-83
INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                     FILING DATE: 24-JAN-1996 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 01
FILING DATE: 12-JUL-1996
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PRIOR APPLICATION DATA:
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APPLICATION NUMBER:
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                                                                                                                                   (415) 397-8338
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IBM PC compatible
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US-09-823-649A-3 (1-11) x US-08-682-853A-12 (1-1600)
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Patent No. 6
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INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER: 1
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                           TYPE: nucleic acid
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Grotelueschen Hall, Jeff S.
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TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 12
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APPLICATION NUMBER: US 0
FILING DATE: 29-NOV-1996
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APPLICATION NUMBER: US 08/682,853
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STATE: California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 0 FILING DATE: 24-JAN-1996
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Brow, Mary Ann D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patentin Release #1.0, Version #1.30
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                                                                                                                                                                                                                                                                                              DNA (genomic)
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                                                                                                                                                            100.00%
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US-09-350-309-12
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                                                                                Patent No. 6348314
GENERAL INFORMATION:
                                                                                                                   Sequence 12,
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CLASSIFICATION DATA:
PRIOR APPLICATION NUMBER: US 08/
APPLICATION NUMBER: US 08/
APPLICATION NATE: 29-NOV-1996
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Improved Cleavage Agents NUMBER OF SEQUENCES: 134
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                                                                                                                                                                                                                       1 LeuSerGlnGluLeuAlaIleProTyrGluGlu 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Ingolia, Diane E. REGISTRATION NUMBER: 40,027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE:
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NUMBER OF SEQUENCES: 69
              Lyamichev, Victor I.
TITLE OF INVENTION: Invasive Cleavge Of Nucleic Acids
                                                                 APPLICANT: Prudent,
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Lyamichev, Victor I.
Lyamichev, Natasha
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                                                  Hall, Jeff G
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                                                                  James R.
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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                                                                                                                                                                                NUMBER OF SEQUENCES: 1: CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                        TITLE OF INVENTION: PATHOGENS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 LeuSerGlnGluLeuAlaIleProTyrGluGlu 11
                                                                                                                     STREET: 220 MONTGOMERY STREET, SUITE 2200 CITY: SAN FRANCISCO
                                                                                  COUNTRY:
                                                                                                         STATE:
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ADDRESSEE: Medlen & Carroll, LLP
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                                                                     94104
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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STATE: California
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TELEFAX: (415) 397-8338
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REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: FORS-02564
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 08/599,491 FILING DATE: 24-JAN-1996
                                                                                                       CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                   Application US/08520946
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                                                                                  UNITED STATES OF AMERICA
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Matches:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: 32,946
FILING DATE:
CLASSIFICATION NUMBER: US/08/520,946
FILING DATE:
CLASSIFICATION NUMBER: 32,837
REGISTRATION NUMBER: 50RS-01756
FELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 1600 base pairs
TYPE: nucleic acid
STANDEDNESS: double
TOPOLOGY: linear
WOLECULE TYPE: DNA (genomic)
US-08-520-946-12

Alignment Scores:
Percent Similarity: 100.00%
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Sequence:
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T08526
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D98157
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AI1082
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45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30
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61.1	61.1	61.1	63.0	63.0	63.0	63.0	63.0	63.0	63.0	63.0	63.0	63.0	63.0	63.0	63.0
153	153	105	1324	1136	629	538	458	415	390	385	382	382	342	309	285
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AI1804	AC1431	D72452	S06187	JQ0494	C86149	G69317	G72377	E84397	S75715	C75221	S32148	S01339	AF2177	C83754	S29368
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                                                                                                                                                                                                  A;Molecule type: DNA
A;Residues: 1-832 <LAM>
A;Residues: 1-832 <LAM>
A;Cross-references: GB:J04639; NID:g155128; PIDN:AAA27507.1; PID:g155129; GB:M26480
C;Superfamily: DNA-directed DNA polymerase I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Thermus aquaticus
C;Date: 29-Jan-1990 #sequence_revision 29-Jan-1990 #text_change 18-Jun-1999
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A;Title: Overproduction of Thermus aquaticus DNA polymerase and its structural analys
A;Reference number: Jx0359; MUID:95204371; PMID:7896728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Accession: JX0359
R;Ishino, Y.; Ueno, T.; Miyagi, M.; Uemori, T.; Imamura, M.; Tsunasawa, S.; Kato, I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Thermus aquaticus
C;Date: 04-Sep-1998 #sequence_revision 04-Sep-1998 #text_change 07-May-1999
                                                                                                                                                                                     C; Keywords: DNA binding; nucleotidyltransferase
                                                                                                                                                                                                                                                                                                           A; Accession: A33530
A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                         R; Lawyer, F.C.; Stoffel, S.; Saiki, R.K.; Myambo, K.; Drummond, R.; Gelfand, D.H. J. Biol. Chem. 264, 6427-6437, 1989
A;Tille: Isolation, characterization, and expression in Escherichia coli of the DNA p. A;Reference number: A33530; MUID:89197950; PMID:2649500
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A; Residues: 1-831 <ISH>
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Best Local :
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678 LSQELAIPYEE 688
                                                                                                                Local Similarity
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                                        1 LSQELAIPYEE 11
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100.0%; Pred. No. 0.031;
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Pred. No. 0.031;
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C;Species: Aquifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 05-Nov-1999
C;Accession: G70332
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A; Accession: G70332
A; Status: preliminary; nucleic acid sequence not shown; translation not shown
                                           A; Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus. A; Reference number: A70300; MUID:98196666; PMID:9537320
                                                                                              Nature 392, 353-358, 1998
                                                                                                                                                                                                                                           conserved hypothetical protein aq_367 - Aquifex aeolicus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                submitted to the EMBL Data Library, May 1994 A; Description: The sequence of S. cerevisiae cosmid 8025
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C;Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 29-Oct-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic Acids Res. 20, 5839, 1992
A;Title: Molecular cloning and nucleotide sequence of the DNA polymerase gene from Therm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Accession:
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                                                                                                                                       R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA-directed DNA polymerase (EC 2.7.7.7) I - Thermus aquaticus
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81.8%;
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! A; Reference number: S60435; MUID: 96158062; PMID: 8585325
F9L1.15 protein - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Datc: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 27-Nov-2001 C;Accession: B86286
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C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 20-Jun-2000
C;Accession: S25321; S60435; S64453; S17019
                                                                                                                                                                                                                                                                                                                                                                                                                           C;Keywords: transmembrane protein F;68-84/Domain: transmembrane #status predicted <TMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Skala, J.; Nawrocki, A.; Goffeau, Yeast 11, 1421-1427, 1995
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A; Residues: 1-326 \ VAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Status: nucleic acid sequence not shown; translation not shown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R; Praekelt, U.M.; Meacock, P.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 thiamin biosynthesis protein thi4 - yeast (Saccharomyces cerevisiae) N; Alternate names: MOil protein; protein G6620; protein YGR144w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Gene: aq_367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-850 < AQF>
                                                                                                                                         RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: SGD:S0003376; MIPS:YGR144w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Gene: SGD: THI4; MOL1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Experimental source: strain $2880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A)Cross-references: EMBL:X72929; NID:g1823241; PIDN:CAA97157.1; PID:g1323242; MIPS:YG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            submitted to the Protein Sequence Database, May 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: EMBL:X85807; NID:g1045249; PIDN:CAA59802.1; PID:g1045250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Residues: 205-326 < SKA>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yeast 8,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S25321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Experimental source: strain VF5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GB:AE000686; NID:g2983038; PIDN:AAC06656.1; PID:g2983047; GB:AE00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Superfamily: thiamin biosynthesis protein thil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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                                                                                                                                                                                                                                                                                                                                                     Local Similarity
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                                                                                                                                                                                                                                                                       3 QELAIPYEE 11
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54.5%;
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77.8%;
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                                                                                                                                                                                                                                                                                                                                                                            Score 38;
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A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.; Sakano, H.; A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Ruthors: Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis. A;Reference number: A86141; MUID:21016719; PMID:11130712
                                                                                                                                                                   R;Okinaka, R.T.; Cloud, K.; Hampton, O.; Hoffmaster, A.R.; Hill, K.K.; Keim, P.; Koehler J. Bacteriol. 181, 5509-5515, 1999
A;Tille: Seguence and organization of pXO1, the large Bacillus anthracis plasmid harbori A;Reference number; A59091; MUID:99445483; PMID:10515943
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                                                     A; Molecule type: DNA
A; Residues: 1-452 < OKI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Gone: PABZ116
C;Superfamily: Methanococcus jannaschii conserved hypothetical protein MJ1154
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A; Experimental source: strain Sterne
                            A;Cross-references: GB:AF065404; NID:q4894216; PIDN:AAD32346.1; PID:q4894258
                                                                                                          A; Status: preliminary
                                                                                                                                         A; Accession: B59096
                                                                                                                                                                                                                                                                                          C;Date: 12-Nov-1999 #sequence_revision 12-Nov-1999 #text_change 11-May-2000
C;Accession: B59096
                                                                                                                                                                                                                                                                                                                                                  hypothetical protein pXO1-42 - Bacillus anthracis virulence plasmid pXO1 C; Species: Bacillus anthracis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   submitted to the EMBL Data Library, July 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Pyrococcus abyssi
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:AJ248284; GB:AL096836; NID:g5457730; PIDN:CAB49268.1; PID:g54577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome, stru
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R; anonymous, Genoscope
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein PAB2116 - Pyrococcus abyssi (strain Orsay)
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72.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 38;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
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                                                                                                                                   A;Map position: linear chromosome C;Superfamily: melibiose-specific alpha-galactosidase
                                                                                                                                                                                                                                                                                                                                                                              A;Reference number: A97359; PMID:11743194
A;Accession: D98157
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                                                                                                                                                                                                                                    C; Genetics:
                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-474 < KUR>
                                                                                                                                                                                                                                                                                                                                                     A; Status:
                                                                                                                                                                                                     A; Gene: AGR_L_436
                                                                                                                                                                                                                                                          A;Cross-references: GB:AE007870; PIDN:AAK88782.1; PID:g15158531; GSPDH:GN00170
                                                        Query Match
Best Local S
                            Matches
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Local Similarity
hes 7; Conserv

Conservative

2;

Mismatches

9; Gaps

0;

68.5%; 63.6%;

Score 37; DB Pred. No. 33;

DB 2; Length 474;

preliminary

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alpha-galactosiduse (meliblase) [imported] - Agrobacterium tumefaciens (strain C58, C; Species: Agrobacterium tumefaciens (c; Lpate: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 17-May-2002 C; Accession: D98157
                                                                                                                                                                                                                               RESULT 11
D98157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Map position: linear chromosome
C;Superfamily: meliblose-specific alpha-galactosidase
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A;Reference number: AB2577; PMID:11743193
A;Accession: AE3130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woerage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alpha-galactosidase melA [imported] - Agrobacterium tumefaciens (strain C58, Dupont) C;Species: Agrobacterium (umefaciens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;N\text{ole:} similar to hypothetical, glutamate rich protein; locus A45555; Plasmodium fa C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Gene: melA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-45/ <KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Ka
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Karp, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Accession: AE3130
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A; Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium
                                      Science 294, 2323-2328, 2001
                                                                                      R; Goodner, B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Experimental source: strain C58 (Dupont)
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Matches 7; Conserv
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nes 7; Conserv
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                                                     , B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Gold F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz,
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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63.6%;
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63.6%;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R.; Monks, D.; Chen, L.; Wood, G.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NO.
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RESULT 14
A40597
C:Species: Deinococcus radiodurans
C:Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 17-Mar-2000
C:Accession: A40597; E75363; S42112; S42235
R:Gutman, P.D.; Euchs, P.; Ouyang, L.; Minton, K.W.
J. Hacteriol. 175, 3581-3590, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     submitted to the EMBL Data Library, December 1996
A;Description: The sequence of C. elegans cosmid F07E5.
A;Reference number: Z21520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      thiazole biosynthetic enzyme - Aspergillus oryzae N;Alternate names: pyrithiamin resistance protein C:Species: Aspergillus oryzae C:Date: 08-Sep-2000 #sequence_revision 08-Sep-2000 #text_change 03-Aug-2001
                                                                                                                        DNA-directed DNA polymerase (EC 2.7.7.7) I - Deinococcus radiodurans (strain R1)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Experimental source: strain Bristol N2; clone F07E5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Biosci. Biotechnol. Biochem. 64, 1416-1421, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Gene: CESP:F07E5.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: EMBL:U80837; PIDN:AAB37908.1; GSPDH:GN00020; CESP:F07E5.9
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63.6%;
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75.0%;
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Pred. No. 44;
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10 LRQELAIPF 18

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A; fitte: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1 A; Reference number: A75250; MUID:20036896; PMID:10567266
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A;Molecule type: DNA
A;Residues: 'MYPCGDGGLSCESIDFALCCLRGRSGNYVQSRTLP',1-12,'T',14-41,'H',43-72,'F',74-92
A;Cross-references: GB:AE002012; GB:AE000513; NID:g6459473; PIDN:AAF11264.1; PID:g64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein yxaB |imported| - Lactococcus lactis subsp. lactis (strain 11.34) (Species: Lactococcus lactis subsp. lactis C;Species: Lactococcus lactis subsp. lactis C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001 C;Accession: C86902
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A;Accession: A40597
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C; Superfamily: DNA-directed DNA polymerase I
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A; Residues: 1-921 <GUT>
                                                                                                                                                                    A;Gene: yxaB
                                                                                                                                                                                                  C; Genetics:
                                                                                                                                                                                                                          A; Experimental source: strain 11.1403
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                                                                                                                                                                                                                                                                                   A; Residues: 1-59 <STO
                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                          A; Title: The complete genome sequence of the lactic acid bacterium Lactococcus lacti:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, Genome Res. 11, 731-753, 2001
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1 LSQELAIPY 9
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                                                        Conservative
                                                                             64.8%;
77.8%;
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53.6%;
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Pred. No.
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                                                        Mismatches
                                                                                      DB 2; Length 59; 7.7;
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          US-09-823-649A-3
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ALIGNMENTS

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al structures of open a	Waksma	X-RAY CRISTALLOGRAPHY (2.3 ANGSTROMS) OF 295-832. MEDLINE=99077817: DubMod=9857206:		,	"Structure of Tag polymerase with DNA at the polymerase active site.";	EOM S.H. Wang J. Steitz T.A.	MEDLINE=96353982: PubMed=8717047;	X-RAY CRYSTALIOGRAPHY 13 O ANGSTRONS)		Proc. Natl. Acad. Sci. U.S.A. 92:9264-9268(1995).		5-A resolution: structural basis !	the large fragment of The	, di Cera	568114;	X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 290-832.	[4]		stal structure of Thermus aquaticus DNA polymerase.";	-S., Suh S.W., Steitz	Med-7	X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS).		1024(1994).	mass spectrometry.";	"Overproduction of Thermus aquaticus DNA polymerase and its	and the second s	. Mivagi M., Uemori T., Inamura M.	04371: DubMed=7896708		SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.	-	3iol. Chem. 264:6427-6437(1989).	ymerase gene from Thermus aquaticus.";	haracterization, and exp		Lawyer F.C., Stoffel S., Saiki R.K., Myambo K., Drummond R.,	MEDLINE=89197950; PubMed=2649500;	SEQUENCE FROM N.A.		NCBI_TaxID-271;	e; Thermus.	Racteria: Thermus/Deinococcus group: Deinococci: Thermales:	CENTROL OF FOLE.	ymera Ymera	JUN-2002 (Rel. 41, Last annotation update)	(Rel. 17, Last se	1991 (Rel.	DECLIFIENC STANDARD; FRI; 632 AA.	HEAQ	17 1

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Ptam; PF01367; 5_3_exonuclease; 1. pfam; PF02739; 5_3_exonuc_N; 1. prannts; PR00868; DNAPCII.
                                                                                                                                                                                                                                                                                                                                                                             InterPro;
InterPro;
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PDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Stru .ur.-based design of Taq DNA polymerases with improved properties of dideoxynucleotide incorporation.";
Proc. Natl. Acad. Sci. U.S.A. 96:9491-9496(1999).
-i- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fab: the Fab is directed against an intermediate in
dynamics of the enzyme.";
Proc. Natl. Acad. Sci. U.S.A. 95:12562-12567(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    polymerase I complexed with deoxyribonucleoside triphosphates.",
Protein Sci. 7:1116-1123(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 I: structural basis for nucleotide incorporation.";
EMBO J. 17:7514-7525(1998).
                    Transferase; DNA-directed DNA polymerase; DNA replication; DNA repair; DNA-binding; 3D-structure.
                                                                             TIGRFAMS; TIGR00593; pola; 1.
PROSITE; PS00447; DNA_POLYMERASE_A; 1.
                                                                                                                                                                                      SMART;
                                                                                                                                                                                                                SMART;
                                                                                                                                                                                                                                                                                                                    Pfam; PF00476; DNA_pol_A;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       x-ray Crystallography (2.3 angstroms).
meDLINE=98445410; PubMed=9770525;
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"Crystal structures of the Klenow fragment of Thermus aquaticus DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 290-832
MEDLINE=98266352; PubMed=9605316;
                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: BELONGS TO THE DNA POLYMERASE TYPE-A FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BIOTECHNOLOGY: Used in the PCR method because of its high
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         thermostability. Has a relatively high error rate because it lacks exonuclease proofreading functionality.
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5KTQ;
1BCX;
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1KTQ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1TAQ;
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                                                                                                                                                       SM00475; 53EXOC; 1.
SM00278; HhH1; 1.
SM00279; HhH2; 1.
                                                                                                                                SM00482; POLAC;
                                                                                                                                                                                                                                                                                                                                                      IPR003584; HHH_2.
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22-DEC-99.
22-DEC-99.
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14-OCT-98
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DNA_pol.
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POLYMERASE (BY SIMILARITY).
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Best Local (
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01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
DNA polymerase I, thermostable (EC 2.7.7.7) (TAC polymerase 1).
                                                       SMART; SM00278; HhH1; 1.
SMART; SM00279; HhH2; 1.
SMART; SM00482; POLAC; 1
Transferase; DNA-directed DNA polymerase; DNA replication; DNA repair; DNA-binding.
                                                                                                                 Pfam: PF00476; DNA_Pol_A; 1.
Pfam: PF01367; 5_3_exonuclease; 1.
Pfam: PF02739; 5_3_exonuc_N; 1.
Pfam: PF02739; 5_3_exonuc_N; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- FUNCTION: THERMOSTABLE ENZYME THAT HAS 5'-TO-3' EXONUCLEASE
ACTIVITY AND NO 3'-TO-5' EXONUCLEASE ACTIVITY.
-!- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE~93285135; PubMed~8508785; Park J.H., Kim J.S., Kwon S.-T., Lee D.-S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.
                           TIGREAMS; TIGRO0593; pola; 1. PROSITE; PS00447; DNA_POLYMERASE_A; 1.
                                                                                                       SMART;
                                                                                                                                                                                                                                                                      PIR; S33287; S33287.
HSSP; P19821; 1TAQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            polymerase."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-GK24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kwon
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Thermus caldophilus
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P80194;
                                                                                                                                                                                              InterPro; IPR003583; HHH_1.
                                                                                                                                                                                                              InterPro;
                                                                                                                                                                                                                       InterPro; IPR002421; 5_3_exonuclease.
InterPro; IPR001098; DNA_pol.
InterPro; IPR002298; DNA_polI.
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                                                                                                                                                                                                                                                                                                                                                                                       the European Bioinformatics Institute.
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-!- SIMILARITY: BELONGS TO THE DNA POLYMERASE TYPE-A FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Purification and characterization of Thermus caldophilus GK24
                                                                                                                                                                               InterPro; IPR003584; HHH_2.
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                                                                                                      SM00475; 53EXOc;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Biochem. 214:135-140(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  155
832 AA;
                                                                                                                                                                                                              IPR000513;
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F1731055B5246F03 CRC64;
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                                                                                                                                                PRINTS; PR00868; DNAPOLI. SMART; SM00475; 53EXOC; 1. SMART; SM00278; HhH1; 1.
                                                                                                                                                                                                                                                                                                                      use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                   DNA polymerase gene (polA) from Thermus thermophilus HB8.";
J. Ferment. Bioeng. 76:285-269(1993).
-I- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate - N diphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
DNA polymerase I, thermostable (EC 2.7.7.7) (Tth polymerase 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P52028;
                                                             SEQUENCE
                                                                                                       TIGRFAMS; TIGR00593; pola; 1.
PROSITE; PS00447; DNA_POLYMERASE_A; 1.
                                                                                                                             SMART; SM00279; HhH2; 1
SMART; SM00482; POLAC;
                                                                                                                                                                              Pfam; PF01367; 5_3_exonuclease; Pfam; PF02739; 5_3_exonuc_N; 1.
                                                                                                                                                                                                                         InterPro; IPR002298; DNA_poll.
InterPro; IPR000513; Exo_N_I.
InterPro; IPR003583; HHH_1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN-HB8 / ATCC 27634;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                DNA-binding.
                                                                                             Transferase; DNA-directed DNA polymerase; DNA replication;
                                                                                                                                                                                                     Pfam; PF00476; DNA_pol_A;
                                                                                                                                                                                                                 InterPro; IPR003584;
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                                                                                                                                                                                                                                                                                                              or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                               -!- SIMILARITY: BELONGS TO THE DNA POLYMERASE TYPE-A FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Cloning, nucleotide sequence, and expression in Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Urabe I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Asakura K., Komatsubara H., Soga S., Yomo T., Oka M., Emi S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=274;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Thermaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Thermus/Deinococcus group; Deinococci; Thermales
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834 AA;
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93798 MW;
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                              100.0%; Score 54; DB 1; Length 834: 100.0%; Pred. No. 0.011;
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                                                                       POLYMERASE (BY SIMILARITY).
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A851FF3C3076348E CRC64;
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Pred. No. 0.011;
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                                                              1A98145DC11A54A9 CRC64;
                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            834 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 834;
                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                     Indels
                                                                                             DNA repair;
                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Caps
                     Gaps
                    0;
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1 LSQELAIPYEE 11
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Query Match
Best Local Similarity
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P30313;
01-APR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "LERLH
                                                                                                                                                                                 TIGREAMS; TIGRE0593; pola; 1.
PROSITE; PS00447; DNA_POLYMERASE_A; 1.
                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF01367; 5_
Pfam; PF02739; 5_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Celsius; can be used at temperatures up to 95 degree Celsius. -!- SIMILARITY: BELONGS TO THE DNA POLYMERASE TYPE-A FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic Acids Res. 20:5839-5839(1992).
-!- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Thermus/Deinococcus group; Deinococci; Thermales.
Thermaceae; Thermus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-APR-1993 (Rel. 25, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
UNA polymerase 1, thermostable (BC 2.7.7.7) (Tfl polymerase 1).
                                                                                                      SEQUENCE 831 AA;
                                                                                                                                                                 Transferase; DNA-directed DNA polymerase; DNA replication;
                                                                                                                                                                                                                                       SMART; SM00485;
                                                                                                                                                                                                                                                            SMART; SM00482;
                                                                                                                                                                                                                                                                                   SMART;
                                                                                                                                                                                                                                                                                                   SMART; SM00278;
                                                                                                                                                                                                                                                                                                                      SMART; SM00475; 53EXOc; 1.
                                                                                                                                                                                                                                                                                                                                                PRINTS; PR00868;
                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00476; DNA_pol_A; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HMBL; X66105; CAA46900.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the European Bioinformatics Institute. There are no restrictions on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -! - MISCELLANEOUS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- BIOTECHNOLOGY: Used in the PCR method because of its high
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  from Thermus flavus."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Akhmetzjanov A.A., Vakhitov V.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-93087201; PubMed-1454544;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-ACM B-1257;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID-274;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Thermus thermophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POLA OR POL
                                                                                                                                DOMAIN
                                                                                                                                              DNA-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; 1PR003584; HHH_2.
InterPro; 1PR001532; XPGC_Rad.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; 158003583; HBH_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro: IPR001098; DNA_pol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Molecular cloning and nucleotide sequence of the DNA polymerase gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR002421;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     680 LSQELAIPYEE 690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              thermostability
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   S26675; S26675.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     S24929; S24929.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P19821; 1TAQ
                                                                                                                                                                                                                                                                                 SM00279;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HPR002298; DNA_pol1.
                                                                                                                    409
                  Conservative
                                                                                                                                                                                                                                                                                 ићи1; 1.
нћн2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                    XPGN; 1
                                                                                                                                                                                                                                                         POLAc; 1.
                                                                                                                                                                                                                                                                                                                                                DNAPOLI.
                                                                                                                                                                                                                                                                                                                                                                                            _3_exonuclease; 1.
                                                                                                    831
93783 MW;
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                                                                                                                                                                                                                                                                                                                                                                  _exonuc_N; 1.
                                   81.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5_3_exonuclease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
              1; Mismatches
                                   Score 44; D
Pred. No. 0.
                                                                                                                         POLYMERASE (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                  96F93CEFA3CA536D CRC64;
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                                                     DB 1;
                                     95;
              ۲.
                                                   Length 831
              Indels
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              0;
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RESULT 6
THI4_YEAST
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01-FEB-1995
                                                                          THI4_YEAST STANDARD; PRT; 326 AA. p32318; 01-0CT-1993 (Rel. 27, Created) 01-0CT-1993 (Rel. 27, Last sequence update) 16-0CT-2001 (Rel. 40, Last annotation update)
                                              Thiazole biosynthetic enzyme, mitochondrial precursor. TH14 OR MOL1 OR ESP35 OR YGR144W OR G6620.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Dover J., Du Z., Favello A., Fulton L., Gattung S., Geisel C., Kirsten J., Kucaba T., Hillier L., Jier M., Johnston L., Langston Y., Latteille P., Louis E.J., Macri C., Marcis E., Menezes S., Mouser L., Nhan M., Rifkin L., Riles L., St Peter H., Trevaskis E., Vaughan K.,
Saccharomycetales; Saccharomycetaceae; Saccharomyces
                Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00134; cyclin; 1.
SMART; SM00385; CYCLIN; 1.
PROSITE; PS00292; CYCLINS; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          G1/S-specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YEAST
                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                             Cyclin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U00061; AAB68375.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Science 265:2077-2082(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Vaugin M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Vignati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=94378003; PubMed=8091229;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Saccharomycetales; Saccharomycetaceae; Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PCL5 OR YHR071W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CG18_YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Complete nucleotide sequence of Saccharomyces cerevisiae chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-FEB-1995 (Rel. 31, 16-OCT-2001 (Rel. 40,
                                                                                                                                                                                                                                       174 LNYELAIPYDE 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPRO04366; Cyclin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  677 LSGELSIPYEE 687
                                                                                                                                                                                                                                                                                                                        Local
                                                                                                                                                                                                                                                                     1 LSQELAIPYEE 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: BELONGS TO THE CYCLIN FAMILY. MOST SIMILAR TO G1/S-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPECIFIC CYCLINS PCLT AND PCL2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S0001113; PCL5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S46696; S46696.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  D., Wilcox L., Wohldman P., Waterston R., Wilson R.,
                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                             Cell cycle; Cell division
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                         229 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Rel. 31, Created)
                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        / AB972;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cyclin PCL5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                           26467 MW; B6839ABB9DB5DD49 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update
                                                                                                                                                                                                                                                                                                                                     Score 42;
                                                                                                                                                                                                                                                                                                                      Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                          No.
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                                                                                                                                                                                                                                                                                                                                        DB 1; Length 229;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                in no
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Query Match
Best Local Similarity
"---hes 7; Conserva
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"The sequence of a 27 kb segment on the right arm of chromosome VII
from Saccharomyces cerevisiae reveals MOLI, NAT2, RPL30B, RSR1, CYS4,
                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Machado C.R., Praekelt U.M., de Oliveira R.C., Barbosa A.C.,
Byrne K.L., Meacock P.A., Menck C.F.;
"Dual role for the yeast TH14 gene in thiamine biosynthesis and DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Praekelt U.M., Meacock P.A.;
"MOLI, a Saccharomyces cerevisiae gene that is highly expressed in early stationary phase during growth on molasses.";
yeast 8:699-710(1992).
                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                        EMBL; X61669; CAA43843.1; -. EMBL; X85807; CAA59802.1; -. EMBL; Z72929; CAA97157.1; -. EMBL; Z72930; CAA97159.1; -.
                                                                                                                                                                                                                                                                                                                                                            or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                         entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                           modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- INDUCTION: REPRESSED BY THIAMINE.
-!- MISCELLANEOUS: EXPRESSED AT HIGH LEVELS IN THE EARLY STATIONARY
PHASE OF BATCH CULTURES GROWING ON MOLASSES, AN INDUSTRIAL MEDIUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         J. Mol. Biol. 273:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Saccharomyces cerevisiae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     van Dyck L., Skala J., de Wergifosse P., Purnelle B., "alla E.,
Nawrocki A., del Bino S., Goffeau A.;
Nawmitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                    CHAIN
                                                                                                                                                   Thiamine biosynthesis; Mitochondrion;
                                                                                                                                                                      Pfam; PF01946; Thi4; 1.
TIGRFAMs; TIGR00292; Thi4; 1
                                                                                                                                                                                                                                                                                                                                                                                                          the European Bioinformatics fustitute. There are no restrictions on use by non-profit institutions as long as its content is in no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SIMILARITY: BELONGS TO THE THI4 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -! - SUBCELLULAR LOCATION: Mitochondrial (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE~98035046; PubMed-9367751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION IN DNA DAMAGE TOLERANCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Praekelt U.M., Byrne K.L., Meacock P.A.;
"Negulation of TH14 (MOL1), a thiamine-biosynthetic gone of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE~95028146; PubMed=7941734;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                THIAMINE REGULATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PEM1/CHO2, NSR1 genes and ten new open reading frames."; Yeast 11:1421-1427(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PEMI/CHO2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=96158062; PubMed=8585325;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 205-326 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=93070608; PubMed=1441749;
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                                                                                                                                        TRANSIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (east 10:481-490(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NOI. Biol. 273:114-121(1997).
FUNCTION: INVOLVED IN BIOSYNTHESIS OF THE THIAMINE PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOLERANCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      THIAZOLE. ALSO SEEMS TO HAVE A ROLE IN MITOCHONDRIAL DNA DAMAGE
                                                                                                                                                                                                                           S0003376; THI4
                                                                                                                                                                                                                                         $17019; $17019.
$25321; $25321.
                                                                                                                                                                                                        IPR002922; Thi4.
                                                                                  326 AA;
                  Conservative
                                                                                  34991 MW;
                               70.4%; Score 38; DB 1; 77.8%; Pred. No. 5.4;

    Mismatches

                                                                                                FAD OR NAD (POTENTIAL)
                                                                                                                   THIAZOLE BIOSYNTHETIC ENZYME
                                                                                                                                   MITOCHONDRION (POTENTIAL)
                                                                                  843790F2CE00BF02 CRC64;
                                                                                                                                                  Transit peptide; FAD;
                                                                                                                                                                                                                                                                                                                                                                                               Usage
                                               Length 326;
                Indels
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              Gaps
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                                                                                                                    DPO1_THEFT
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                                                           Matches
                                                                                     Query Match
                                                                                                                                                                                                        SMART; SM00475; 53EXOC; 1.
SMART; SM00278; HhH1; 1.
SMART; SM00279; HhH2; 1.
SMART; SM00482; POLAC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the MMBH outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-JUN-2002 (Rel. 41, Last annotation update) DNA polymerase I, thermostable (EC 2.7.7.7) (TFI polymerase 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DP01_
                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                  Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=98170158; PubMed=9509419;
Jung S.E., Choi J.J., Kim H.K., K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Thermus filiformis.
                                                                                                                                    DOMAIN
                                                                                                                                               DNA-binding.
                                                                                                                                                                                                                                                                    PRINTS; PR00868; DNAPOLI.
                                                                                                                                                                                                                                                                                                                              InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBI,; AF030320; AAC46079.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             + {DNA}(N).
-!- SIMILARITY: BELONGS TO THE DNA POLYMERASE TYPE-A FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Thermus/Deinococcus group; Deinococci; Thermales
                                                                                                                                                             Transferase; DNA-directed DNA polymerase; DNA replication; DNA repair;
                                                                                                                                                                             PROSITE; PS00447; DNA_POLYMERASE_A; 1.
                                                                                                                                                                                                                                                                                                                                              Inter/ro;
                                                                                                                                                                                                                                                                                                                                                                         InterPro;
                                                                                                                                                                                                                                                                                                                                                                                         InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                     InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Cloning and analysis of the DNA polymerase-encoding gene from Thermus
678 LSQELGIDYKE 688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         127 QELEIPYED 135
                             1 LSQELAIPYEE 11
                                                                        [,ocal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION: THERMOSTABLE ENZYME THAT HAS 5'-TO-3' EXONUCLEASE ACTIVITY AND NO 3'-TO-5' EXONUCLEASE ACTIVITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  THEFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cells 7:769-776(1997).
                                                                                                                                                                                                                                                                               PF01367; 5_3_exonuclease; 1. PF02739; 5_3_exonuc_N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                    P19821;
                                                                                                                                                                                                                                                                                                               PF00476; DNA_pol_A;
                                                          Similarity
8; Conser
                                                                                                                                                                                          TICK00593; pola; 1
                                                                                                                                                                                                                                                                                                                              IPR003584; HHH_2
                                                                                                                                                                                                                                                                                                                                                                         IPR002298;
                                                                                                                                                                                                                                                                                                                                                           IPR000513;
                                                                                                                                                                                                                                                                                                                                                                                         IPR001098;
                                                                                                                                                                                                                                                                                                                                                                                                     IPR002421; 5_3_exonuclease.
                                                                                                                    833 AA;
                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Thermus.
                                                                                                                                                                                                                                                                                                                                                                                                                  ITAQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                   833
93890 MW;
                                                                       70.4%;
72.7%;
                                                                                                                                                                                                                                                                                                                                                                                       DNA_pol
                                                                                                                                                                                                                                                                                                                                              HHH
                                                                                                                                                                                                                                                                                                                                                                       DNA_polI.
                                                                                                                                                                                                                                                                                                                                                         EXO_N_I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kim H.K., Kwon S.-T.;
                                                           <u>س</u>و
                                                                       Score 38; DB
Pred. No. 14;
                                                                                                                   POLYMERASE (BY SIMILARITY).
; 51BF8B0417EEFC4D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  833 AA.
                                                                                     DB 1; Length 833;
                                                          2:
                                                           Indels
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                                                        Gaps
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RESULT 8

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RESULT 9
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ID DPO1
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ON POI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
Gutman P.D., Fuchs P., Ouyang L., Minton K.W.; "Identification, sequencing, and targeted mutagenesis of a DNA polymerase gene required for the extreme radioresistance of
                                                                                                                                                                                                                                                                                                      P52027;
01-0CT-1996 (Rel. 34, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-UUN-2002 (Rel. 41, Last annotation update)
DNA polymerase I (EC 2.7.7.7) (POL I).
POLA OR DRI707.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         characterization and application as a dominant selectable marker for transformation.";
                                                                                         MEDI.INE=93273728; PubMed=8501062;
                                                                                                                      STRAIN=R1
                                                                                                                                                                                                                                                                                          Deinococcus radiodurans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AF217503; AAF25444.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/aunounce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9UUZ9;
                                                                                                                                                 SEQUENCE OF 36-956 FROM N.A
                                                                                                                                                                                                         NCBI_TaxID=1299;
                                                                                                                                                                                                                                    Deinococcaceae; Deinococcus
                                                                                                                                                                                                                                                         Bacteria; Thermus/Deinococcus group; Deinococci; Deinococcales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DPO1_DEIRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DEIRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NP_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TRANSIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Thiamine biosynthesis; Mitochondrion; Transit peptide; FAD; NAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TIGRFAMS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro: IPR002922; Thi4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SUBCELLULAR LOCATION: Mitochondrial (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- FUNCTION: INVOLVED IN BIOSYNTHESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Biosci. Biotechnol. Biochem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kubodera T., Yamashita N., Nishimura A.;
"Pyrithiamine resistance gene (ptrA) of Aspergillus oryzae: cloning,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=20399355; PubMed=10945258;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-HLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota; Bungi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Aspergillus oryzae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   THIA OR PTRA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Thiazole biosynthetic enzyme, mitochondrial precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         THI4_ASPOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-0CT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   138 ELGVPY DE 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 ELAHYEE H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         THIAZOLE (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PF01946; Thi4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the Swiss Institute of Bioinformatics and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TIGR00292; Thi4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      327 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ascomycota; Pezizomycotina; Eurotiomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         35099 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66.7%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FAD OR NAD (POTENTIAL).
; 7C561EE06742B2AE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 36; DB
Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            THIAZOLE BIOSYNTHETIC ENZYME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64:1416-1421(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         327 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OF THE THIAMINE PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          There are no
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ξ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 327;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                restrictions on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL outstation
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                                                                Best Local
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CONFLICT
CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        radiodurans R1.";
Science 286:1571-1577(1999).
-i- EUNCTION; IN ADDITION TO POLYMERASE ACTIVITY, THIS D
EXHIBITS 3' TO 5' AND 5' TO 3' EXONUCLEASE ACTIVITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D., Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L., Moffat K.S., Qin H., Jiang L., Papphile W., Crosby M., Shen M., Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C., Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D., Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
                                                                                                                                                                                 Hydrolase;
CONFLICT
                                                                                                                                                                                                                                                                                                          Pfam; PF01367; 5_3_exonuclease; Pfam; PF02739; 5_3_exonuc_N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                          HSSP;
                                                                                                                                                                     CONFLICT
                                                                                                                                                                                                        Transferase;
                                                                                                                                                                                                                                                SMART; SM00482;
                                                                                                                                                                                                                                                          SMART; SM00279; HhH2; 1
                                                                                                                                                                                                                                                                        SMART; SM00278; HhH1; 1.
                                                                                                                                                                                                                                                                                    SMART; SM00475; 53EXOc;
                                                                                                                                                                                                                                                                                                PRINTS; PR00868;
                                                                                                                                                                                                                                                                                                                                     Pfam; Pr00476; DNA_pol_A; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                               TIGR; DR1707
                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AE002012;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; L14581; AAC36974_1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=20036896; PubMed=10567266,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Deinococcus radiodurans."
                                                                                                                                                                                                                     PROSITE; PS00447; DNA_POLYMERASE_A; 1.
                                                                                                                                                                                                                                                                                                                                                     InterPro;
                                                                                                                                                                                                                                                                                                                                                                           InterPro;
                                                                                                                                                                                                                                                                                                                                                                                        InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                     InterPro;
803
                                                                                                                                                                                                                                                                                                                                                                InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Genome sequence of the radioresistant bacterium Deinococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                               Local
                          I LSQELAIPYEE 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteriol. 175:3581-3590(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBUNIT: SINGLE-CHAIN MONOMER WITH MULTIPLE FUNCTIONS. SIMILARITY: BELONGS TO THE DNA POLYMERASE TYPE-A FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    S MILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the FMBL outstation -
LSNDLGIPYAE 813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (DNA) (N)
                                                  Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                        19821; 2KTQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                   IPR002421; 5_3_exonuclease. IPR001098; DNA_pol.
                                                                                                                                                                                                                                  TIGR00593;
                                                                                                                                                                                                                                                                                                                                                  IPR003584;
                                                                                                                                                                                                                                                                                                                                                              IPR003583;
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                                                                                                                          406
540
956
                                                    Conservative
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                                                                                                     105659 MW;
                                                               66.7%;
63.6%;
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                                                                                                                                                                                                                                                                                                                                                              HHH_1.
                                                                                                                                                                                                                                                                                                                                                                           EXO_N_I.
                                                                                                                                                                                                                                                                                                                                                                                        DNA_polI.
                                                             Score 36; DB 1;
Pred. No. 40;
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-> R (IN
-> V (IN
                                                    Mismatches
                                                                                                     6ABBF117D75AB84A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             There are no restrictions on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Usage
                                                                           Length 956;
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RESULT 10 VE6_HPV31

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P17386;
01-AUG-1990
01-AUG-1990
15-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZN_FING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Nucleotide sequence of human papillomavirus type 31: a cervical neopilasia-associated virus.";

Virology 171:306-311(1989).
-!- FUNCTION: THIS PROTEIN MAY BE INVOLVED IN THE ONCOGENIC POTENTIAL OF THIS VIRUS (CERVICAL NEOPILASIA-ASSOCIATED VIRUS).
-!- FUNCTION: EXHIBIT A STRONG, BUT NON SPECIFIC AFFINITY FOR DOUBLE STRONG ON THE ONLY THE ONLY
                        Miele L., Strack B., Kruft V., Lanka E.; "Gene organization and nucleotide sequence of the primase region of IncP plasmids RP4 and R751.";
                                                                                                                                                                                                                                                                                Wscherichia coli.
Plasmid IncP-beta R751
                                                                                                                                                                                                                                                                                                                                      TRAC
                                                                                                                                                                                                                                                                                                                                                    01-AUG-1992 (Rel. 23, Croated)
01-AUG-1992 (Rel. 23, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
DNA primase trac (EC 2.7.7.-) (Replication primase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                TRC5_ECOLI STANDARD P27190; P27191; P27185;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ECOLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              esu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
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DNA Seq. 2:145-162(1991).
                                                                                                 MEDLINE-92297959; PubMed=1818755;
                                                                                                                                 STRAIN=HB101
                                                                                                                                                 SEQUENCE FROM N.A., AND SEQUENCE OF
                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; Pr00518; E6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; J04353; AAA46950.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIINE*89299478; PubMed=2545036; Goldsborough M.D., Disilvestre D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                          NCBI_TaxID-562;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDED DNA (IN VITRO)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
7: Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Rel. 15, Last sequence update) (Rel. 41, Last annotation update
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Rel. 15, Created)
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; 17713 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Mismatches
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Pred. No. 9.1;
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                                                                                                                                                       2-11; 219-234 AND 702-714
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                                                                                                                                                                                                                                                                                                                                     KCY_AQUAE
067907;
15-DEC-1998
15-DEC-1998
                                                                                    Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L., Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay M., Huber Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;
"The complete genome of the hyperthermophilic bacterium Aguifex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRANSFERRED INTO THE RECIPIENT CELL DURING BACTERIAL CONJUGATION.
CATALYZES THE SYNTHESIS OF SHORT OLLGORIBONUCLEOTIDE PRIMERS WITH
CPA OR PCPA AT THBIT 5'-TERMINI ON A SINGLE STRANDED TEMPLATE DNA
-i- ALTERNATIVE PRODUCTS: 3 ISOFORMS; TRAC-2 (SHOWN HERE), TRAC-3 AND
TRAC-4; ARE PRODUCED BY ALTERNATIVE INITIATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     [2]
SEQUENCE FROM N.A.
             -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- SIMILARITY: BELONGS TO THE CYTIDYLATE KINASE FAMILY. SUBPAMILY 1.
                                            -i- CATALYTIC ACTIVITY: ATP + (d)CMP = ADP + (d)CDP
                                                          Nature 392:353-358(1998)
                                                                                                                                                      MEDLINE-98196666; PubMed-9537320;
                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                              Bacteria; Aquificae;
                                                                                                                                                                                                                                                           CMK OR AQ_2153.
Aquifex aeolicus.
                                                                                                                                                                                                                                                                                                          Cytidylate kinase
                                                                                                                                                                                                                                                                                                                           16-0CT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (AUG-1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Thomas C.M.;
                                                                                                                                                                                                               NCBI_TaxID=63363;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INIT_MET
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              986 QYLAVPYEQ 994
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(Rel.
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                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                         37, Created)
37, Last sequence update)
40, Last annotation updat
(EC 2.7.4.14) (CK) (Cytid
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66.7%;
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DNA
FOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 35;
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PRIMASE, ISOFORM TRAC-3.
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(Cytidine monophosphate kinase)
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Matches 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P22353;
01-AUG-1991 (Rel. 19, Created)
01-EB-1995 (Rel. 31, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
01-OCT-1996 (Rel. 34, Last annotation update)
Mitochondrial 60S ribosomal protein L8 (YmL8).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collabora between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commer
                                          EMBL; X53841; CAA37834.1; -. EMBL; Z34288; CAA84060.1; -. HMBL; Z49338; CAA89354.1; -.
                                                                                                                                                                                                                                                                                                            Vandenbol M., Durand P., Dion C., Portetelle D., Hilger F.; "Sequence of a 17.1 kb DNA fragment from chromosome X of Saccharomyces cerevisiae includes the mitochondrial ribosomal protein
                                                                                                                                                                                                                                                                                                                                                                                                                     ribosomal proteins in Saccheromyces cerevisiae.";
Nucleic Acids Res. 18:1521-1529(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Transferase; Kinase; ATP-binding; Complete proteome.
NP_BIND 7 15 AMP (HY SIMILARITY).
SEQUENCE 222 AA; 25400 MW; 523BDCDFB48128C8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                        entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                              use by non-profit institutions as long modified and this statement is not removed
                                                                                                                                                            the European Bioinformatics Institute. The use by non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                  MEDI.INE-95282514; PubMed-7762302;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A., AND PARTIAL SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HSSP; P23863;
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                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-90221879; PubMed-2183197;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Saccharomyces cerevisiae (Baker's yeast)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR003136; Cytidylate_k
Pfam; PF02224; Cytidylate_kin; 1.
                                                                                                                                                                                                                                                                                  Yeast 11:57-60(1995)
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                                                                                                                                                                                                                                                -!- SIMILARITY: BELONGS TO THE L17P FAMILY OF RIBOSOMAL PROTEINS
                                                                                                                                                                                                                                                                   SUBCELLULAR LOCATION: Mitochondrial
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                                                                                                                                                                                              the Swiss Institute of Bioinformatics and the
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Pred. No.
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                                                                                                                                                          There are no restrictions on 
ng as its content is in no
                                                                                                                                          Usage
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S0003599; MRPL8. \$14890; \$14890. \$47128; \$47128.

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Q913C3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
3-methyl-2-oxobutanoate hydroxymethyltransferase (EC 2.1.2.11)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                    SEQUENCE
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or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                              the European Bioinformatics Institute. Tuse by non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathogen.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M T., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=ATCC 15692 / PAO1;
MEDLINE=20437337; PubMed=10984043;
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                                                                                                                                                                                                                                                    Pfam; PF02548; Pantoate_transf; 1.
                                                                                                                                                                                                                                                                                             EMBL; AE004587; AAG04987.1; -.
                                                                                                                                                                                                                                                                                                                                                                           modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Garber R .., Coltry L., Tolentino E., Westbrock-Wadman S., Yuan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Ketopantoate hydroxymethyltransferase).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TIGRFAMs;
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                                                                                                                                                                                         Complete proteome
                                                                                                                                                                                                               Pantothenate biosynthesis; Transferase; Methyltransferase;
                                                                                                                                                                                                                                                                         InterPro;
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          197 LSEELAIP 204
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                                                                                                            Local
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                                               1 LSQELAIP 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ure 406:959-964(2000).

CAPALYTIC ACTIVITY: 5,10-methylenetetrahydrofolate + 3-methyl-2-
oxobutanoate = tetrahydrofolate + 2-dehydropantoate.

PARTHWAY: Pantothenate blosynthesis; first branch; first step.

SIMILARITY: BELONGS TO THE PAND FAMILY.
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                                                                                                         Similarity
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                                                                                                                                                                  273 AA;
                                                                                        Conservative
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45.5%;
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26945 MW; Al30EFD95E8719BA CRC64;
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          InterPro: IPR02735; eIF5_eIF2B.
Pfam; PF01873; eIF5_eIF2B; 1.
ProDom; PD004078; eIF5_eIF2B; 1.
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RESULT 15
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EMBL; M21813; AAA34589.1; -. EMBL; Z67751; CAA91607.1; -. EMBL; Z73594; CAA97959.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Ellipse the European Bioinformatics Institute. There are no restitute to the surface of 
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nature 387:103-105(1997).
-i- FUNCTION: EIF-2 FUNCTIONS IN THE EARLY STEPS OF PROTKIN SYNTHESIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-88311063; PubMed-3136928;
Donahue T.F., Cigan A.M., Pablich E.K., Valavicius B.C.;
"Mutations at a Zn(II) finger motif in the yeast eIF-2 beta gene after ribosomal start-site selection during the scanning process.";
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01-OCT-1989 (Rel. 12, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                         or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                             entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                       use by non-profit institutions as long modified and this statement is not removed.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Saccharomyces cerevisiae (Baker's yeast).
Eukaryola; Fungi; Ascomycola; Saccharomycolina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUI3 OR TIF212 OR YPL237W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryotic translation initiation factor 2 beta subunit (eIF-2-beta).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P09064;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SIMILARITY: BELONGS TO THE EIF-2-BETA / EIF-5 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-97313271; PubMed-9169875;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPLEX HINDS TO A 40S RIBOSOMAL SUBUNIT, FOLLOWED BY MRNA BINDING TO FORM A 43S PREINITIATION COMPLEX, JUNCTION OF THE 60S RIBOSOMAL SUBUNIT TO FORM THE 80S INTITATION COMPLEX IS PRECEDED BY HYDROLYSIS OF THE GTP BOUND TO EIF-2 AND RELEASE OF AN EIF-2-GDP HINARY COMPLEX, IN ORDER FOR EIF-2 TO RECYCLE AND CATALYZE ANOTHER ROUND OF INITIATION, THE GDP BOUND TO FIF-2 MOST EXCHANGE WITH GTP BY WAY OF A REACTION CATALYLED BY EIF-2B.

**SUBUNIT: HETEROTRIMER COMPOSED OF AN ALPHA, A BETA, AND A GAMMA THAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BY FORMING A TERNARY COMPLEX WITH GTP AND INITIATIOR TRNA. THIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FUNCTION: EIF-2 FUNCTIONS IN THE EARLY STEPS OF PROTEIN SYNTHESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AB972;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nere are no restrictions as its content is in
                                                                                                                                                                                                                                                                                                                                                                                                         Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL outstation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 a collaboration
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\$29368; \$29368. \$0006158; \$UI3.

Title: Perfect score:

on:

Scoring table: Sequence:

BLOSUM62

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Minimum DB seq length: 0
Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
                                                                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            January 15, 2003, 10:29:39; Search time 25.5714 Seconds (without alignments) 88.635 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             671580 seqs, 206047115 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gapop 10.0 , Gapext 0.5
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1: sp_archea:
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                                                                                        Q9REF0
P91228
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                         Q9CDK0
Q9JEU9
Q9CKQ5
Q9CKQ5
Q9A3W3
Q99X18
                                                                                                                                   Q9XI48
Q9V1T1
                                                                                                                                                        Q8XS63
                                                                                                               Q8U6Z1
                                                                                                                                                                                                                       SUMMARIES
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                                 Q8svp8 ei
Q9cdk0
Q9jeu9
Q9ckq5 i
Q9a3w3
                                                                                        Q8u6zl agrobacteri
Q9ref0 bradyrhizob
P91228 caenorhabdi
                                                                                                                       Q9x148 arabidopsis
Q9v1tl pyrococcus
Q9x312 bacillus an
                                                                                                                                                                                       Description
   Q99x18
Q8rb89
Q98c69
                                                                                                                                                        Q8xs63 ralstonia s
O66691 aquifex aeo
                                                                             encephalito
            staphylococ
thermoanaer
    rhizobium l
                                   caulobacter
                                             pasteurella
                                                        human immun
                                                                   lactococcus
                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 1
Q8xs63
                                             Query Match
Best Local
   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q8XS63 PRELIMINARY; PRT; 519 AA.
Q8XS63;
Q1-MAR-2002 (TrEMBLrel. 20, Created)
Q1-MAR-2002 (TrEMBLrel. 20, Last sequence update)
Q1-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Probable bifunctional: precorrin-3 methyltransferase and precorrin-6x
reductase oxidoreductase protein (EC 2.1.1.131).
CBLJH OR RSP0618 OR RS03749.
                                                                                                         Salanoubat M., Génin S., Artiguenave F., Gouzy J., Mangenot S., Arlat M., Billault A., Brottler P., Cames J.C., Cattolico L., Chandler M., Choisne N., Claudel-Renard C., Cunnac S., Demange N., Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T., Siguier P., Thebault P., Whalen M., Wincker P., Levy M., Weissenbach J., Boucher C.A.; "Genome sequence of the plant pathogen Ralstonia solanacearum."; mature 415:497-502(2002).

EMBLJ, A646079; Can17769.1; -.

InterPro: IPROGN723; CbiJ.

InterPro: TROGN723; CbiJ.
                                                                 Pfam; PF02571; CbiJ; 1.
Pfam; PF00590; TP_methylase; 1.
TIGRFAMs; TIGR00715; precor6x_red; 1.
                                            Transferase; Methyltransferase; Plasmid; Complete proteome SEQUENCE 519 AA; 55892 MW; ED701EC2F7D56392 CRC64;
                                                                                                InterPro; IPR000878; Cor/por_Metransf.
                                                                                                                                                                                                                       MEDLINE-21681879; PubMed-11823852;
                                                                                                                                                                                                                                   STRAIN-GMI1000;
                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                NCBI_Tax1D=305;
                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; beta subdivision; Ralstonia group;
                                                                                                                                                                                                                                                                                               Plasmid megaplasmid
                                                                                                                                                                                                                                                                                                           Ralstonia solanacearum (Pseudomonas solanacearum)
   Local Similarity hes 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1448
1469
1531
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747
757
757
805
986
989
1230
72.2%; Score 39; DB 77.8%; Pred. No. 27; tive 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0903Z6
093YS5
09NJ08
P77542
0937B6
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Q59971
Q5989F3
0 Q94LB4
0 Q44755
P97150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   L Q9CXB2
Q59311
7 Q9VIY0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5 Q9KEL7
7 Q8TXR1
Q93NQ2
Q93WR8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9XIE2
Q8RSH6
Q9JP28
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Q94964
Q94973
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Q92FP6
Q8YAQ3
Q8TMG8
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                    DB 16; Length 519;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9a4i8 caulobacter
Q92fp6 listeria in
Q8yaq3 listeria mo
Q8tmg8 methanosarc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q8txr1 methanopyru
Q93nq2 escherichia
Q93wr8 medicago va
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q937b6 pseudomonas
Q9xie2 arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9v1i5 drosophila
Q9u3z6 drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q941b4 oryza sativ
Q44755 borrelia bu
P97150 escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9ya31 aeropyrum p
Q59971 streptomyce
Q989f3 rhizobium 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9cxb2 mus musculu
Q59311 clostridium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q94964 drosophila
Q94973 drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q94849 drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9jp28 pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q8rsh6 uncultured
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q93ys5 arabidopsis
Q9nj08 drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P77542 escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9v1y0 pyrococcus
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Database

7: 8: 9: 10: 12: 13:

sp_mhc:*

Result

Score

Match

Length

Query

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RESULT 2
066691
 RESULT 3
Q9XI48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local
        STRAIN-CV. COLUMBIA;
Vysotskaia V.S., Schwartz J.R., Yu G., Toriumi M., Lenz C., Liu S.,
Lee J., Liu A., Li J., Kremenetskaia I., Luros J., Gonzalez A.,
Altafi H., Araujo R., Brooks S., Buehler E., Chao Q., Conn L.,
Conway A.B., Dunn P., Hansen N., Huizar L., Khan S., Kim C., Palm C.,
Rowley D., Shinn P., Walker M., Davis R.W., Ecker J.R.,
                                                                                                                                                                 Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
                                                                                                                                                                                                                                              09x148;
01.NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro: IPR001993; Mitoch_carrier.
Pfam; PF00563; BAL; 1.
Pfam; PF00990; GGDEF; 1.
SMART; SM00267; DUF1; 1.
SMART; SM00052; DUF2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical protein; Complete proteome. SEQUENCE 850 AA; 97669 MW; C02DCEF91DBCDEB0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 392:353-358(1998).
EMBL; AE000686; AAC06656.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L., Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay M., Huber Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                              Q9XI48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00215; MITOCH_CARRIER; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TIGRFAMS; TIGRO0254; GGDEF; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    aeolicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Aquificae; Aquificales; Aquificaceae; Aquifex.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Aquifex aeolicus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical protein AQ_367.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    066691;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   066691
Federspiel N.A., Theologis A.;
                                                                                                                                      NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001633; EAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "The complete genome of the hyperthermophilic bacterium Aquifex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-98196666; PubMed=9537320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=63363;
                                                                                                                                                                                                                                                                                                                                                                                        227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             346 LAQELALPY 354
                                                                                                                                                                                                                                                                                                                                                                                                                       1 LSQELAIPYEE 11
                                                                                                                                                                                                                                                                                                                                                                                        SRHMDVPYEE 237
                                                                                                                                                                                                                                 15 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   l Similarity
6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                       Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  72.2%; 54.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 39;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
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RESULT 4
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Best Local Similarity
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01-MAY-2000
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATP-binding. spouence 1451 AA; 163602 MW;
                                                                                                                                                                                                                    01-NOV-1999
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9VIT1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Probom; PD000006; ABC_transportr; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00005; ABC_tran; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Arabidopsis thaliana chromosome 1 BAC F9L1 sequence."; Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases EMBL; AC007591; AAD39650.1; -.
STRAIN=STERNE;
                                                                                                                                       Plasmid virulence plasmid PX01
                                                                                                                                                                  Bacillus anthracis
                                                                                                                                                                                               PX01-42.
                                                                                                                                                                                                                                                                      Q9x312;
01-NOV-1999
                                                                                                                                                                                                                                                                                                                         Q9X312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART; SM00471; HDc; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 417 AA; 47906 MW; 59C62CB32C441833 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            structure and evolution."; Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID-29292;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein PAB2116 PAB2116.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9V1T1;
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InterPro; IPR003439; ABC_transportr.
                     SEQUENCE FROM N.A.
                                                                     NCBI_TaxID=1392;
                                                                                               Bacillaceae;
                                                                                                                  Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF01966; HD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro: IPRO02819; HD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AJ248284; CAB49268.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-ORSAY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pyrococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaccae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Pyrococcus abyssi genome sequence: insights into archaeal chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     491 LSNELSVPYDK 501
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                                                                                                                                                                                                               (TrEMBLrel. 12, Created)
(TrEMBLrel. 12, Last sequence update)
(TrEMBLrel. 19, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Trembline). 13, last sequence update) (Trembline). 21, Last annotation update)
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                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                          Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        68.58;
72.78;
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54.5%;
                                                                                                               Bacillus/Clostridium group; Bacillales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 38;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Mismatches
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Pred. No. 54;
                                                                                                                                                                                                                                                                                                                      PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 17; Length 417;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 10;
                                                                                                                                                                                                                                                                                                                      ΑA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C., Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A., Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D. Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M., Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M., Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Keim P., Koehler T.M., Lamke G., Kumano S., Mahillon J., Manter D., Martinez Y., Ricke D., Svensson R., Jackson P.J.;
"Sequence and organization of pXOI, the large Bacillus anthracis plasmid harboring the anthrax toxin genes.";
J. Bacteriol. 181:6509-6515(1999).
                                                                                                                                                                                                                                                             Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M., Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L., Houmiel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F., Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B., Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P., Okura Y.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rhizobiaceae; Rhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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Okinaka R.T., Cloud K., Hampton O., Hoffmaster A.R., Hill K.K.,
                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                   "Genome sequence of the plant pathogen and biotechnology agent agrobacterium tumefaciens {\sf C58."};
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-21608550; PubMed-11743193;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Agrobacterium tumefaciens (strain C58 / ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MELA OR ATU4665 OR AGR_L_436
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                                                                                                                                                   Complete proteome.
                                                                                                                                                                   EMBL;
                                                                                                                                                                                                    Science 294:2323-2328(2001).
                                                                                                                                                                                                                                                    Cielo
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                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                      Science 294:2317-2323(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nester E.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_{TaxID}=176299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria; alpha subdivision: Rhizobiaceae group;
                                                                                                                                                                                                                                                                                                                                                                                                                                      "The genome of the natural genetic engineer Agrobacterium tumefaciens
200 LAHDLDIPYEE 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               219 ISQEVAIPSED 229
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                               1 LSQELAIPYEE 11
                                                                                                                                                                   AE009395; AAL45459.1; ALT_INIT
AE008220; AAK88782.1; -.
                                                                                                                                                                                                                                                    C., Slater S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AF065404; AAD32346.1;
                                                                                 Similarity
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                                                                                                                                   474 AA;
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                                                                   Conservative
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                                                                                 63.68;
                                                                                                                                     53483 MW;
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63.6%;
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                                                                                 Pred. No.
                                                                                                   Score 37;
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                                                                                                 DB 16; Length 474;
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                                                                   Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9REF0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bradyrhizobium japonicum.
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Bradyrhizobium group; Bradyrhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "The dnaKJ operon belongs to the sigm32-dependent class of heat shock genes in Bradyrhizobium japonicum."; Mol. Gen. Genet. 254:195-206(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9REF0;
01-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9REF0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAY-1997 (TrEMBLIRE) 03, Created)
01-MAY-1997 (TrEMBLIRE) 03, Last sequence update)
01-DEC-2001 (TrEMBLIRE) 19, Last annotation update
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Minder A.C., Fischer H.M., Hennecke H., Narberhaus F.; "Role of HreA and CIRCE in the heat shock regulatory network of Bradyrhizobium japonicum.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Minder A.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical
                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical 46.7 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mol. Microbiol. 39:1186-1198(2001).
EMBL; Y09633; CAH60666.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-110SPC4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-97261868; PubMed-9108282;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=110SPC4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID-375;
                                                            None;
                                                                                                 MEDLINE=99069613; PubMed=9851916;
                                                                                                                                          STRAIN-BRISTOL N2;
                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                       NCBI_TaxID-6239;
                                                                                                                                                                                                                                                                                                                                                                                                         Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P91228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00857; Isochorismalase; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        critical for an efficient symbiosis with the soybean
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Phosphatidylcholine levels in Bradyrhizobium japonicum membranes are critical for an efficient symbiosis with the soybean host plant.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Minder A.C., de Rudder K.E.E., Narberhaus F., Fischer H.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=21150465; PubMcd=11251836;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=110SPC4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=20082837; PubMed-10613857;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
Genome sequence of the nematode C. elegans: a platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      125 LSKULATIHAE 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 LSQELATEYEE II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteriol. 182:14-22(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PR000868; Isochorismatase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        240 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Narberhaus F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25.4 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Geiver O.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25406 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Babst M., Hennecke H., Fischer H.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        152ED79DACA1A2E5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         240 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2; Length 240;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            update)
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RESULT 9
Q8SVP8
ID Q8SV
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Best Local Similarity
Thes 7; Conserve
                       Q9CDK0
                                           RESULT 10
                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q8SVP8;
01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
  Q9CDK0
                                                                                                                                                                                                                                                                                                                                                                                  Weissenbach J., Vivares C.P.; "Genome sequence and gene compaction of the eukaryote parasite Encephalitozoon cuniculi.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Encephalitozoon cuniculi.
Eukaryota; Microsporidia; Unikaryonidae; Encephalitozoon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein ECU04_1610.

ECU04_1610.
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PROSITE; PS00687; ALDEHYDE_DEHYDR_GLU; UNKNOWN_1

Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases EMBL; U80837; AAB37908.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "The sequence of C. eleg
Submitted (JAN-1997) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 investigating biology. The C. elegans Sequencing Consortium.", Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                     Nature 414:450-453(2001).
EMBL; AL590444; CAD25350.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Katinka M.D., Duprat S., Cornillot E., Metenier G., Thomarat F., Prensier G., Barbe V., Peyretaillade E., Brottier P., Wincker P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-GB-M1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q8SVP8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Waterston R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Du Z., Goela D.;
                                                                                                                                                                                                                                                                                          Initiation factor; Hypothetical protein SEQUENCE 627 AA; 72118 MW; BBC37862
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Delbac F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=21576510; PubMed=11719806;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-GB-M1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=6035;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Direct Submission.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                472
                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                         1 LSQELAIPYEE 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 LSQELAIPYEE 11
                                                                                                              LSEELSVAYED 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ISPELAVPNEE 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                     El Alaoui H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           412 AA;
                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             elegansto the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           46671 MW; 8CBACE59E416A294 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66.7%;
                                                                                                                                                                                                                         54.5%;
                                                                                                                                                                                                                                                 66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peyret P., Saurin W., Gouy M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cosmid F07E5.";
EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                 Score 36;
                                                                                                                                                                                                    Pred. No. 1.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
    PRT;
                                                                                                                                                                                                                                                                                               BBC37862A41B820D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               627 AA
    59 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             84;
                                                                                                                                                                                                                                                    DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 412;
                                                                                                                                                                                                                                                 Length 627;
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                                                                                                                                                                                                      Indels
                                                                                                                                                                                                      0;
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                                                                                                                                                                                                      Gaps
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Q0JEUD

ID USLEU

AC QJEUD

DT 01-OC

DT 01-DC

DT 01-DC

DT 01-DC

ILIMAN

OC VITUS

ON WCBL

RN [1]

RN [1]

RN EDLI

RN EDLI

RA Yamac

RA Tamac

RA Tam
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           밁
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                     Q9CKQ5
                                                                                                                                                    Qy
    B
                                           RESULT 12
                                                                                                                뮵
                                                                                                                                                                                                    Best Local Similarity Matches 6; Conserv
                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
  Q9CKQ5
                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                             Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                      Arch. Virol. 144:2291-2311(1999).
EMBL; AF120196; AAF68138.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Congo."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Yamaquchi-Kabata Y., Taniquchi Y., Ido E., Kaptue L., M'pelle P., Parra H.J., Ikeda M., Hayami M., Miura T.; "Genetic diversity of HIV-1 group M from Cameroon and Republic of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human immunodeficiency virus type 1.
Viruses; Retroid viruses; Retroviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9JEU9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9JEU9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "The complete genome sequence of the lactic acid bacterium Lactococcus lactis ssp. lactis IL1403."; Genome Res. 11:731-733(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bolotin A., Wincker P., Mauger S., Jallic
Weissenbach J., Whrlich S.D., Sorokin A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=1360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YXAB OR LL2219.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9CDK0;
                                                                                                                                                                                                                                                                                                                                       NON_TER
                                                                                                                                                                                                                                                                                                                                                                                     InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-20129484; PubMed-10664385;
Mboudjeka I., Bikandou B., Zekeng L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=CNG30,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID-11676;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Integrase (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AE006450; AAK06317.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=21235186: PubMed=11337471;
Bolotin A., Wincker P., Mauger S., Jaillon O., Malarme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-IL1403;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptococcaceae; Lactococcus
                                                                                                                                                                                                                                                                                                                    NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
                                                                                                                47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10 LRQELAIPF 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 LSQELAIPY 9
                                                                                                                                                         1 LSQELAIPY 9
                                                                                                           IAQELGIPY 55
                                                                                                                                                                                                                                                                                                                                                        PF00665; rve; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Retroid viruses;
                                                                                                                                                                                                                                                                                                                                                                                     IPR001584; Rve.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        59 AA; 7043 MW;
                                                                                                                                                                                                                                                                                            95 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                    95
                                                                                                                                                                                                                                                                                            10490 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64.8%;
77.8%;
                                                                                                                                                                                                                       64.8%;
66.7%;
                                                                                                                                                                                                 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           80903DC52808162A CRC64;
                                                                                                                                                                                                                                            Score 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 35;
Pred. No.
                                                                                                                                                                                                                         Pred. No.
                                                                                                                                                                                                                                                                                            AFB8FD5EC6765D32 CRC64;
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
202 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Takehisa J., Harada Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             B
                                                                                                                                                                                                                                               DB 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lentivirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  <del>ب</del>
                                                                                                                                                                                                                                            Length 95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 59;
                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                 Gaps
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RESULT 13
Q9A3W3
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                                                                                                                                                                       A TO DESCRIPTION OF THE PROPERTY OF THE PROPER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            망
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                                                        Matches
                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9CKQ5;
01-JUN-2001
01-JUN-2001
01-JUN-2002
                                                                                                                                                  InterPro; LPKUVVVII.
Plam; PF00043; GST_C; 1.
Pfam; PF02798; GST_N; 1.
Pfam; PF02798; GST_N; 1.
Transferase; Complete proteome.
708 AA; 22885 MW;
                                                                                                                                                                                                                                                                                                                                                                                 Nierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E., Eisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R., Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B., DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H., Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K., Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K., Kolonay J.F., Tran K., Wolf A., Vanathevan J., Ermolaeva M., White O., Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M., "Complete genome sequence of Caulobacter crescentus."; "Complete genome sequence of Caulobacter crescentus."; "Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Glutathione S-transferase family protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur V.; "Comple 3 genomic sequence of Pasteurella multocida Pm70."; Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
EMBL; AE006192; AAK03635.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical PM1551.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Caulobacter crescentus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9A3W3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9A3W3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF02798; GST_N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR004046; GST_Cterm.
InterPro; IPR004045; GST_Nterm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE*21145866; PubMed=11248100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-PM70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pasteurella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pasteurella multocida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=21173698;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID-155892;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID-747;
                                                                                                                                                                                                                                                                                                             InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20 LLKELAIPFE 29
                                                                                   Local Similarity
1 LSQELAIPYE 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 LSQELAIPYE 10
                                                                                                                                                                                                                                                                                                                                        CC3088; -
                                                                                                                                                                                                                                                                                                                                                                  AE005972; AAK25050.1; -.
                                                        6
                                                                                                                                                                                                                                                                                                             IPR004046; GST_Cterm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      202 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (TrEMBLrel. 17, Created)
(TrEMBLrel. 17, Last sequence update)
(TrEMBLrel. 21, Last annotation update)
1 protein PM1551.
                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein; Complete proteome.
02 AA; 23180 MW; 5E6D95AE3FE02E73 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PubMed=11259647;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CB15;
                                                                                64.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alpha subdivision; Caulobacter group;
                                                        ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2;
                                                                                Score 35; DB
Pred. No. 65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                    A48AC2988C284DD1 CRC64;
                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   208 AA
                                                                                                           DB 16; Length 208;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 16; Length 202;
                                                     <u>ب</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                        0;
                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                        0
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IVE OR TTE0933

01-JUN-2002 (TREMBLrel. 21, Created)
01-JUN-2002 (TREMBLrel. 21, Last sequence update)
01-JUN-2002 (TREMBLRel. 21, Last annotation update)
Branched-chain amino acid aminotransferase/4-amino-4-deoxychorismate

Thermoanaerobacter tengcongensis.
Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;

Thermoanaerobacteriales; Thermoanaerobacteriaceae;

Thermoanaerobacter

Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J. Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling Tan H., Chen R., Wang J., Yu J., Yang H.;

SEQUENCE FROM N.A. STRAIN=MB4T / JCM11007;

NCBI_TaxID=119072;

MEDLINE=21992816; PubMed=11997336;

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099X18
AC AC DITON
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SPECIES-S.aureus (strain Mu50), and S.aureus (strain N315);
MEDLINE-21311952; PubMed-11418146;
MEDLINE-21311952; PubMed-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical protein SAV0203.
SAV0203 OK SA0197.
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q99X18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00211; ABC_TRANSPORTER; UNKNOWN_1.
Hypothetical profein; Complete proteome.
SEQUENCE 240 AA; 27319 MW; 29C122944033DE4E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lancet 357:1225-1240(2001).

EMBL; AP003358; BAB56365.1; -.

EMBL; AP003129; BAB41418.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Staphylococcus aureus (strain Mu50 / ATCC 700699), and Staphylococcus aureus (strain N315).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q99X18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00005; AHC_tran; 1.
Probom; PD000006; ABC_transportr; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR003593; AAA_ATPase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                aureus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=158878,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Staphylococcus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Whole genome sequencing of meticillin-resistant Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro: IPR003439; ABC_transportr.
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18 LLEELSLPYE 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
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RT "A complete sequence of T. tengcongensis genome.";
RL Genome Res. 12:689-700(2002).
DR EMBL, RED13059; AAMAZ189.1; -.
KW Transferase; Aminotransferase; Complete proteome.
SQ SEQUENCE 291 AA; 32346 MW; 105072D27AB06FFE CRC64;
SEQUENCE 291 AA; 32346 MW; 105072D27AB06FFE CRC64;

Query Match
Best Local Similarity 54.8%; Score 35; DB 16; Length 291;
Best Local Similarity 54.5%; Pred. No. 92;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0; ",
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0; ",

29 1 LSGELAIPYEE 11
:::|| | | | | | | |
Db 218 IARELNIPFEE 228

Search completed: January 15, 2003, 12:35:45
Job time: 32.5714 secs
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Score

Query Match Length DB

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Description

SUMMARIES

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OM protein - nucleic search, using frame_plus_p2n model
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Searched:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -CQ-CG912_1/USPTO_Spool/US09823649/runat_14012003_151001_29119/app_query.fasta_1.1393
-CD=N_Geneseq_101002 -QFMT=fastap -SUFFIX-rng -MINMATCH=0.1 -LOOPCL-0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MAIRIX-blosum62 -TRANS-human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE-pct -THR_MIN-0 -ALIGN-15
-MODE=LOCAL -OUTFMT=pto -NORM-ext -HEAPSIZE=500 -MINLEN=0 -MAILEN=2000000000
-MODE=LOCAL -OUTFMT=0 - NORM-ext -HO12003_151001_29119 -NCPU=6 -TCPU=3
-USBR=US09823649_@CGN_1_1_0_@runat_14012003_151001_29119 -NCPU=6 -TCPU=3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_THREDIS-120
-NO_XLPXY -NO_MMAP -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-WARN_TIMEDUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Command line parameters: .. *
-MODEL=frame+_p2n.model -DEV=x1h
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Ygapop 10.0,
Fgapop 6.0,
Delop 6.0,
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54
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1: /SIDS2/gcgdata/geneseg/genesegn-emb1/NA1980.DAT:*

2: /SIDS2/gcgdata/geneseg/genesegn-emb1/NA1983.DAT:*

3: /SIDS2/gcgdata/geneseg/geneseqn-emb1/NA1983.DAT:*
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Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                    | SIDS2/gcgdata/geneseq/geneseqn-emb1/NA199.DAT: *
                                                                                                                                                                                                                                                                                                                                                                                                                       /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1986.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1987.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1988.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1989.DAT:*
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/SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*
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			DNA cleavage;				0 вр.	ALIGNMENTS	ABA97303	ABA97301	AAF57663	AAU24225	AAQ24223 AAQ24224	AAQ23993	AAQ24324	AAQ23995	AAQ24325	AAQ23994 AAQ24013	AAQ24326	AAQ23996 AAQ24320	AAD24823	AAD24819 AAD24822	AAQ24327	AAQ23997 AAQ24321	AAS00718	AAS00717	AAT32327	AAZ29461	AAT47960	AAX27132	AAT4/951	AAT47959	AAZ29460	AAQ24322	AAQ23998	AAV63407	AAV65786	AAT76647	AAT70347	AAQ80745	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
			RNA cleavage; 5' nuclease; ds.					S	sensit	sensiti	T. aquaticus (iqq) Wild type Taq DNA	ied Tag	Modified Tag polym	, T	Mutant thermostabl	Mutant thermostabl	Mutant thermostabl	Mutant thermostabl	Mutant thermostabl	Mutant thermostabl	Polylysine (PL)	Sulfolobus acidoca	Mutant thermostabl	Mutant thermostabl	Chimeric Caullag DN	Chimeric CauTaq DN	Thermus flavus DNA	Thermostable DNA d	Mutant Tag polymer	FY4 polymerase cod	FY2 polymerase cod	Mutant Tag polymer	Thermostable DNA d	Mutant thermostabl	Mutant thermostabl	DNA sequence of a	Thermus aquaticus Nucleotide sequenc	e 5' nucle	s deficie	5' Nuclease Irom T Mutant Thermus agu	

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the Lotal score distribution.

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RESULT 2
AAT27686
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The Tag DNA-polymerase (DNAP) gene was amplified by PCR. Amplified fragments were ligated into pTTQ18 vector, which contains the hybrid trp-lac (tac) promoter. An amplification/scloction protocol was used to isolate clone 4B containing a mutated Tag DNAP gene (mutTag) (sequence given in AAQ80746) having normal 5 nuclease activity but less than 1% of the wt Tag DNAP activity. mutTag was cut from pTTQ18 by EcoRI-SalI digestion and cloned into pET-3c.
                                                                                                                                                                                                                                            p53; mutant; mutation; cleavage; nuclease; cleavase; Thermus; Escherichia; Saccharomyces; Campylobacter; Mycobacterium; Shigella; Staphylococcus; identification; detection; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             1133 CTCTCCCAGGAGCTAGCCATCCCTTACGAGGAG 1165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Thus clone was digested with BstXI and BamHI. The DNA was treated with DNAPEC1 Klenow fragment and dNTPs, blunt-ended and religated, resulting in an in-frame deletion of 903 nucleotides. The DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5' Nuclease(s) derived from thermostable DNA polymerase(s) - have cleavage activity with reduced synthetic ability, used for detection of specific target sequences.
30-AUG-1995;
09-NOV-1994;
                                            09-NOV-1995;
                                                                         23-MAY-1996
                                                                                                        W09615267-A1.
                                                                                                                                                                                                                Thermus aquaticus
                                                                                                                                                                                                                                                                                                          Mutant Thermus aquaticus DNA polymerase coding sequence (Clone 4F).
                                                                                                                                                                                                                                                                                                                                                                                                  AAT27686 standard; DNA; 1600 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1600 BP; 287 A; 518 C; 553 G; 242 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 5; Page 95-96; 159pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Brow MAD, Dahlberg JE, Lyamichev VI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    04-JUN-1993;
                                                                                                                                                                                                                                                                                                                                      18-NOV-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                     AAT27686;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence of the resulting 5' nuclease is given in AAQ80745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (THIR-) THIRD WAVE TECHNOLOGIES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-JUN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 LeuSerGlnGluLeuAlaIleProTyrGluGlu 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93US-0073384.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94WO-US06253
94US-0337164
              95US-0520946
                                             95WO-US14673
                                                                                                                                    /product= Mutant DNA polymerase.
                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0.0649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches:
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QY

1133 CTCTCCCAGGAGCTAGCCATCCCTTACGAGGAG 1165

1 LeuSerGlaGluLeuAlalleProTyrGluGlu 11

Db 113 RESULT 3 AAT70347

AAT70347 standard; DNA; 1600 BP

Thermus aquaticus

Synthetic

03-APR-1998 (first entry)

AAT70347;

Synthesis deficient Tag DNA polymerase gene clone 4F.

DNA polymerase; tag polymerase gene; DNAP; 5' nuclease activity; Cleavase BB; DNA cleavage; reduced synthetic activity; ss.

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US-09-823-649A-3 (1:11) x AAT27686 (1-1600)
                                                              Query Match:
                                                                                                                                                                           Alignment Scores:
                                                                                   Best Local Similarity:
                                                                                                          Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                              The method may also be used for the identification of viruses, especially hepatitis C virus and simian immunodeficiency virus. Thermus aquaticus (Taq) DNA polymerase was amplified using two primers (ART27679, ART27680). The Taq polymerase DNA was inserted into the BamHI restriction site of the expression vector pET-3c and mutant genes were created from that construct. This mutant was created after the material distriction of the construct.
                                                                                                                                                    . No.:
                                                                                                                                                                                                                                                                               genes were created from that construct. This mutant was created after the vector was digested with BstXI and BamHI. The DNA was then treated with the Klenow fragment of DNAPEC1 to trim both 3' overhangs to blunt ends which were then ligated together, resulting in an in frame deletion of 903 nucleotides. The resulting mutant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alternatively, microbial gene sequences. Cleavage products are compared to the cleavage products of reference gene sequences method is used for detecting mutation in the man p53 gene; for jobality for a sequence of micro
                                                                                                                                                                                                                   Sequence 1600 BP; 286 A; 519 C; 553 G; 242 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       identifying strains of microorganisms, especially bacteria selected from the the group of members of the genera Campylobacter, Escherichia, Mycobacterium, Salmonella, Shigella and Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cleavage of nucleic acids using an enzyme, especially a nuclease selected from the group consisting of Cleavase (RTM) BN enzyme,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cleavage of nucleic acids to detect mutation(s) - allows detection esp. in human p53 gene, to identify strains of microorganisms and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P-PSDB; AAR96267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oldenburg MC, Olive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Brow MAD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09-MAR-1995;
07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       oligonucleotide containing a human p53 gene sequence or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              polymerase, Escheri
Radl/Radl0 complex.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 2A; Page 257-258; 433pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            viruses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1996-259862/26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (THIR-) THIRD WAVE TECHNOLOGIES INC.
                                                                                                                                                                                                                                                               Taq polymerase is also referred to as the Cleavase BB enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Thermus aquaticus DNA polymerase,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dahlberg JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Escherichia coli ExoIII and the Saccharomyces cerevisiae Domplex. The nucleic acid substrate is preferably an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95US-0402601.
95US-0484956.
                                                              100.00%
100.00%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fors L, Heisler LM, Lyamichev VI;
                                       Caps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Thermus thermophilus DNA
                                                                 indels:
                                                                                     Mismatches:
                                                                                                        Conservative:
                                                                                                                               Matches:
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RESULT 4
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                                                                                                                                                                                                        AAQ24007
                                                                                                                                                                                                                                                                                                                                                                                                                US-09-823-649A-4 (1-11) x AAQ24008 (1-2043)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Thermostable DNA polymerases with altered 5'-3' exo nuclactivity - having conserved regions mutated or deleted, in e.g. PCR, sequencing and detection assays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5'-3' nuclease activity may facilitate higher sensitivity allelic discrimination in a combined polymerase ligase chain reaction (PLCR) assay. An enhanced amt. of 5'-3' exonuclease activity may be desirable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 polymerases are useful in many recombinant DNA techniques, esp. nucleic acid amplification by PCR, self-sustained sequence replication (SSR) and high temp. DNA sequencing. The absence of the control of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The sequence is that of Thermus species sps17 polymerase DNA which has been mutated. The mutation designated pSPSd2-151 causes the polymerase enzyme produced to exhibit a different amt. of 5'-3'
Mutant thermostable DNA polymerase psPSd2-73.
                                                            22-OCT-1992 (first entry)
                                                                                                                                                                           AAQ24007 standard; DNA; 2277
                                                                                                                                                                                                                                                                                                    1576 CTCTCCCAGGAGCTCTCCATCCCCTACGAGGAG 1608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NO. .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   a range of recombinant proteins having 5'-3' exonuclease activity to a complete lack of activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  in enzymes used in homogeneous assays for the amplification and detection of a target nucleic acid sequence. Mutation of the DNA encoding particular regions of the enzymes can be used to prepare
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 11; Page 59; 185pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1992-150885/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-SEP-1990;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9206200-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2043 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          See also AAQ23993-Q24013, AAQ24320-36 and AAQ24343-60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             exonuclease activity than the native enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (CETU ) CETUS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-SEP-1990;
                                                                                                                                                                                                                                                                                                                                                      1 LeuSer***GluLeuSerIleProTyrGluGlu 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gelfand DH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               90US-0590213.
90US-0590466.
90US-0590490.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           91WO-US07035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       339 A; 697 C; 703 C; 304 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.8
48.00
90.91%
90.91%
96.00%
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     for use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              XSX
                                                                                                                                                                                                           Дb
                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match:
                                                                                                                     AAQ24006
                                                                                                                                                     RESULT 5
                                                                                                                                                                                                                                                                                                                             US-09-823-649A-4 (1-11) x AAQ24007 (1-2277)
                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-SEP-1990;
28-SEP-1990;
28-SEP-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               polymerases are useful in many recombinant DNA techniques, esp. nucleic acid amplification by PCR, self-sustained sequence replication (SSR) and high temp. DNA sequencing. The absence of 5'-3' nuclease activity may facilitate higher sensitivity allelic discrimination in a combined polymerase ligase chain reaction (PLCR) assay. An enhanced amt. of 5'-3' exonuclease activity may be desirable
                                                                                                                                                                                                        1810 CTCTCCCAGGAGCTCTCCATCCCCTACGAGGAG 1842
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                detection of a target nucleic acid sequence. Mutation of the DNA encoding particular regions of the enzymes can be used to prepare a range of recombinant proteins having 5'-3' exonuclease activity to a complete lack of activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The sequence is that of Thermus species sps17 polymerase DNA which has been mutated. The mutation designated ps9802-73 causes the polymerase enzyme produced to exhibit a different ant. of 5'-3' exonuclease activity than the native enzyme. Thermostable DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Thermostable DNA polymerases with altered 5'-3' exo nuclease activity - having conserved regions mutated or deleted, for use in e.g. PCR, sequencing and detection assays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       old_sequence
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                               AAQ24006;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2277 BP; 378 A; 779 C; 779 G; 341 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    See also AAQ23993-Q24013, AAQ24320-36 and AAQ24343-60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 11; Page 59; 185pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P-PSDB; AAR23154.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Abramson RD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (CETU ) CETUS CORP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        W09206200-A
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                                                                                        AAQ24006 standard; DNA; 2367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-APR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   in enzymes used in homogeneous assays for the amplification and
                                                                                                                                                                                                                                                             1 LeuSer***GluLeuSerIleProTyrGluGlu 11
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sequence."
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                                                                                                                                                                                                                                                               DB:
                                                                                                                                                                                                                                                                        Query Match:
                                                                                                                                                                                                                                                                                   Best Local Similarity:
                                                                                                                                                                                                                                                                                                                     Alignment Scores: Pred. No.:
                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
                                                                                                                                                                                        1168 CTCTCCCAGGAGCTCTCCCATCCCCTACGAGGAG 1200
                                                                                                                                                                                                                                                                                                                                                                                        detection of a target nucleic acid sequence. Mutation of the DNA encoding particular regions of the enzymes can be used to prepare a range of recombinant proteins having 5'-3' exonuclease activity to a complete lack of activity.
                     Thermus species sps17
                                             5'-3'; exonuclease; PCR; amplification; SSR; sequencing; PLCR;
                                                                    Mutant thermostable DNA polymerase pSPSd2-199.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           has been mutated. The mutation designated pSPSdA288 causes the polymerase enzyme produced to exhibit a different amt. of 5'-3' exonuclease activity than the native enzyme. Thermostable DNA polymerases are useful in many recombinant DNA techniques, esp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-SEP-1990;
                                                                                                                                         AAQ24009 standard; DNA; 1899 BP
                                                                                                                                                                                                                                                                                                                                                        Sequence 1635 BP; 267 A; 572 C; 559 G; 237 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   discrimination in a combined polymerase ligase chain reaction (PLCR) assay. An enhanced amt. of 5'-3' exonuclease activity may be desirable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nucleic acid amplification by PCR, self-sustained sequence replication (SSR) and high temp. DNA sequencing. The absence of 5'-3' nuclease activity may facilitate higher sensitivity allelic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 11; Page 59; 185pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Abramson RD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-SEP-1991;
                                                                                            22-OCT-1992 (first entry)
                                                                                                                    AAQ24009;
                                                                                                                                                                                                                                                                                                                                                                               See also AAQ23993-Q24013, AAQ24320-36 and AAQ24343-60.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        activity - having conserved regions mutated or deleted, for use
in e.g. PCR, sequencing and detection assays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Thermostable DNA polymerases with altered 5'-3' exo nuclease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P-PSDB; AAR23157.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1992-150885/18.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-SEP-1990;
28-SEP-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-APR-1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The sequence is that of Thermus species sps17 polymerase DNA which
                                                                                                                                                                                                                                                                                                                                                                                                                                        in enzymes used in homogeneous assays for the amplification and
                                                                                                                                                                                                               1 LeuSer***GluLeuSerIleProTyrGluGlu 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gelfand DH;
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90US-0590466
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Location/Qualifiers
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RESULT 3
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                                                                                                                                                                                AAQ24008
                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
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                                                                                                                                                                                                                                                     1432 CTCTCCCAGGAGCTCTCCATCCCCTACGAGGAG 1464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     detection of a target nucleic acid sequence. Mutation of the DNA encoding particular regions of the enzymes can be used to prepare a range of recombinant proteins having 5'-3' exonuclease activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nucleic acid amplification by PCR, self-sustained sequence replication (SSR) and high temp. DNA sequencing. The absence of 5'-3' nuclease activity may facilitate higher sensitivity allelic discrimination in a combined polymerase ligase chain reaction (PLCR) assay. An enhanced amt. of 5'-3' exonuclease activity may be desirable in enzymes used in homogeneous assays for the amplification and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The sequence is that of Thermus species sps17 polymerase DNA which has been mutated. The mutation designated psp82d-199 causes the polymerase enzyme produced to exhibit a different amt. of 5'-3' exonuclease activity than the native enzyme. Thermostable DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                old_sequence
Mutant thermostable DNA polymerase pSPSd2~151.
                                                                                                                                                     AAQ24008 standard; DNA; 2043 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1899 BP; 320 A; 647 C; 647 G; 285 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        See also AAQ23993-Q24013, AAQ24320-36 and AAQ24343-60.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                polymerases are useful in many recombinant DNA techniques, esp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 11; Page 59; 185pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             activity - having conserved regions mutated or deleted,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1992-150885/18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Abramson RD, Gelfand DH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-SEP-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-SEP-1990;
28-SEP-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-SEP-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-APR-1992
                                                  22-OCT-1992 (first entry)
                                                                                                        AAQ24008;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  to a complete lack of activity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Thermostable DNA polymerases with altered 5'-3' exo nuclease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P-PSDB; AAR23156.
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                                                                                                                                                                                                                                                                                                        1 LeuSer***GluLeuSerIleProTyrGluGlu 11
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/*tag= a
/note= "nucleotides 4-597 deleted from the native
sequence."
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900S-0590490
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5'-3'; exonuclease; PCR; amplification; SSR; sequencing; PLCR; ss

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AAQ92369
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                           Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            thermostable polymerase modified to have reduced synthetic activity, where the 5' nuclease is tapable of cleaving a linear nucleic acid duplex structure to create a single, single-stranded cleavage product. The methods are used for the specific detection of nucleic acid sequences, via a cleavage-based procedure, but without the need for amplification of target sequences. Thermostable polymerases, altered to have nuclease, but not polymerase activity are preferably used due to their specificity. The cleavage product specifically formed is detected, preferably by the use of radioactively labelled oligonucleotides. These
Key
                             Thermus filiformis.
                                                        DNA-polymerase; Tfil; thermostable enzyme; ss
                                                                                         Tfil DNA-polymerase.
                                                                                                                       28-OCT-1995
                                                                                                                                                                                                                                                  2029 CTCTCCGGGGAGCTTTCCATCCCCTACGAGGAG 2061
                                                                                                                                                                                                                                                                                                                                                                                                                         No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2496 BP; 402 A; 830 C; 854 G; 410 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             describes a method for detecting the presence of a nucleic acid molecule. The method uses a thermostable 5' nuclease derived from a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Fig 2; 91pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Detection of target nucleic acid molecules - uses modified thermostable enzymes with specific cleavage activity to create specific detection products from oligo:nucleotide(s) and target
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1999-023438/02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Brow MAD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             04-JUN-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-JUN-1994;
07-DEC-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US5837450-A
                                                                                                                                                       AAQ92369;
                                                                                                                                                                                     AAQ92369 standard; DNA; 2512 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence encodes a thermostable DNA polymerase enzyme. The sequence is used in the course of the invention. The specification
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (THIR-) THIRD WAVE TECHNOLOGIES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-NOV-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     can be used in e.g. forensic testing or paternity determination
                                                                                                                                                                                                                                                                                1 LeuSer***GluLeuSerIleProTyrGluGlu 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dahlberg JE,
                                                                                                                         (first entry)
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Location/Qualifiers
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90.91%
96.00%
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                                                                                                                                                                                                                                                                                                                                            Caps:
                                                                                                                                                                                                                                                                                                                                                               Mismatches: Indels:
                                                                                                                                                                                                                                                                                                                                                                                              Conservative:
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AAQ86927
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nucleotidyltransferase DNA-directed enzyme) which has reverse-
transcriptase activity in the presence of mg2+. The enzyme is a
versatile DNA-polymerase suitable for use in DNA synthesis from DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDS
                                                                                                                                                                                                                                                                                                                                           2034 CTCTCCCAGGAGCTCTCCATCCCCTACCAGGAG 2066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2512 BP; 415 A; 862 C; 854 G; 381 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           reactions are performed in the same buffer. The enzyme has a hig
salt tolerance and is also suitable for use in cycled fluorescent
22-AUG-1986;
                          11-APR-1995
                                                                                                                                                                                                                                  05-DEC-1995
                                                                                                                                                                                                                                                                                     AAQ86927 standard; DNA; 4947 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and RNA templates, and for automated DNA sequencing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The sequence encodes thermostable DNA-polymerase Tfil (DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 7; Fig 1; 40pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bergquist PL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-NOV-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-NOV-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-1995
                                                     US5405774-A
                                                                                                                                                Thermus species sps17.
                                                                                                                                                                          Polymerase; Thermus; enzyme; thermostable; exonuclease;
                                                                                                                                                                                                     Tsps17 polymerase gene.
                                                                                                                                                                                                                                                             AAQ86927;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA sequencing using dye-primers and dye-terminators.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                transcriptase activity in the presence of magnesium ions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New heat-stable DNA polymerase from Thermus filiformis - has reverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1995-206929/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (PACI-) PACIFIC ENZYMES 1993 LTD
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                                                                                                                                                                                                                                (first entry)
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86US-0899241.
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/*tag=
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                                                                             /product= Thermostable polymerase
                                                                                                                     Location/Qualifiers
                                                                                             /*tag=
                                                                                                       1246..3738
                                                                                                                                                                                                                                                                                                                                                                                                                                        48.00
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Indels:
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Conservative:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The enzyme has a high
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DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alignment Scores:
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22-AUG-1986;
17-JUN-1987;
12-JAN-1988;
15-MAY-1990;
28-SEP-1990;
5' Nuclease(s) derived from thermostable DNA polymerase(s) - cleavage activity with reduced synthetic ability, used for detection of specific target sequences.
                                                                                                                                                                                                                                                                                                                                                                                      3316 CTCTCCCAGGAGCTCTCCATCCCCTACGAGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence encodes the thermostable polymerase of Thermus species sps17. It may be mutated to encode an Asp residue at position 43 instead of the wild type Gly residue. This substitution is shown to result in a 100 fold decrease in the 5'-3' exonuclease activity with no change to the polymerase activity of the enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA for Thermus species sps17 DNA polymerase - modified to encode an N-terminal deletion to reduce 5'\cdot 3' exo:nuclease activity
                                                                                                                                              06-JUN-1994;
                                                                                                                                                                                                                                                                  5' Nuclease from Taq DNAP
                                                                                                                                                                                                                                                                                                                                        AAQ80745 standard; DNA; 1600 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4947 BP; 822 A; 1601 C; 1774 G; 750 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (HOFF ) HOFFMANN LA ROCHE INC
                                                WPI; 1995-036504/05.
                                                                                                                       04-JUN-1993;
                                                                                                                                                                                            W09429482-A
                                                                                                                                                                                                                  Thermus aquaticus YT-1.
                                                                                                                                                                                                                                         DNA-polymerase; DNAP; Taq; DNA cleavage; RNA cleavage; 5' nuclease;
                                                                                                                                                                                                                                                                                           19-JUL-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        No.:
                                                                                               (THIR-) THIRD WAVE TECHNOLOGIES INC
                                                                                                                                                                                                                                                                                                                                                                                                             1 LeuSer***GluLeuSerIleProTyrGluGlu ll
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1995-154582/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Columns 5-12; 26pp; English.
                                                                       Dahlberg JE,
                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gelfand DH, Greenfield IL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93US-0119754.
86US-0899241.
87US-0063509.
88US-0143441.
                                                                                                                       93US-0073384.
                                                                                                                                              94WO-US06253.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90US-0590213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                90US-0523394
                                                                                                                                                                                                                                                                                                                                                                                                                                                              5
48.00
90.91%
90.91%
96.00%
                                                                       Lyamichev VI;
                                                                                                                                                                                                                                                                                                                                                                                                                                    (1-4947)
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative: Mismatches: Indels: Gaps:
                                                                                                                                                                                                                                                                                                                                                                                        3348
                                                                                                                                                                                                                                                                                                                                                                                                                                                              4947
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Best Local Similari
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAT27686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-823-649A-4 (1-11) x AAQ80745 (1-1600)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alignment Scores: Pred. No.:
                                                                                                                                                            30-AUG-1995;
09-NOV-1994;
09-MAR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The Taq DNA-polymerase (DNAP) gene was amplified by PCR. Amplified fragments were ligated into pTTQ18 vector, which contains the hybrid trp-lac (tac) promoter. An amplification/selection protocol was used to isolate clone 4B containing a mutated Taq DNAP gene (mutTaq) (sequence given in AAQ80746) having normal 5' nucleas activity but less than 18 of the wt Taq DNAP activity. mutTaq was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cut from pTTQ18 by EcoRI-Sall digestion and cloned into pET-3c. Thus clone was digested with BstXI and Bam#I. The DNA was treated with DNA;ECI Klenow fragment and dnPbs, blu-t-ended and religated resulting in an in-frame deletion of 903 nucleotides. The DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1133 CTCTCCCAGGAGCTAGCCATCCCTTACGAGGAG 1165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 5; Page 95-96; 159pp; English.
                                     WPI; 1996-259862/26.
P-PSDB; AAR96267.
                                                                            Oldenburg MC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1600 BP; 287 A; 518 C; 553 G; 242 T; 0 other;
                                                                                                                                                                                                                   09-NOV-1995;
                                                                                                                                                                                                                                                                         W09615267-A1.
                                                                                                                                                                                                                                                                                                                                                                   Thermus aquaticus.
                                                                                                                                                                                                                                                                                                                                                                                             Escherichia; Saccharomyces; Campylobacter; Staphylococcus; identification; detection;
                                                                                                                                                                                                                                                                                                                                                                                                                         p53; mutant; mutation; cleavage; nuclease; cleavase; Thermus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mutant Thermus aquaticus DNA polymerase coding sequence (Clone 4F).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAT27686;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAT27686 standard; DNA; 1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence of the resulting 5' nuclease is given in AAQ80745
                                                                                                                     (THIR-) THIRD WAVE TECHNOLOGIES
                                                                                                                                                                                                                                             23-MAY-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 LeuSer***GluLeuSerIleProTyrGluGlu 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity:
                                                                                         Dahlberg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                              Olive
                                                                                                                                              95US-0520946.
94US-0337164.
95US-0402601.
95US-0484956.
                                                                                                                                                                                                                  95WO-US14673
                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
14..1600
                                                                                                                                                                                                                                                                                                  /product- Mutant DNA polymerase.
                                                                                                                                                                                                                                                                                                                /*1 ag-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5.97
45.00
90.91%
81.82%
90.00%
                                                                              JE,
                                                                                                                      INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Caps:
                                                                                         Heisler LM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative: Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels:
                                                                                                                                                                                                                                                                                                                                                                                              Mycobacterium; Shigelia ds.
                                                                                         Lyamichev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The DNA was treated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1600
1
1
0
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Cleavage of nucleic acids to detect mutation(s) - allows detection $esp.\ in\ human\ p53\ gene,\ to\ identify\ strains\ of\ microorganisms\ and$

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AAT70347
ID AAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-823-649A- (1-11) x AAT27686 (1-1600)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Escherichia, Mycobeterium, Salmonella, Shigella and Staphylococcus. Escherichia, Mycobeterium, Salmonella, Shigella and Staphylococcus. The method may also be used for the identification of viruses, especially hepatitis C virus and simian immunodeficiency virus. Thermus aquaticus (Taq) DNA polymerase was amplified using two primers (AAT27679, AAT27680). The Taq polymerase DNA was inserted into the BamHI restriction site of the expression vector pET-3c and mutant genes were created from that construct. This mutant was created after the vector was digested with BstXI and BamHI. The DNA was then treated with the Klenow fragment of DNAPEcl to trim both 3' overhangs to blunt ends which were then ligated togethor, resulting in an in frame deletion of 903 nucleotides. The resulting mutant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cleavage of nucleic acids using an enzyme, especially a nuclease selected from the group consisting of Cleavase (RTM) BN enzyme, Thermus aquaticus DNA polymerase, Thermus thermophilus DNA polymerase, Escherichia coli ExoIII and the Saccharomyces cerevisiae
                                                                                                                                             07-DEC-1992;
04-JUN-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alternatively, microbial gene sequences. Cleavage products are compared to the cleavage products of reference gene sequences method is used for detecting mutation in the human p53 gene; for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Radi/RadiO complex. The nucleic acid substrate is preferably an oligonucleotide containing a human p53 gene sequence or
   Brow MAD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA polymerase; tag polymerase gene; DNAP; 5' nuclease activity; Cleavase BB; DNA cleavage; reduced synthetic activity; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         03-APR-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1133 CTCTCCCAGGAGCTAGCCATCCCTTACGAGGAG 1165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     from the the group of members of the genera Campylobacter, Escherichia, Mycobacterium, Salmonella, Shigella and Staph
                                                                    (THIR-) THIRD WAVE TECHNOLOGIES INC
                                                                                                                                                                                                                                                        06-JUN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                 US5614402-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Thermus aquaticus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthesis deficient Taq DNA polymerase gene clone 4F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAT70347;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAT70347 standard; DNA; 1600 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1600 BP; 286 A; 519 C; 553 G; 242 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Taq polymerase is also referred to as the Cleavase BB enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     identifying strains of microorganisms, especially bacteria selected
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 2A; Page 257-258; 433pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ě.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 LeuSer***GluLeuSerIleProTyrGluGlu 11
Dahlberg JE,
                                                                                                                                         92US-0986330.
93US-0073384.
                                                                                                                                                                                                                                                        94US-0254359.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      45..00*
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Lyamichev VI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cleavage products are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The
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δÃ

Вb

Example 2; Page 245; 457pp; English

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAT76647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
                                                                                                                     Brow MAD,
Olive DM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1133 CTCTCCCAGGAGCTAGCCATCCCTTACCAGGAG 1165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence, clone 4F encodes a Tag DNA polymerase enzyme that has normal 5' nuclease activity, but reduced synthetic ability. This sequence was derived from the mutTag construct described in AAT70343. The entire mutTag gene was cut from the plasmid, and cloned into pET-3c. This clone was digested with BstXI and BamHI, at unique
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sites. The 3' overhang of BstXi was trimmed to a blunt end, while the 5' overhang of BsmH! was filled in. The blunt ends were lighted together. This resulted in an in-frame deletion of 903 nucleotides. The enzyme encoded by the present protein is also referred to as Cleavase BB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Thermostable 5' nuclease derived from thermostable polymerase - has
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1997-201481/18.
                                                                                                                                                                                                                                             02-DEC-1996;
24-JAN-1996;
                                                                                                                                                                                                                                                                                                                                                        W09727214-AL
                                                                                                                                                                                                                                                                                                                                                                                    synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                     Thermus aquaticus YT-1.
                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acid cleavage; DNA cleavage; RNA cleavage; 5' nuclease; Taq; DNA polymerase; Cleavase BB; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tag gene 5' nuclease clone 3F (Cleavase BB).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAT75647;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAT76647 standard; DNA; 1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1600 HP; 286 A; 519 C; 553 C; 242 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 2A; Columns 79-82; 93pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             reduced synthetic activity useful in nucleic acid detection assays
                                          characterisation of nucleic acid sequences and variations in nucleic
                                                        Thermostable structure-specific nuclease(s) - used for detection and
                                                                                       WP1; 1997-393613/36.
                                                                                                                                                                   (THIR-) THIRD WAVE TECHNOLOGIES INC.
                                                                                                                                                                                                 02-DEC-1996;
                                                                                                                                                                                                               12-JUL-1996;
29-NOV-1996;
                                                                                                                                                                                                                                                                                           22-JAN-1997;
                                                                                                                                                                                                                                                                                                                           31-JUL-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 LeuSer***GluieuSerIleProTyrGluGlu 11
                                                                                                                     Prudent JR;
                                                                                                                                   Dahlberg JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (lirst entry)
                                                                                                                                                                                               96US-0758314.
                                                                                                                                                                                                            96US-0756386.
                                                                                                                                                                                                                                                                                             97WO-US01072.
                                                                                                                                                                                                                             9508-0682853.
                                                                                                                                                                                                                                               9605-0599491.
                                                                                                                                                                                                                                                              96US-0759038.
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45.00
90.91%
81.82%
90.00%
                                                                                                                                     Hall JG, Kaiser MW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative:
                                                                                                                                     Lyamichev VI;
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cc altered Thermus aquaticus DNA polymerase (Taq) gene in which cc altered Thermus aquaticus DNA polymerase (Taq) gene in which cc nucleotides 875-1778 of the wild-type gene coding sequence are cd eleted. Mutant gene mutTaq (see AAT76643) was used as the starting cc material for the construct. Cleavase BB is a thermostable cc structure-specific nuclease preferred for use in nucleic acid cc leavage methods of the invention. Mutant genes (AAT7644-47) cc were constructed in order to determine which portions of the Taq cc were constructed in order to determine which portions of the Taq cc polymerase domain can be altered without eliminating 5' nuclease cc polymerase domain can be altered without eliminating 5' nuclease cc activity. The invention relates to means for the detection and cc characterisation of nucleic acid (NA) sequences and variations in the structure on the structure of the specific manner. The 5' nuclease activity of various enzymes cc (see AAN4/210-13) is used to cleave the target dependent cleavage structure, thereby indicating the presence of specific NA sequences cc or specific variations of them.
                                                                                                                                     Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                        Alignment Scores: Pred. No.:
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                                     δÃ
                                                                          US-09-823-649A-4 (1-11) x AAT76647 (1-1600)
                                                                                                                        DB:
                                                                                                                                                                                                         Score:
Sequence 1600 BP; 286 A; 519 C; 553 G; 242 T; 0 other;
                                                                                                                          5.97
45.00
90.91%
81.82%
90.00%
                                                                                                                          Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                             Length: Matches:
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Search completed: January 15, 2003, 12:55:32 Job time : 134.143 secs

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Title:
Perfect score:
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No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -MODEL-frame+_p2n.model -DBY=x1b
-MODEL-frame+_p2n.model -DBY=x1b
-MODEL-frame+_p2n.model -DBY=x1b
-MODEL-frame+_p2n.model -DBY=x1b
-Q=/Cgn2_1/USPTO_Sp001/CMS09423649/runat_14012003_151002_29127/app_query.fasta_1.1393
-DB-ISSUEQ _Patents_ NA -OPM=fastap -SUFFIX=rni -MINNATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DCCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-NOLE-LOCAL -OUTPM=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-UNDEFLOCAL -OUTPM=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=20000000
-USER=US09823649_@CGN_1_1_35_@runat_14012003_151002_29127 -NOPU=5 -TCPU=3
-NO_XLPXY -NO_MMAD -LARGEQUERY -NEG_SCORES=0 -WALT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPPD=10 -XGAPEXT=0.5 -FGAPDP=6 -FGAPEXT=7
-YGAPDP=10 -YGAPDXT=0.5 -DELOP=6 -DELEXT=7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Post-processing: Minimum Match 0%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Maximum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Minimum
                                                                                                                                                                                                                                                                                                                                                                                                                                          Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Command line parameters:
                                                                                                                                                                                                                                                                                              score
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BB
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seq
                                                                                                                                                                                                                                                                                                 greater
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                                                                                                                                                                                                                                                                             No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             length: 2000000000
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Listing first 45 summaries
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Copyright (c) 1993 - 2003 Compugen Ltd
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
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US-07-977-434-5
US-08-458-819-5
PCT-US-91-07035-5
US-08-973-844C-2
US-08-98-39A-2
US-08-483-043-2
US-08-481-238-2
US-08-481-266-2
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US-08-599-491-2
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ALIGNMENTS

RESULT 1 US-07-977-434-5

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Sequence 5, Application US/07977434
Patent No. 5466591
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Gelfand, I APPLICANT: Abramson,
                                                                                                                                                                                                                                   SOFTWARE: WordPerfect 2.1 CURRENT APPLICATION DATA:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                              FILING DATE: 28-SEP-PRIOR APPLICATION DATA:
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APPLICATION NUMBER:
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STATE:
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                              APPLICATION NUMBER: US 5 FILING DATE: 28-SEP-1990
                                                                                                                                                                                   CLASSIFICATION: 435
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                                                                                                                                                                                                                                                    OPERATING SYSTEM:
SOFTWARE: WordPe:
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5' TO 3' EXONUCLEASE MUTATIONS OF THERMOSTABLE DNA POLYMERASES
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                                                                                     Sequence 5, Application US/08458819 Patent No. 5795762
                                                                    GENERAL INFORMATION:
APPLICANT: Gelfand,
APPLICANT: Abramson,
TITLE OF INVENTION:
TITLE OF INVENTION:
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TELEPHONE: (510) 814-2972
INFORMATION FOR SEQ ID NO: 5:
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APPLICATION NUMBER:
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REGISTRATION NUMBER: 31,822
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                5' TO 3' EXONUCLEASE MUTATIONS OF
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Matches:
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Indels:
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INFORMATION FOR SEQ ID NO:
           MOLECULE
HYPOTHETICAL: NO
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CURRENT APPLICATION DATA:
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PRIOR APPLICATION DATA:
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ORIGINAL SOURCE:
                                             MOLECULE TYPE:
                                                                                                                            SEQUENCE CHARACTERISTICS:
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PRIOR APPLICATION DATA:
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                                                                                               TYPE:
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                                                            TOPOLOGY:
                                                                             STRANDEDNESS:
                                                                                                         LENGTH:
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                                                                                         nucleic acid
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                                                                                                         2493 base pairs
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                                           DNA (genomic)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Gelfand, David H. APPLICANT: Abramson, Richard TITLE OF INVENTION: 5' TO 3'
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APPLICATION NUMBER: US 745,121
FILING DATE: 15-AUG-1991
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MEDIUM TYPE: Floppy disk
                 PRIOR APPLICATION DATA:
                                                                 PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US 063,509
FILING DATE: 17-JUN-1987
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APPLICATION NUMBER:
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APPLICATION NUMBER: US 590,466
FILING DATE: 28-SEP-1990
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APPLICATION NUMBER: [
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                               APPLICATION NUMBER: FILING DATE: 21-DEC
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APPLICATION NUMBER:
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                                               WO PCT/US90/07641
                                                                                                                                                   US 899,241
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 US 585,471
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US-08 074-384C:2
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                                                                                                                                                                                                                                                                      APPLICANT: Dahlberg, James E. APPLICANT: Lyamichev, Victor I. APPLICANT: Brow, Mary Ann D. TITLE OF INVENTION: SYNTHESIS-DE TITLE OF INVENTION: POLYMERASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
                                             SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                           COMPUTER READABLE FORM:
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ANTI-SENSE:
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LENGTH: 2493 base pair
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APPLICATION NUMBER: U
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                 APPLICATION NUMBER: FILING DATE: 04-JUI
                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                           MEDIUM TYPE:
                                                                                                                                                              COUNTRY:
                                                                                                                                                                                           CITY: San Francisco
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CLASSIFICATION:
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PRIOR APPLICATION DATA:

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INFORMATION FOR SEQ ID NO: 2:
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APPLICATION NUMBER: US 07/986,330
APPLICATION NUMBER: US 07/986,330
APPLICATION DATE: 07-DEC-1992
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             TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410]
                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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ATTORNEY/AGENT INFORMATION:
                                                                                                    ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: US 08/073,384
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 TELEFAX:
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                                                                                                                                                                                                                                   CLASSIFICATION: 435
                                                                                                                                                                                                                                                  FILING DATE:
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                                                                   NAME: CARROLL, PETER G. REGISTRATION NUMBER: 32,837
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1: 220 MONTGOMERY STREET, SUITE 2200

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LYAMICHEV, VICTOR I.

BROW, MARY ANN D.

VENTION: 5' NUCLEASES DERIVED FROM THERMOSTABLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          415/397-8338
(415) 397-8338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DAHLBERG, JAMES E.
                                                                                                                                                                                                                                                                                                                                                                                                                   UNITED STATES OF AMERICA
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US-08-483-043-2
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                                                    ; MOLECULE TYPE: US-08-483-043-2
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                                                                                                                                                                    TELEFAX: 415/397-8338
INFORMATION FOR SEQ ID NO: 2:
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APPLICANT: Brow, Mar
TITLE OF INVENTION:
TITLE OF INVENTION:
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                                                                                                                                                    SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                        FILING DATE: 04-JUN-13937
FILING DATE: 04-JUN-13937
APPLICATION NUMBER: US 07/986,330
TITING DATE: 07-DEC-1992
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                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
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Brow, Mary Ann D.
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; Sequence 2, Application US/08471066B
; Patent No. 5837450
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US-08-471-066B-2
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INFORMATION FOR SEQ ID NO: :
                                                                                                                                                                                                                                                                                      . No. :
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COMPUTER: IBM PC campatible
COMPUTER: IBM PC campatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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APPLICANT: LYAMICHEV, VICTOR I.
APPLICANT: BROW, MARY ANN D.
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                                                                                                            1 LeuSer***GluLeuSerIleProTyrGluGlu 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: CARROLL, PETER G.
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: FO
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INFORMATION FOR SEQ ID NO:
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APPLICATION NUMBER: 1
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APPLICANT: Brow, Mary Ann D.
TITLE OF INVENTION: 5' Nucleases Derived From Thermostable
                   APPLICANT: DAHLBERG, JAMES E.
APPLICANT: LYAMICHEV, VICTOR
APPLICANT: BROW, MARY ANN D.
APPLICANT: OLDENBURG, MARY C.
APPLICANT: HEISLER, LAURA
                                                                                                                                                                                                                      2029 CTCTCCGGGGAGCTTTCCATCCCCTACGAGGAG 2061
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APPLICATION NUMBER: 1
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APPLICATION NUMBER: US 08/254,359
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TITLE OF INVENTION: DETECTION OF p53 MUTATIONS
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SOFTWARE: PatentI
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               HEISLER,
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                                                                      VICTOR I.
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RESULT 10
US-08-757-653-2
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                                                                                                                        Sequence 2, Application US/08757653
Patent No. 5843669
                                                                                                         GENERAL INFORMATION:
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               APPLICANT: Lyamichev, Victor I.
APPLICANT: Lyamichev, Natasha
TITLE OF INVENTION: Clearage Of Nucleic Acid Using
TITLE OF INVENTION: Thermostable FEN-1 Endonuclease
                                                                                                                                                                                                                    2029 CTCTCCGGGGAGCTTTCCATCCCCTACGAGGAG 2061
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SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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APPLICATION NUMBER:
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APPLICATION NUMBER: 1
FILING DATE: 09-NOV-
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APPLICATION NUMBER: US 0
FILING DATE: 09-MAR-1995
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ADDRESSEE: HAVERSTOCK, MEDLEN & CARROLL
NUMBER OF SEQUENCES:
                                                                                       APPLICANT:
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                                                                                   Kaiser, Michael W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (415) 397-8338
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SYSTEM: PC-DOS/MS-DOS
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                 Thermostable FEN-1 Endonucleases
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ADDRESSEE: Medlen & Carroll, LLP
                 SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                          APPLICANT: PRODENT, JAMES R.
THILE OF INVENTION: DETECTION OF NUCLEIC ACID
THILE OF INVENTION: INVADER-DIRECTED CLEAVAGE
                                                                                                                                                                                                                                                                                                                                                  APPLICANT: GROTELUESCHEN HALL, JEFF S. APPLICANT: LYAMICHEV, VICTOR
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: BROW, MARY ANN D.
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REGISTRATION NUMBER:
                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICATION NUMBER: US/08/599,491
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CALIFORNIA
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                                                                                                                                                 UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                      OLIVE, DAVID M.
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                                                                                                                                                                                                                                                                                                 DETECTION OF NUCLEIC ACID SEQUENCES BY
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23-JAN-1996

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Query Match: DB:
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INFORMATION FOR SEQ ID NO:
                 TELEFAX: (415) 397-8338 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
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APPLICANT: Lyamichcorrection
                                                                                                   PRIOR APPLICATION NUMBER: US 08/599,491
APPLICATION NUMBER: US 08/599,491
FILING DATE: 24-JAN-1996
ATTORNEY/AGENT IMPORMATION:
NAME: Ingolia, Diane E.
REGISTRATION NUMBER: 40,027
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                                                  REFERENCE/DOCKET NUMBER: FO TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 705-8410
                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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LENGTH: 2496 base pairs
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SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                FILING DATE:
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CLASSIFICATION:
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California
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415) 397-8338
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Best Local Similarity:
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No.:
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REFERENCE/DOCKET NUMBER: FO TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 705-8410
                                                                                    FILING DATE: 24-JAN-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 29-NOV-
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TYPE: r
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STRANDEDNESS: double
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                                                     REGISTRATION NUMBER:
                                                                                                                                                         APPLICATION NUMBER: FILING DATE: 12-JUI
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                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 08/758,314
                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: PCT/US97/01072
FILING DATE: 21-JAN-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                   40,027
                                    FORS-02736
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; LENGTH: 2496 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic
US-08-682-853A-2
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                                                                                                                  REFERENCE/DOCKET NUMBER: FORS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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LENGTH: 2496 base pair
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APPLICATION NUMBER: US 08/599,491
FILING DATE: 24-JAN-1996
ATTORNEY/AGENT INFORMATION:
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TITLE OF INVENTION: DETECTION OF NUCLEIC ACID SEQUENCES BY ITTLE OF INVENTION: INVADER-DIRECTED CLEAVAGE
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                                                                                                                                                                                                                                          NAME: Ingolia, Diane E. REGISTRATION NUMBER: 40
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STREET: 220 Montgomery Street, Suite 2200
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STRANDEDNESS: double
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United States Of America
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Grotelueschen Hall, Jeff S.
Lyamichev, Victor
Olive, David M.
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                       DNA (genomic)
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Alignment Scores:

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DPO1_DEIRA
THI4_YEAST
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PURC_BACSU
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PURC_BACSU
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IDI1_MCUSE
IDI1_RAT
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ALIGNMENTS

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                                                                                                       MEDLINE=96353982; PubMed=8717047;
Eom S.H., Wang J., Steitz T.A.;
"Structure of Tag polymerase with DNA at the polymerase active site.";
                                                                                                                                                                                                   Korolev S., Nayal M., Barnes W.M., di Cera E., Waksman G.; "Crystal structure of the large fragment of Thermus aquatious polymerase I at 2.5-A resolution: structural basis for thermostability.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DPO1_THEAQ P19821;
"Crystal structures of open and closed forms of binary and ternary complexes of the large fragment of Thermus aquaticus DNA polymerase
                               MEDLINE=99077817; PubMed=9857206;
Li Y., Korolev S., Waksman G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-95204371; PubMed-7896728; Ishino Y., Ueno T., Miyagi M., Uemori T., Imamura M., Tsunasawa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Isolation, characterization, and expression in Escherichia coli the DNA polymerase gene from Thermus aquaticus.";
J. Biol. Chem. 264:6427-6437(1989).
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15-JUN-2002 (Rel.
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                                                              X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF
                                                                                           Nature 382:278-281(1996).
                                                                                                                                                                                                                                                                                                                            Kim Y., Eom S.H., Wang J., Lee D.-S., Suh S.W., Steitz T.A.;
"Crystal structure of Thermus aquaticus DNA polymerase.";
                                                                                                                                                                                                                                                                                                                                                        x-ray crystallography (2.4 angstroms).
medline=95364959; PubMed=7637814;
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                                                                                                                                                        K-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).
                                                                                                                                                                                                                                                               MEDLINE=96016150;
                                                                                                                                                                                                                                                                                X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 290-832
                                                                                                                                                                                                                                                                                                               Nature 376:612-616(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A., AND PARTIAL SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-89197950;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Thermaceae; Thermus
                                                                                                                                                                                                                                                                                                                                                                                                                                   "Overproduction of Thermus aquaticus DNA polymerase and its
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 LSXELSIPYEE 11
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-1991 (Rel. 17, Last sequence update)
-2002 (Rel. 41, Last annotation update)
-lymerase I, thermostable (BC 2.7.7.7) (Tag polymerase 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F.C., Stoffel S.,
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X-RAY CRYSTALLOGRAPHY (2.30 ANGSTROMS) OF 293-831.

MEDLINE-99380545; PubMed=10449720;

Li Y., Mitaxov V., Woksman G.;

"Structure-based design of Taq DNA polymerases with improved properties of dideoxynucleotide incorporation.";

Proc. Natl. Acad. Sci. U.S.A. 96:9491-9496(1999).

-!- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
PROSTIE; PS00447; DNA-POLYMERASE_A; 1.

Transferase; DNA-directed DNA polymerase; DNA replication; DNA-binding; 3D-structure.

DOMAIN 410 832 POLYMERASE (BY CTUTTOTE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBI outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1: structural basis for nucleotide incorporation.";
EMBO J. 17:7514-7525(1998).
                                                                           SMART; SM00279; HhH2;
SMART; SM00482; POLAC;
                                                                                                         SMART; SM00475; 53EXOC; 1.
SMART; SM00278; HhH1; 1.
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thermostability. Has a relatively high error rate because it lacks
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Proc. Natl. Acad. Sci. U.S.A. 95:12562-12567(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fab: the Fab is directed against an intermediate in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Crystal structure of Taq DNA polymerase in complex with an inhibitory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Murali R., Sharkey D.J., Daiss J.L., Murthy H.M.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Crystal structures of the Klenow fragment of Thermus aquaticus DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=98266352; PubMed=9605316;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 290-832
                                                                                                                                                                                                        InterPro;
                                                                                                                                                                                                                                   InterPro;
                                                                                                                                                                                                                                                    InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Y., Kong Y., Korolev S., Waksman G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              exonuclease proofreading functionality.
SIMILARITY: BELONGS TO THE DNA POLYMERASE TYPE-A FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             + [DNA](N).
                                                                                                                                                                                                                                                                                                                                                           1BGX;
                                                                                                                                                                                                                                                                                                                                                                                                       3KTQ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A33530; A33530.
                                                                                                                                                                                                                                                                                                 1QTM;
                                                                                                                                                                                                                                                                                                                                                                                        4 KTQ;
                                                                                                                                                                                                                                                                                                                                                                                                                                     1KTQ;
                                                                                                                                                       PF01367; 5_3_exonuclease; 1. PF02739; 5_3_exonuc_N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              J04639; AAA27507.1; -. D32013; BAA06775.1; -.
                                                                                                                                                                                   PF00476; DNA_pol_A;
                                                                                               SM00279; HhH2; 1
                                                                                                                                                                                                     1PR003584; HHH_2
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                                                                                                                                                                                                                                                                 IPR001098;
                                                                                                                                                                                                                                                                                 1PR002421;
                                                                                                                                                                                                                                                                                                            10 SEP 98.
14 OCT 98.
12-MAR 97.
16-AUG-99.
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01-NOV-1997 (Rel.
15-JUN-2002 (Rel.
                                            TIGRFAMS; TIGR00593; pola; 1.
PROSITE; PS00447; DNA_POLYMERASE_A; 1.
                                                                                                                       SMART; SM00278; HhH1; 1.
SMART; SM00279; HhH2; 1.
                                                                                                                                                                                               Pfam; PF00476; DNA_PO1_A; 1.
pfam; PF01367; 5_3_exonuclease; 1.
pfam; PF07739; 5_3_exonuc_N; 1.
pxints; pr00868; DNAPOLI.
pxints; pr00868; DNAPOLI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or send an email to license@ish-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                entitles requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EWBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              + {DNA}(N).
-!- SIMILARITY: BELONGS TO THE DNA POLYMERASE TYPE-A FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=93285135; PubMed=8508785; Park J.H., Kim J.S., Kwon S.-T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 1-21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (AUG-1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kwon S.-T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=GK24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Thermus caldophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-JUN-2002 (Rel. 41, Last annotation update)
DNA polymerase I, thermostable (EC 2.7.7.7) (TAC polymerase 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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                                                                                                SMART; SM00482; POLAC;
                                                                                                                                                                           SMART; SM00475; 53EXOC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR; $33287; $33287.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U62584; AAB81398.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      - | - CATALYTIC ACTIVITY: N deoxynucleoside triphosphate - N diphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P80194;
                      Transferase; DNA-directed DNA polymerase; DNA replication; DNA repair.
                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Purification and characterization of Thermus caldophilus GK24 DNA
                                                                                                                                                                                                                                                                                                             InterPro;
                                                                                                                                                                                                                                                                                                                                      InterPro;
                                                                                                                                                                                                                                                                                                                                                               InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         . J. Biochem. 214:135-140(1993).
FUNCTION: THERMOSTABLE ENZYME THAT HAS 5'-TO-3' EXONUCLEASE ACTIVITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         _THECA
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                                                                                                                                                                                                                                                                                                                                      IPR003583;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Thermus/Deinococcus group; Deinococci; Thermales
                                                                                                                                                                                                                                                                                                                                                                                                                 IPR001098;
                                                                                                                                                                                                                                                                                                           IPR003584; HHH_2
                                                                                                                                                                                                                                                                                                                                                               IPR000513;
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35, Last sequence update)
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                                                                                                                                                                                                                                                                                                                                      HHH_1
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                                                                                                                                                                                                                                                                                                                                                                                        DNA_poli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Park J.H., Kim H., Lee D.-S.;
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; F1731055B5246F03 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lee D. -S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            834 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             There are no restrictions on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 between the Swiss Institute of Bioinformatics and the EMBL outstate the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                J. Ferment. Bioeng. 76:265-269(1993).
-!- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
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DNA polymerase 1, thermostable (FC 2.7.7.7) (Tth polymerase 1).
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01-0CT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HUBHT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA polymerase gene (polA) from Thermus thermophilus HB8.";
J. Ferment. Bioeng. 76:265-269(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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                                                                                                                 SEQUENCE
                                                                                                                                                                       Transferase; DNA-directed DNA polymerase; DNA replication; DNA-binding.
                                                                                                                                                                                                                                                                                     SMART; SM00482; POLAC;
                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF01367; 5_3_exonuclease; 1. Pfam; PF02739; 5_3_exonuc_N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSSP; P19821; 1TAQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; D28878; BAA06033.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or send an email to licensewisb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Urabe I.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Asakura K., Komatsubara H., Soga S., Yomo T., Oka M., Emi S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-HB8 / ATCC 27634;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Thermus/Deinococcus group; Deinococci; Thermales;
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                                                                                                                                                                                                                                  PROSITE; PS00447; DNA_POLYMERASE_A; 1.
                                                                                                                                                                                                                                                                                                                                                                        SMART; SM00475; 53EXOc; 1.
                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PR00868; DNAPOLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR003584; HHL_2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A
                                                                                                                                                                                                                                                       rigreams; rigr00593; pola; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; 1PR003583;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  interPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR002421; 5_3_exonuclease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SIMILARITY: BELONGS TO THE DNA POLYMERASE TYPE-A FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Cloning, nucleotide sequence, and expression in Escherichia coli of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=274;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         680 LSQELAIPYEE 690
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PF00476; DNA_POI_A; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9;
                                                                                                                    834 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       115000841
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     Conservative
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93798 MW;
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94049 MW;
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                             81.8%;
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                             Score 45; DB 1;
Pred. No. 0.3;
                                                                                                                 POLYMERASE (BY SIMILARITY)
; 1A98145DClla54A9 CRC64;
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Pred. No. 0.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POLYMERASE (BY SIMILARITY).
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1 LSXELSIPYEE 11

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RESULT 6
CIW5_HUMAN
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                                                                                                                                                                    16-OCT-2001
16-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Dover J., Du Z., Favello A., Fulton L., Gattung S., Geisel C., Kirsten J., Kucaba T., Hillier L., Jier M., Johnston L., Langston Y., Latteille P., Louis E.J., Macri C., Mardis E., Menezes S., Mouser L., Nhan M., Rifkin L., Riles L., St Peter H., Trevaskis E., Vaughan K., Vignati D., Wilcox L., Wohldman P., Waterston R., Wilson R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-FEB-1995 (Rel. 31, Last sequence update) 16-0CT-2001 (Rel. 40, Last annotation updat Gl/s-specific cyclin PCL5.
PCL5 OR YHR071W.
                                                                  16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
Potassium channel subfamily K member 5 (Acid-sensitive potassium channel protein TASK-2) (TWIK-related acid-sensitive K+ channel in the chan
                                                                                                                                                                                                                                 CIW5_HUMAN
095279;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 modified and this statement is not removed. Usage by and for commercial entities retries a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P38794;
01-FEB-1995
Eukaryota; Metazoa;
                        Homo sapiens (Human)
                                                         KCNK5 OR TASK2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00134; cyclin; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; U00061; AAB68375.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or send an a ail to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Science 265:2077-2082(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=94378003; PubMed=8091229;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-S288C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=4932;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CG18_YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -1- SIMILARITY: BELONGS TO THE CYCLIN FAMILY. MOST SIMILAR TO G1/S-SPECIFIC CYCLINS PCLA AND PCL2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Complete nucleotide sequence of Saccharomyces cerevisiae chromosome
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                                                                                                                                                                                                                                                                                                                                                                                                        174 LNYELAIPYDE 184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 LSXELSIPYEE 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBN outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        S0001113; PCL5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SM00385; CYCLIN; 1.
E; PS00292; CYCLINS; FALSE_NEC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cell cycle; Cell division
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IPR004366; Cyclin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    229 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Rel. 31, Created)
                                                                                                                                                                                               (Rel. 40, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                               STANDARD,
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   Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26467 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No.
                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    B6839ABB9DB5DD49 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                               499 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 229;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                                Best Local
Matches
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01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Genome polyprotein [Contains: Nuclear inclusion protein A (NI-A) (NIA)
(BC 3.4.22.44) (49 kDa proteinase) (49 kDa-Pro); Nuclear inclusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    J. Biol. Chem. -!- FUNCTION: I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential)
-1- TISSUE SPECIFICITY: ABUNDANT EXPRESSION IN KIDNEY, ALSO DET
IN LIVER, PLACENTA AND SMALL INTESTINE. IN THE KIDNEY, EXPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=99030343; PubMed=9812978;
                                                                                                                                                                                                                                                                                                               SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genew;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AF084830; AAC79458.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  channel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Reyes R., Duprat F., Lesage F., Fink M., Salinas M., Farman N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                         P20234;
                                                                                                        POLG_OMV
                                                                                                                                                                                                                                                                                                                               CARBOHYD
                                                                                                                                                                                                                                                                                                                                                              TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001622;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000636; M+channel_nlg.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR003280; K+channel_2pore
                                                                                                                                                                                     478 ELSVPYEQ 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     onic channel; "Transmembrane; ton transport; Potassium transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         lycoprotein
                                                                                                                                                                                                                    4 ELSIPYEE 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Biol. Chem. 273:30863-30869(1998).
FUNCTION: PH DEPENDENT, VOLFAGE INSENSITIVE, OUTWARDLY RECTIFYING POTASSIUM CHANNEL. OUTWARD RECTIFICATION IS LOST AT HIGH EXTERNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHANNELS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MISCELLANEOUS: INHIBITED BY QUININE, QUININDINE AND EXTERNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBUNIT: HOMODIMER (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACIDIFICATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EXPRESSED IN PROXIMAL TUBULES OR GLOMERULI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IN LIVER, PLACENTA AND SMALL INTESTINE. IN THE KIDNEY, EXPRES IS RESTRICTED TO THE DISTAL TUBULES AND COLLECTING DUCTS. NOT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    K+ CONCENTRATIONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     603493;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HGNC:6280; KCNK5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                from human kidney
                                                                                                                                                                                                                                                  Similarity
6; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PR01333;
                                                                                                                                                                                                                                                                                                               499 AA;
                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                             250
                                                                                                                                                                                                                                                                                                                                                                                                           113
134
                                                                                                                                                                                                                                                                                                                                                                             190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ion_trans;
                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZPOREKCHANEL.
                                                                                                                                                                                                                                                                                                                                           26
112
133
157
180
215
250
325
                                                                                                                                                                                                                                                                                                             55130 MW;
                                                                                                                                                                                                                                                              74.0%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kichannel_pore.
                                                                                                                                                                                                                                                                               Score 37;
                                                                                                                                                                                                                                                              Pred. No.
                                                                                                                                                                                                                                                                                                                              N-LINKED (GLCNAC
                                                                                                                                                                                                                                                                                                                                             CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                          POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                          PORES FORMING 2 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                          CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                          PORE-FORMING 1 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CYTOPLASMIC (POTENTIAL).
                                                                                                        PRT';
                                                                                                                                                                                                                                                                                                               E871A7A4823DDA00 CRC64;
                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                               DH 1; Length 499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IN THE KIDNEY, EXPRESSION
                                                                                                                                                                                                                                                                                                                              (POTENTIAL).
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                                                                                                                                                                                                                                                  VE6_HPV31
                                                                                                                                                                                                                                                                               RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                         P17386;
01-AUG-1990 (Rel. 1
01-AUG-1990 (Rel. 1
15-JUN-2002 (Rel. 4
Human papillomavirus type 31.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Burger J.T., Brand R.J., Rybicki E.P.;
Burger J.T., Brand R.J., Rybicki E.P.;
Submitted (NOV-1990) to the EMBL/GenBank/DDBJ databases.

Sibmitted (NOV-1990) to the EMBL/GenBank/DDBJ databases.

Sibmitted (NOV-1990) to the EMBL/GenBank/DDBJ databases.

Sibmitted (NOV-1990) to the EMBL/GenBank/DDBJ databases.

FUNCTION: NUCLEAR INCLUSION PROTEIN A HAS PROTEOLYTIC ACTIVITY.

SIDMITTED TO ACTIVITY.

FUNCTION: NUCLEAR INCLUSION PROTEIN A HAS PROTEOLYTIC ACTIVITY.

FUNCTION: NUCLEAR INCLUSION PROTEIN A HAS PROTEIN ACTIVITY.

FUNCTION: NUCLEAR INCLUSION PROTEIN A HAS PROTEOLYTICAL ACTIVITY.

FUNCTION: NUCLEAR INCLUSION PROTEIN A HAS PROTEIN ACTIVITY.

FUNCTION: NUCLEAR INCLUSION PROTEIN A HAS PROTEOLYTIC ACTIVITY.

FUNCTION: NUCLEAR INCLUSION PROTEIN A HAS PROTEIN ACTIVITY.

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FUNCTION PROTEIN A HAS PROTEIN A 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00767; Poty_coat; 1.
Pfam; PF00863; Peptidase_C4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entities requires a license agreement (See http://www.isb-sib.ch/announce or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the European Bioinformatics Institute. There are no restuse by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -i- PTM: THE VIRAL RNA OF POTYVIKUSES IS EXPRESSED AS A SINCLE POLYPROTEIN WHICH UNDERGOES POSTTRANSLATIONAL PROFESITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ornithogalum mosaic virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein B (NI-B) (NIB) (RNA-directed RNA polymerase) (EC 2.7.7.48);
Coat protein (CP)] (Fragment).
                                                                                                                                                                                                                        VE6_HPV31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Coat protein; Polyprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEROPS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; D00615; BAA00490.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=12204;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001730; Peptidase_C4.
InterPro; IPR001592; Poty_coat.
                                                                                                                                                                                                                                                                                                                                                              698 KLSIPYEE 705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity les 7; Conserv
                                                                              protein.
                                                                                                                                                                                                                                                                                                                                                                                                                   4 ELSIPYEE 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: NI-A PROTEINASE BELONGS TO PEPTIDASE FAMILY C4. SIMILARITY: BELONGS TO THE POTYVIRUSES POLYPROTEIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gln+(Ser or Gly) for the enzyme from tobacco etch virus. The natural substrate is the viral polyprotein, but other proteins and oligopeptides containing the appropriate consensus sequence are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROCESSING RESULTING IN THE PRODUCTION OF AT LEAST EIGHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CATALYTIC ACTIVITY: N nucleoside triphosphate - N diphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      [RNA](N)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JQ0494; JQ0494.
PS; C04.005; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INDIVIDUAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PF00680; RNA_dep_RNA_pol; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IPR001254; Ser_protease_Try.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IPR001205; RNA_pol_P3D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1136 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Transferase; Thiol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                        STANDARD;
                                                                                                         15, Last sequence update)
41, Last annotation update)
                                                                                                                                                             15, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           365
883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  74.0%;
87.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   128914 MW; 0A7AE0527743FD61 CRC64;

    Mismatches

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 37; DB
Pred. No. 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COAT PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUCLEAR INCLUSION PROTEIN A NUCLEAR INCLUSION PROTEIN B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protease; RNA-directed RNA polymerase;
                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                        149 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               There are no restrictions on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 1136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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THI4_ASPOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hest Local Similarity 63.68; Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Nucleotide sequence of human papillomavirus type 31: a cervical neoplasia-associated virus."; Virology 171:306-311(1989).
                                                                                                                                                                                                                                                                                                                                                                16-oct-2001 (Rel. 40, Created)
16-oct-2001 (Rel. 40, Last sequence update)
16-oct-2001 (Rel. 40, Last annotation update)
Thiazote blosynthetic enzyme, mitochondrial precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZN_FING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             use by non-profit institutions as long modified and this statement is not removed.
     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDED DNA (IN VITRO).
                                                                                                                     Biosci. Biotechnol. Biochem. 64:1416-1421(2000).
                                                                                                                                                                     "Pyrithtamine resistance gene (ptrA) of Aspergillus oryzae: cloning, characterization and application as a dominant selectable marker for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001334; E6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR; A32444; W6WL31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the European Bioinformatics Institute. There are no rest
use by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -1- FUNCTION: EXHIBIT A STRONG, BUT NON SPECIFIC AFFINITY FOR DOUBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Goldsborough M.D., Disilvestre D.,
                                                                        -!- SUBCELLULAR LOCATION: Mitochondrial (Potential).
                                                                                                                                                       transformation.";
                                                                                                                                                                                                    Kubodera T., Yamashita N., Nishimura A.;
                                                                                                                                                                                                                     MEDLINE=20399355; PubMed=10945258;
                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                        NCBI_TaxID-5062;
                                                                                                                                                                                                                                                                                                    Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
                                                                                                                                                                                                                                                                                                                       Bukaryota; Fungi;
                                                                                                                                                                                                                                                                                                                                     Aspergillus oryzae.
                                                                                                                                                                                                                                                                                                                                                        THIA OR PTRA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     THI4_ASPOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oncogene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Early protein; DNA-binding; Nuclear protein; Zinc-finger;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ptam; PF00518; E6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; J04353; AAA46950.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- FUNCTION: THIS PROTEIN MAY BE INVOLVED IN THE ONCOGENIC POTENTIAL OF THIS VIRUS (CERVICAL NEOPLASIA-ASSOCIATED VIRUS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=89299478; PubMed=2545036;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID-10585;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Papillomavirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15 LSSALEIPYDE 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 LSXELSIPYEE 11
                                                                                                        THIAZOLE (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   149 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               103
                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                       Ascomycota; Pezizomycotina; Eurotiomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17713 MW; 61D2N86C362767D9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Temple G.F., Lorincz A.T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   327 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            restrictions on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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non-profit institutions as long as its content is

SO PTT

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Best
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P21662; P22546;
01-MAY-1991 (Rel
01-AUG-1991 (Rel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-AUG-1991 (Rel. 19, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Neuroendocrine convertase 1 precursor (EC 3.4.21.93) (NEC 1) (PC1)
(Prohormone convertase 1) (Proprotein convertase 1) (PC3) (Furin homolog) (Propeptide professing protease).

PCSK1 OR NEC1 OR NEC-1 OR ATT-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                       processing of Proc. Natl.
"Identification of a cDNA encoding a second putative prohormone convertase related to PC2 in AtT20 cells and islets of Langerhans.";
                                                                                                               "Cloning and primary sequence of a mouse candidate prohormone convertase PC1 homologous to PC2, Furin, and Kex2: distinct chromosomal localization and messenger RNA distribution in brapituitary compared to PC2."; Mol. Endocrinol. 5:111-122(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                     "Isolation and functional expression of a mammalian processing enzyme, murine prohormone convertase 1.", Proc. Natl. Acad. Sci. U.S.A. 88:6834-6838(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=91319778; PubMed=1862107;
Korner J., Chun J., Harter D., Axel R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse), and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Thiamine biosynthesis; Mitochondrion; Transit peptide; FAD; NAD.
TRANSIT 1
MITOCHONDRION (POTENTIAL).
CHAIN 7 327 THIAZOLE BIOSYNTHETIC ENZYME.
NP_BIND 77 107 FAD OR NAD (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entities requires
                               MEDIINE=91110525; PubMed=1988934; Smeekens S.P., Avruch A.S., Lamendola J., Chan S.J., Steiner D.F.;
                                                                  SPECIES=M.cookii;
                                                                                                                                                                                                  Seidah N.G., Marcinkiewicz M., Benjannet S., Mattei M.-G., Lazure C., Mbikay M., Chretien
                                                                                                                                                                                                                               MEDLINE=91203919; PubMed=2017186;
                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPECIES-Mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus cookii (Cook's mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TIGRFAMS;
                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                   Nakayama K., Hosaka M., Hatsuzawa K., Murakami K.;
"Cloning and functional expression of a novel endoprolease involved in prohormone processing at dibasic sites.";
J. Biochem. 109:803-806(1991).
                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=92041727; PubMed=1657897;
                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10090,
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AMS; TIGR00292; Thi4; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            a license agreement (See http://www.isb-sib.ch/announce/
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75.0%;
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Pred. No.
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7C561EE06742B2AE CRC64;
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EMBL; X57088; CAAA0368.1; A
EMBL; M5589; AAA39894.1;
EMBL; M55668; AAA39375.1; A
EMBL; M59196; AAA39732.1;
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Chretien M.;
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CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPECIES-Mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 214-478 FROM N.A. SPECIES-Mouse; TISSUE-Pituitary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Proc. Natl. Acad. Sci. U.S.A.
[5]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- CATALYTIC ACTIVITY: Release of protein hormones, neuropeptides and
renin from their precursors, generally by cleavage of -Lys-Arg-|-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chretien
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PIR; A37951; A37951.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FUNCTION: INVOLVED IN THE PROCESSING OF HORMONE AND OTHER PROTEIN PRECURSORS AT SITES COMPRISED OF PAIRS OF BASIC AMINO ACID RESIDUES. SUBSTRATES INCLUDE PONC, RENIN, ENREPHALIN, DYNORPHIN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COFACTOR: CALCIUM DEPENDENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      furin gene products: tissue-specific
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                                                                                                                                                                                                                                                                                                                                                                           ; PS00137;
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9:415-424(1990).
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SUBTILASE_SER; 1.
SUBTILASE_SER; 1.
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  72.0%;
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N-LINKED (GLCNAC. . .)
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                                                                                                                                                     CHARGE RELAY SYSTEM (BY SIMILARITY).
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                                                                                                                                                                                                                                    AMPHIPATHIC (POTENTIAL).
                                                                                                                                                                                                                                                                                   NEUROENDOCRINE CONVERTASE
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                        Length 753;
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01-AUG-1991 (Rel. 19, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
Mitochondrial 60S ribosomal protein L8 (YML8).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     _YEAST
                                                                                                                                                                                                                                                                                                                                                                                                              modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                 Ribosomal protein; Mitochondrion CONFLICT 82 82 D -:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           the European Bioinformatics Institute. There are no rest use by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIINE-95282514; PubMed-7762302;
Vandenbol M., Durand P., Dion C., Portetelle D., Hilger F.;
"Sequence of a 17.1 kb DNA fragment from chromosome X of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MRPL8 OR YJL063C OR J1125 OR HRD238
                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                               TIGRFAMS;
                                                                                                                                                                                                                                                            ProDom; PD004277;
                                                                                                                                                                                                                                                                                                                                                                                    EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Cloning and characterization of nuclear genes for two mitochondrial ribosomal proteins in Saccharomyces cerevisiae."; Nucleic Acids Res. 18:1521-1529(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Saccharomycetales; Saccharomycetaceae; Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RM08_YEAST
                                                                                                                                                                                                                                  PROSITE; PS01167; RIBOSOMAL_L17; 1.
                                                                                                                                                                                                                                                                            Pfam; PF01196; Ribosomal_L17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Yeast 11:57-60(1995)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=4932;
                                                             193 LLKEMSLPYDE 203
                                                                                                                                                                                                                                                                                            InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -1- SIMILARITY: BELONGS TO THE L17P FAMILY OF RIBOSOMAL PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  690 SAKLSIPYE 698
                                                                                                                                     Local
                                                                                         1 LSXELSIPYEE 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBCELLULAR LOCATION: Mitochondrial
                                                                                                                                                                                                                                                                                                                         $14890; $14890.
$47128; $47128.
                                                                                                                                                                                                                                                                                                           S0003599; MRPL8
                                                                                                                                                                                                                                                                                                                                                   X53841; CAA37834.1; -. Z34288; CAA84060.1; -. Z49338; CAA89354.1; -.
                                                                                                                        Similarity
6; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the Swiss Institute of Bioinformatics and the
                                                                                                                                                                                                                                                                                          IPR000456; Ribosomal_L17.
                                                                                                                                                                                                                                               TIGR00059; L17;
                                                                                                                                                                                    238 AA;
                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Grohmann L., Graack H.-R., Isono K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                             Ribosomal_L17; 1
                                                                                                                                                                                      26945 MW;
                                                                                                                                      54.5%;
                                                                                                                                                       70.0%;
                                                                                                                        ω
                                                                                                                                        Pred. No. 8;
                                                                                                                                                     Score 35;
                                                                                                                                                                                                    D -> G (IN REF. 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                    A130EFD95E8719BA CRC64;
                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        238 AA.
                                                                                                                                                     DB 1; Length 238;
                                                                                                                        2;
                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL outstation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequences and the specific localization of each transcript to endocrine and neuroendocrine tissues in rats.";
Endocrinology 129:3053-3063(1991).

-!- FUNCTION: INVOLVED IN THE PROCESSING OF HORMONE AND OTHER PROTEIN PRECURSORS AT SITES COMPRISED OF PAIRS OF BASIC AMINO ACID RESIDUES. SUBSTRATES INCLUDE POMC, RENIN, ENKEPHALIN, DYNORPHIN,
                                                                                                                                                                                            PROSITE; PS00136; SUBTILASE_ASP; 1.
PROSITE; PS00137; SUBTILASE_HIS; 1.
PROSITE; PS00138; SUBTILASE_SER; 1.
                                                                                                                                                                                                                                                                                                                                                                                        EMBL; M76705; AAA40945.1; EMBL; M83745; AAA41476.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                  entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Manumalia; Eutheria; Rodentia; Sciurognathi; Muridae;
        CARBOHYD
                     CARBOHYD
                                        CARBOHYD
                                                                                                                      DOMAIN
                                                                                                                                     CHAIN
                                                                                                                                                                                                                                            PRINTS; PR00723; SUBTILISIN. Probom; PD000717; Pdomain;
                                                                                                                                                                                                                                                                            Pfam; PF00082; Peptidase_S8; Pfam; PF01483; P; PARTIAL.
                                                                                                                                                                                                                                                                                                                                            MEROPS; $08.072
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EWBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- CATALYTIC ACTIVITY: Release of protein hormones, neuropeptides and
renin from their precursors, generally by cleavage of -Lys-Arg-[-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         rat insulinoma cell line based on similarities to Kex2 and furin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hakes D.J., Birch N.P., Mezey A., Dixon J.E.;
"Isolation of two complementary deoxyribonucleic acid clones from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=92063860; PubMed=1954888;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Prohormone-converting enzymes: regulation and evaluation using antisense RNA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=92168040; PubMed=1791845;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Prohormone convertase 1) (Proprotein convertase 1). PCSK1 OR NEC1 OR NEC-1 OR BDP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Neuroendocrine convertase 1 precursor (EC 3.4.21.93) (NEC 1) (PC1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-DEC-1992
01-DEC-1992
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                                                                                                     DOMAIN
                                                                                                                                                 PROPEP
                                                                                                                                                                   SIGNAL
                                                                                                                                                                                                                                                                                                                                                                         PIR; A4155b; KXRTCI.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-DEC-1992 (Rel. 24, Last sequence up 16-OCT-2001 (Rel. 40, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 £28840;
                                                                                                                                                                                                                                                                                                          InterPro; IPR000209; Peptidase_S8
                                                                                                                                                                                                                                                                                                                           InterPro; IPR002884;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S8. FURIN SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bloomquist B.T., Kipper B.A., Mains R.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION: LOCALIZED IN THE SECRETION GRANULES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COFACTOR: CALCIUM DEPENDENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOMATOSTATIN AND INSULIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Endocrinol. 5:2014-2024(1991).
                                                                                                                                                                                                                                                                                                                                                           Q45670;
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                                                                                                                                                                                 protease;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence update)
                                                                                                                                                                               Glycoprotein; Zymogen; Calcium;
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                      CHARGE RELAY
                                                                                                 AMPHIPATHIC (POTENTIAL)
                                                                                                                  CATALYTIC
                                                                                                                                 NEUROENDOCRINE CONVERTASE 1.
                                                                                                                                                  POTENTIAL
                                                                                                                                                                POTENTIAL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
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                                                                                  SYSTEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Muridae; Murinae; Rattus.
                                                                                  (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-MAY-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
DNA polymerase I (EC 2.7.7.7) (POL I).
POLA OR DR1707.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CONFLICT
                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the FMBH outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DEIRA
                                                                                                                                entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                             "Identification, sequencing, and targeted mutagenesis of a polymerase gene required for the extreme radioresistance of Deinococcus radiodurans.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gutman P.D., Fuchs P., Ouyang L., Minton K.W.; "Identification, sequencing, and targeted mutagenesis of a DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                         HSSP; P19821
TIGR; DR1707
                                                                                                                                                                                                                                                                                                                                                                                                                   Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M., Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C., Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D. Ketchum K.A., Neison K.E., Salzberg S., Smith H.O., Vonter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P52027;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DPO1_DEIRA
                              InterPro;
                                            InterPro;
                                                                                       EMBL; AE002012;
                                                                                                    EMBL; L14581; AAC36974.1; -.
                                                                                                                                                                                                                                                                                                                                                                           radiodurans R1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D., Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=20036896; PubMed=10567266;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=93273728; PubMed=8501062;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 36-956 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Deinococcaceae; Deinococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Thermus/Deinococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Deinococcus radiodurans
                                                                                                                                                                                                                                                                                                                                                                             Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      689 SAKLSVPYE 697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          . Bacteriol. 175:3581-3590(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
nes 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 SXELSIPYE 10
                                                                                                                                                                                                                                                      SUBUNIT: SINGLE-CHAIN MONOMER WITH MULTIPLE FUNCTIONS. SIMILARITY: BELONGS TO THE DNA POLYMERASE TYPE-A FAMILY.
                                                                                                                                                                                                                                                                                                  CATALYTIC ACTIVITY: N deoxynucleoside triphosphate - N diphosphate
                                                                                                                                                                                                                                                                                                                    SIMILARITY)
                                                                                                                                                                                                                                                                                    (DNA)(N)
                                                                       19821; 2KTQ.
                                                                                                                                                              non-profit institutions as long and this statement is not removed.
 IPR000513;
                            IPR002421;
IPR001098;
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514
752 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                        AAF11264.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                34, Created)
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514
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DNA_poli.
Exo_N_I.
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                           DNA_pol
                                         5_3_exonuclease.
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E -> A (IN REF. 2).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         group; Deinococci; Deinococcales;
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                                                                                                                                                              Usage
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InterPro; IPR003584; HHH_2.
Pfam; PF00476; DNA_POL_A; 1.
Pfam; PF001367; 5_3_exonuclease; 1
Pfam; PF02739; 5_3_exonuc_N; 1.
PRINTS; PR00868; DNAPOLI.
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CONFLICT
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CONFLICT 48 48 5 -> A (IN REF. 1).

CONFLICT 77 77 H -> D (IN REF. 1).

CONFLICT 108 108 F -> K (IN REF. 1).
                   Praekelt U.M., Byrne K.L., Meacock P.A.; "Regulation of TH14 (MOLI), a thiamine-biosynthetic gene of Saccharomyces cerevisiae."; Yeast 10:481-490(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     van Dyck L., Skala J., de Wergifosse P., Purnelle B., Talla
Nawrocki A., del Bino S., Goffean A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Saccharomyces cerevisiae (Baker's yeast).
Eukaryola: Fungi: Ascomycola: Saccharomycot::::: Saccharomyceles:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-OCT-2001 (Rel. 40, Last annotation update)
Thiazole biosynthetic enzyme, mitochondrial precursor.
THI4 OR MOL1 OR ESP35 OR YGK144W OR G6620.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-1993
01-OCT-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMART; SM00279; HhH2; 1.
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                                                                                                                                                                                                   Skala J., Nawrocki A., Goffeau A.;
"The sequence of a 27 kb segment on the right arm of chromosome VII from Saccharomyces cerevisiae reveals MOL1, NAT2, RPL30B, MSR1, CYS/PEMI/CHO2, MSR1 genes and ten new open reading frames.";
Yeast 11:1421-1427(1995).
                                                                                                                                                                                                                                                                                                                                                                       STRAIN-S288c
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   early stationary phase during growth on Yeast 8:699 710(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Praekelt U.M., Meacock P.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDI.INE-93070608; PubMed=1441749;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P32318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00447; DNA_POLYMERASE_A; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TICKFAMS;
                                                                                                                         MEDLINE-95028146; PubMed-7941734;
                                                                                                                                                                                                                                                                                                                                        MEDLINE-96158062; PubMed-8585325;
                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 205-326 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID-4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Saccharomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                THI4_YEAST
                                                                                                                                                      THIAMINE REGULATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "MOLL, a Saccharomyces cerevisiae dene that is highly expressed in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      803 LSNDLGIPYAE 813
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TICR00593; pola;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  956 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Rel. 27, Created)
(Rel. 27, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POLAC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            53EXOc;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HhH1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        108
128
406
540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Saccharomycetaceae; Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  105659 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            70.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P -> R (IN REF.
L -> V (IN REF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6ABBF117D75AB84A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                326 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 956;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
STRAIN-JAL-1 / DSM 2661 / ATCC 43067;

MEDITIME-96337999; PubMed-8688087;

Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,

Sutton G.G., Blake J.A., FilzGerald L.M., Clayton R.A., Gocayne J.D.,

Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,

Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,

Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Wguyen D.

Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,

Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Machado C.R., Praekelt U.M., de Oliveira R.C., Barbosa A.C.,
Byrne K.L., Meacock P.A., Menck C.F.;
"Dual role for the yeast THI4 gene in thiamine biosynthesis and DNA
                                                                                                                                                                                                                                                                                                                                              01-NOV-1997
01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                 Y103_METJA
Q57567;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                    Hypothetical protein MJ0103.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Thiamine biosynthesis; Mitochondrion; Transit peptide; FAD; NAD.
TRANSIT 1
MITOCHONDRION (POTENTIAL).
CHAIN 7 326 THIAZOLE BIOSYNTHETIC ENZYME.
NP_BIND 67 97 FAD OR NAD (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X85807; CAA59802.1; -. EMBL; Z72929; CAA97157.1; -. EMBL; Z72930; CAA97159.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 damage tolerance.
                                                                                                                                                                                                             NCBI_TaxID=2190;
                                                                                                                                                                                                                               Methanocaldococcaceae; Methanocaldococcus.
                                                                                                                                                                                                                                                 Archaea; Euryarchaeota; Methanococci; Methanococcales;
                                                                                                                                                                                                                                                                    Methanococcus jannaschii
                                                                                                                                                                                                                                                                                                                            16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              128 ELEIPYED 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF01946; Thi4; 1.4
TIGRFAMs; TIGR00292; Thi4; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SGD; S0003376; THI4.
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PIR; S25321; S25321.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; X61669; CAA43843.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- MISCELLANEOUS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=98035046; PubMed=9367751,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION IN DNA DAMAGE TOLERANCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           interPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 ELSIPYEE 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity es 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mol. Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: BELONGS TO THE THI4 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WOL. Biol. 273:114-121(1997).
FUNCTION: INVOLVED IN BIOSYNTHESIS OF THE THIAMINE PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBCELLULAR LOCATION: Mitochondrial (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MISCELLANEOUS: EXPRESSED AT HIGH LEVELS IN THE EARLY STATIONARY PHASE OF BATCH CULTURES GROWING ON MOLASSES, AN INDUSTRIAL MEDIUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INDUCTION: REPRESSED BY THIAMINE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOLERANCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          THIAZOLE. ALSO SEEMS TO HAVE A ROLE IN MITOCHONDRIAL DNA DAMAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IPR002922; Thi4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        326 AA;
                                                                                                                                                                                                                                                                                                                                            (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                            (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                            35, Created)
35, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34991 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     68.0%;
75.0%;
                                                                                                                                                                                                                                                                                                                                            Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 34;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              843790F2CE00BF02 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                   433 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 326;
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                                                                                                                                                        Matches
                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                             between the Swiss Institute of Bioinformatics and the EMBL outstation - the Buropean Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Science 273:1058-1073(1996).
-i- SIMILARITY: BELONGS TO THE UPP0063 FAMILY.
                                                                                                                                                                                                                             Hypothetical protein; Complète proteome. SEQUENCE 433 NA; 49866 MW; F82576531DF12142 CRC64;
                                                                                                                                                                                                                                                                    InterPro; iPR000385; MoaA_NifB_PqqE.
Pfam; PF01444; MoaA_NifB_PqqE; 1.
                                                                                                                                                                                                                                                                                                             TIGE; MJ0103;
                                                                                                                                                                                                                                                                                                                           EMBL; U67467; AAH98083.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.; "Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                             33 EVEIPYEE 40
                                                                                                                                                                          roca1
                                                                                                                 4 ELSIPYEE 11
                                                                                                                                                      Similarity 6; Conserv
                                                                                                                                                        Conservative
                                                                                                                                                                        68.0%;
75.0%;
                  2003, 11:21:23
                                                                                                                                                                        Score 34;
Pred. No.
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                                                                                                                                                                                         DB 1; Length 433;
                                                                                                                                                      1; Indels
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Minimum DB
Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Run on:
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                                                                                                                                                                                                                                                                                                                                                                                                                                Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Post-processing: Minimum Match 0%
                                                                                                                                                                                                                   pred. Nc. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
                                                                                                                                                                    Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seg length: 0
seg length: 20
  protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           length: 2000000000
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112:
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115:
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50
                                                                                                                                                                              Query
                                                                                                                                                                     Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          671580 seqs, 206047115 residues
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78.0
78.0
76.0
74.0
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72.0
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70.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GenCore version 5.1.3 Coppright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                    sp_vertebrate:*
sp_unclassified:*
sp_rvirus:*
sp_bacteriap:*
                                                                                                                                                                                                                                                                                                                                     sp_organelle:*
sp_phage:*
                                                                                                                                                                                                                                                                                                                                                          sp_mhc:*
                                                                                                                                                                                                                                                                                                                                                                       sp_mammal:*
                                                                                                                                                                                                                                                                                                                                                                               sp_invertebrate:*
                                                                                                                                                                                                                                                                                                                                                                                                  sp_fungi:*
                                                                                                                                                                                                                                                                                                                                                                                                            sp_bacteria:*
                                                                                                                                                                                                                                                                                                                                                                                                                     sp_archea:*
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1 Q9JK62
094248
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Q8SVP8
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09A3W3
094849
1 Q8VEI0
2 Q9YMM5
Q8TC35
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                                                                                                                    066691
Q8U6Z1
                                                                                                           Q989F3
                                                                                                                                         Q44755
                                                                                                                                                  Q9XI48
                                                                                                                                                                                                   SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           671580
 Ošsvp8 encephalito
049528 arabidopsis
0943343 caulobacter
094849 drosophila
08vm51 ymantria d
08tc35 homo sapien
                                                                               094248 schizosacch
                                                                                                                                                                     Description
                                                                                       Q989f3 rhizobium l
Q9q4w5 ornithogalu
Q9jk62 mus musculu
                                                                                                                    066691 aquifex aeo
Q8u6z1 agrobacteri
                                                                                                                                       Q9xi48 arabidopsis
Q44755 borrelia bu
                                                                    Q8rb89 thermoanaer
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228	199	153	153	132	118	16215	6815	1234	1085	1028	1028	1028	697	597	577	428	417	359	359	269	235	233	233	225	184	2894	1026	738
42.	44	16	16	10	16	ഗ	(A)	Ŋ	S		,ı	4	17	ω	10	17	17	16	16	Ŋ	17	16	16	16	16	17	끄	Ç
Q961Z4	Q9NWW6	Q8Y3I4	Q926Q7	Q9%QG2	P72904	Q9NFS3	Q917U4	Q24690	Q24363	P97528	8HML60	Q90Q52	Q8TJQ4	059717	Q9F"FX2	8S1.1.80	Q9V1T1	Q8Y7Q5	Q92СJ1	Q9N610	21XU60	Q8YAQ3	Q92FP6	Q92IY9	Q55139	Q58791	Q62845	Q9XWY5
Q96iz4 homo sapien	5	Q8y3i4 listeria mo	Q926q7 listeria in		P72904 synechocyst	Ω	drosophi	irosophi		P97528 rattus norv	SOB	Q9uq52 homo sapien	met	059717 schizosacch	Q9ftx2 oryza sativ			Q8y7q5 listeria mo	1	Q9n610 leishmania	Q9uxi2 sulfolobus	Q8yaq3 listeria mo	Q92fp6 listeria in	ь	Q55139 synechocyst	Q58791 methanococc	5	Q9xwy5 caenorhabdi

ALIGNMENTS

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Query Match
Best Local Similarity
Matches 7; Conserv
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Q9X148;
01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation updat
                                                                                                                                                                                               STRAIN-CV. (MIMBIA:

VYSOLSKAIA V.S., Schwartz J.R., Yu G., Toriumi M., Lenz G., Liu S.,

VYSOLSKAIA V.S., Schwartz J.R., Yu G., Toriumi M., Lenz G., Liu S.,

VYSOLSKAIA V.S., Schwartz J.R.,

Altafi H., Araujo K., Brooks S., Buchler E., Chao Q., Conn L.,

Altafi H., Araujo K., Brooks S., Huchler E., Chao Q., Conn L.,

Conway A.B., Dunn P., Hansen N., Hulzar L., Khan S., Kim C., Palm C.,

ROWLEY D., Shinn P., Walker M., Davis R.W., Ecker J.R.,

Pederspiel N.A., Theologis A.;

Parabidopsis thaliana chromosome 1 BAC F9L1 sequence.";

**Submitted** (JUN 199) to the EMBL/GenBank/DDBJ databases.

EMBL; AC007591; AAD39650.1; -.
                                                               ATP-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                          InterPro; IPK003593; AAA_ATPase.
InterPro; IPK003439; ABC_transportr.
Pfam; PF00005; ABC_tran; 2
ProDom; PD000006; ABC_transportr; 1.
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⊮9ы1.15.
                                                                                                         SMART; SM00382; AAA; 1.
                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A
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 Conservative
                    80.0%;
                                                                         163602 MW;
                  Score 40; DB
Pred. No. 34;
   Mismatches
                                                                         0D35414D9C370A85 CRC64;
                                   DB 10; Length 1451;
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   Indels
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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1996 (TIEMBLIEL 01, Created)
01-NOV-1996 (TIEMBLIEL 01, Last sequence update)
01-DEC-2001 (TIEMBLIEL 19, Last annotation update)
                                          Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L., Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay M., Huber R., Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;
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01-AUG-1998 (TrEMBLrel. 07, Last seq
01-JUN-2002 (TrEMBLrel. 21, Last ann
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Nature 392:353-358(1998).
               aeolicus
                  "The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.":
                                                                                       MEDLINE=98196666; PubMed=9537320;
                                                                                                       STRAIN-VF5
                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                              NCBI_TaxID=63363;
                                                                                                                                                                Bacteria;
                                                                                                                                                                              Aquifex aeolicus
                                                                                                                                                                                                        Hypothetical protein AQ_367
                                                                                                                                                                                                                                                                 066691;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                burgdorieri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Genomic sequence of a Lyme disease spirochaete, Borrella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-98065943;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                   2 SXELSIPYEE 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AE001137; AAC66681.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     U43739; AAA85591.1;
                                                                                                                                                              Aquificae; Aquificales; Aquificaceae; Aquifex.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , Butler-Loffredo L., Kieleczawa J., Medalle J., Luft B.J.; (DEC-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Spirochaetales;
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                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PubMed=9403685;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           70752 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                               78.0%;
70.0%;
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                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                 850 AA
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Conservative

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Indels

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1 LSXELSIPYEE 11

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Query Match
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7; Conserve
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                                                                                                                                                                                                                            Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M., Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L. Houmiel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F., Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B., Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                          Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P., Okura V.K., Zhou Y., Chen L., Wood C.E., Almedda N.F. Jr., Woo L., Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr., Chenbanan P., Clendenning J., Deatherage G., Gillet W., Grant C., Katyavin T., Levy R., Li M.-J., McClelland E., Palmieri A., Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A., Raymond C., Rouse G., Saenphinmachak C., Wi Z., Romero P., Gordon D. Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M., Cordon Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M., Chumler P., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-2002 (TrEMB), rel. 21, Created)
01-JUN-2002 (TrEMB), rel. 21, Last sequence up
01-JUN-2002 (TrEMB), rel. 21, Last annotation
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                                                                                                                                                          "Genome sequence of the plant pathogen and biotechnology agent Agrobacterium tumefaciens C58."; Science 294:2323-2328(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMART; SM00267; DUF1; 1.
SMART; SM00052; DUF2; 1.
                                                                                                      Complete proteome.
                                                                                                                      EMBL; AE009395; AAL45459.1; ALT_INITERMBL; AE008220; AAK88782.1; -.
                                                                                                                                                                                                                                                                                                                        MEDLINE-21608551; PubMed-11743194;
                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                           Science 294:2317-2323(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                               Nester E.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-21608550; PubMed-11743193;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=176299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rhizobiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Agrobacterium tumefaciens (strain C58 / ATCC 33970)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MELA OR ATU4665 OR AGR_L_436.
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PROSITE; PS00215; MITOCH_CARRIER; UNKNOWN_1.
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InterPro; IPR000160; GGDEF.
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                                                                                                                                                                                                               Cielo C.,
                                                                                                                                                                                                                                                                                                                                                                                                          "The genome of the natural genetic engineer Agrobacterium tumetaciens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        227 ISREMDVPYEE 237
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                                                                                                                                                                                                               Slater S.;
                                                                                     474 AA;
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                                76.0%;
63.6%;
                                                                                     53483 MW;
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54.5%;
               Score 38; DB Pred. No. 26; 2; Mismatches
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                                                                                     16C1085B5A12B21B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                474 AA.
                                                 DB 16; Length 474;
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Best Local :
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                                                                                                                           InterPro; IPR001592; Poty_coat.
InterPro; IPR001205; RNA_pol_P3D.
Pfam; PF00767; Poty_coat; 1.
                                                                                                                                                                                                                 Mackenzie A., Gibbs A.;
"Potyviruses in Australia.";
"Dotyviruses in Australia.";
Submitted (NOV-199) to the EMBL/GenBank/DDBJ databases.
EMBL; AF203528; AAF22752.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-JUN-2002 (TrEMBLrel. 21, Polyprotein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mochizuk Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto
Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,
Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-2001 (TrEMBLrel. 18, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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01-0CT-2001
                                                      SEQUENCE
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PROSITE; PS01324; GLYCOSYL_HYDROL_F4; UNKNOWN_1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Phyllobacteriaceae; Mesorhizobium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rhizobium loti (Mesorhizobium loti)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alpha-galactosidase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q989F3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q989F3
                                                                                NON_TER
                                                                                                             Pfam;
                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=12204;
                                                                                                                                                                                                                                                                                                                                                                                                               Potyvirus
                                                                                                                                                                                                                                                                                                                                                                                                                                      Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ornithogalum mosaic virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AP003009; BAB52744.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mesorhizobium loti.'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Complete genome structure of the nitrogen-fixing symbiotic bacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |: :| |||||
200 LAHDLDIPYEE 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  188 LAHDLSLPYDE 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ŲΊ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
nes 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 LSXELSIPYEE 11
                                                                                                    PF00680; RNA_dep_RNA_pol; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PR00732; GLHYDRLASE4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7:331-338(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IPR001088; GH_4.
                                                      465 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    461 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51818 MW;
                                                      53264 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    74.0%;
54.5%;
74.0%; Score 37; DB 12; Length 465;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18,
18,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6C29F18157E4F6EC CRC64;
                                                         3D4B484C259FF636 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    465 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 16; Length 461;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sasamoto S.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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RESULT 7
Q9JK62
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REPRESENTATION OF THE PROPERTY OF THE PROPERTY
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Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1481 ELSVPYEQ 488
                                                                                Murphy L., Harris \upsilon.; Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                          Schizosaccharomyces pombe (Fission yeast).
Fukaryota; Funqi: Ascomycota; Schizosaccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY-1999 (TIEMBLITE). 10, Created)
01-MAY-1999 (TIEMBLITE). 10, Last sequence update)
01-JUN-2002 (TIEMBLITE). 21, Last annotation update
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Functional properties of mouse "RASK-2 potassium channel."; Submitted (NOV-2000) to the EMBL/GenBanK/DDBJ databases. EMBL, AR559395; ARF868688.1; -. EMBL; AR519542; ANG35065.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Roux J., Bathanin J.;
"Mouse two P domain potassium Channel TASK2."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN=129/SVJ; TISSUE~KIDNEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-2000 (TrEMBLITE).
01-OCT-2000 (TrEMBLITE).
01-JUN-2002 (TrEMBLITE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9JK62;
01-0CT-2000
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                                                                                                                                                                                                                                                                                                                                                  Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                Schizosaccharomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SPCC737.08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical coiled-coil protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     094248;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR003280; Kichannel_2pore.
InterPro; IPR001622; Kichannel_pore.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MGD; MGI:1336175; Kenk5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cid L.P., Niemeyer M.I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID-10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse)
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STRAIN=972H-;
                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                  STRAIN=972H-;
                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PR01333; 2POREKCHANEL
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                                                                                                                                                                                                                                                                                                                    NCBI_TaxID-4896
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27 KLSIPYEE 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 ELSIPYEE 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 ELSIPYEE 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       502 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PREBLIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       55976 MW; E4C7E7CC71B4:055 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chordata;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      74.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15, Created)15, Last sequence update)21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sepulveda F.V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 44;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PKT; 4717 AA.
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QREASULT 9

RESULT 10
Q8SVP
ID Q8SVP
AC Q8SVP
DT 01-JU
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DT 01-JU
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Matches 7
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01-JUN-2002 (TTEMBLrel. 21, Last sequence update)
01-JUN-2002 (TTEMBLrel. 21, Last annotation update)
Branched-chain amino acid aminotransferase/4-amino-4-deoxychorismate
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InterPro; IPR002048; EF-hand.
InterPro; IPR002035; VWE_A.
Pfam; PF00004; AAA; 3.
SMART; SM00327; VWA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wood V., I
Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Thermoanaerobacter tengcongensis.
Bacteria; Firmicutes; Bacillus/Clostridium group; Chermoanaerobacteriales; Thermoanaerobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00018; EF_HAND; UNKNOWN_1.
PROSITE; PS50234; VWFA; 1.
SEQUENCE 4717 AA; 537775 MW; B2B0
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                      SEQUENCE FROM N.A. STRAIN-GB-M1;
                                                                                                                                                                                                                                                                                                                    Q8SVP8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIINE-21992816; pubMed-11997336;
Bac Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S.,
Chen Y., Xu, Y., Lai X., Huang L., Dong
Tan H., Chen R., Wang J., Yu J., Yang H.;
"A complete sequence of T. tengcongensis genome
Genome Res. 12:689-700(2002).
EMBL; AE013059; AAM24189.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=MB4T / JCM11007;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q8RB89;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2663 LITKLSLPYEE
  Genoscope;
                                                                                                  Eukaryota; Microsporidia;
NCBI_TaxID=6035;
                                                                                                                                                           Encephalitozoon cuniculi.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=119072;
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IARELNIPFEE 228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         291 AA;
                                                                                                                                                                                                        (TrEMBLrel. 21, Created)
(TrEMBLrel. 21, Last sequence update)
(TrEMBLrel. 21, Last annotation update)
1 protein ECU04_1610.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32346 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       72.0%;
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63.6%;
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Pred.
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2; Mismatches
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Pred. No. 4.
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                                                                                                                                                                                                                                                                                                                                                     PRT;
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105072D27AB06FFE CRC64;
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                                                                                                                                    Encephalitozoon
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X., N
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Ling
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RESULT
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Best Local
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    Matches
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01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
Hypothetical 206.8 kDa protein F28J12.260 in chromosome IV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Katinka M.D., Duprat S., Cornillot E. Prensier G., Barbe V., Peyretaillade Delbac F., El Alaoui H., Peyret P., S
                                                                                                                   EU Arabidopsis sequencing pr
Submitted (MAR-2000) to the
                                                                                                                                                                                                                                                            Hilbert H., Braun M., Holzer
Mewes H.W., Lemcke K., Mayer
Submitted (MAR-2000) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                 Bevan M., Hilbert H.,
Bancroft I., Mewes H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core en
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein-like).
F28J12.260 OR AT4G18600
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Genome sequence and gene compaction of Encephalitozoon cuniculi."; Nature 414:450-453(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Weissenbach J., Vivares C.P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. STRAIN=GB-M1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (APR-2001) to [2]
                                                             Hypothetical SEQUENCE 1
                                                                                         EMBL; AL1021710; CAA16740.1; EMBL; AL161549; CAB78862.1;
                                                                                                                                                                                                  Mueller M.W., Muendlein Mayer K.F.X.;
                                                                                                                                                                                                                                                                                                                                         Submitted
                                                                                                                                                                                                                                                                                                                                                                       STRAIN-CV.
                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (FEB-1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-CV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             eurosids II; Bra
NCBI_TaxID-3702;
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                                                                                                                                                                                  Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
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   Similarity
7; Conserv
                                                                                                                                                                                                                                                                                                                                  Opsis Sequencing Project:
(FEB-1998) to the EMBL/GenBank/DOBJ databases
                                                           al protein.
1890 AA;
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                                                                                                                                                                                                                                                                                                                                                                       COLUMBIA;
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63.6%;
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                72.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 W., Mayer K.,
                                                             206846 MW;
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                                                                                                                                                                                                                  Α.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cornillot E., Metenier G., Thomarat F., eyretaillade E., Brottier P., Wincker P., Peyret P., Saurin W., Gouy M.,
                                                                                                                                      project;
Score 36; DB
Pred. No. 2.8e
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 36;
Pred. No.
   سر
                                                                                                                                                                                                                  Felber
                                                                                                                                                                                                                                                               EMBL/GenBank/DDBJ databases
                                                                                                                        EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                             X E
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                                                                                                                                                                                                                                                                                                                                                                                                                                Holzer E., Brandt A., Duesterhoeft
K., Schueller C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein
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                                                                                                                                                                                                                                                                             Brandt A.,
.X ;
                                                             4B72F3701F425B30 CRC64;
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                                                                                                                                                                                                               Mewes H.W., Lemcke
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the
                DB 10;
2.8e+02;
                                                                                                                                                                                                                                                                                            Duesterhoeft
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           eukaryote parasite
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                              Length 1890;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Gene 11-1
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Best Local
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Interpro; IPRUU401-.
Pfam; PF00043; GST_C; 1.
Pfam; PF02798; GST_N; 1.
Pfam; PF02798; GST_N; 1.
Pfam; PF02798; GST_N; 1.
22885 MW; Ad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q94849;
01-FEB-1997
01-FEB-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9A3W3 PRELIMINARY; PRT; 208 AA.
(9A3W3;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Glutathione S-transferase family protein.
                                       "Pattern of ecological shifts in the diversification of Hawaiian Drosophila inferred from a molecular phylogeny."; Curr. Biol. 5:1129-1139(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1137 SLEESVPYEE 1146
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SEQUENCE FROM N.A.

CHEATN-ATCC 19089 / CB15;
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                                                                                                                                                            Cohen J.;
                                                                                                                                                                                              MEDLINE-96120851; PubMed-8548285; Kambysellis M.P., Ho K.F., Craddock E.M., Piano F.,
                                                                                                                                                                                                                                 SEQUENCE FROM N.A. MEDLINE=96120851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila buzzatii (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=21173698; PubMed=11259647;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Caulobacter crescentus
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                                                                                                                                                                                                                                                                                                                                                                                                               Ephydroidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Pterygota; Neoptera; Endopterygota; Diptera;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Yolk protein 1 (Fragment).
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7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (TremBirel. 02, Created)
(TremBirel. 02, Last seq
(TremBirel. 17, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                          Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                70.0%;
70.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last annotation update)
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Pred. No. 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 16; Length 208;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Brachycera; Muscomorpha;
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                                                                                                                                                                                                       Parisi M.,
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RESULT 14
Q8VEI0
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 SWWA60
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Best Local Similarity
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                                                                                                                                                                                                                                                  Q9YMM5;
                                             MEDIINE-99124785; PubMed-9887315;
Kuzio J., Pearson M.N., Harwood S.H., Funk C.J., Evans J.T.,
Slavicek J.M., Rohrmann G.F.;
"Sequence and analysis of the genome of a baculovirus pathogenic for
Lymantria dispar.";
Virology 253:17-34(1999).
                                                                                                                                                                                                       Ol-MAY-1999 (TrEMBLIE). 10, Created)
01-MAY-1999 (TrEMBLIE). 10, Last seq
01-DEC-2001 (TrEMBLIE). 19, Last and
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                                                                                                                                                                                     Ldorf-102 peptide.
Lymantria dispar multicapsid nuclear polyhedrosis virus (LdMNPV).
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (DBC-2001) to the EMBL/GenBank/DDBJ databases EMBL; BC018462; AAH18462.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-2002 (TrEMBLEEL 20, La
01-MAR-2002 (TrEMBLEEL 20, La
Hypothetical 32.1 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q8VELO;
01-MAR-2002 (Tremblice).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                              Nucleopolyhedrovirus.
                                                                                                                                                                        Viruses; dsDNA viruses,
                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical protein SEQUENCE 279 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse)
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             Kuzio J.
                        SEQUENCE FROM N.A.
                                                                                                                                                  NCBI_TaxID=10449;
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75.0%;
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Pred. No.
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                                                                                                                                                                                                                                                                EKT;
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                                                                                                                                                                          Baculoviridae;
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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Maximum Match 100%
Listing first 45 summaries
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
    BIJOSUM62
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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           Sequence 2 from patent US
AR023961
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1 (bases 1 to 2496)
Brow, M.Ahn.D., Hall, J.Steven.Grotelueschen., Lyamichev, V.,
Olive, D. Michael. and Prudent, J.Robert.
Detection of nucleic acid sequences by invader-directed cleavage
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Kaiser, M.W., Lyamichev, V.I. and Lyamichev, N.
Cleavage of nucleic acid acid using thermostable methoanococcus
jannaschii FEN-1 endonucleases
Patent: US 5843669-A 2 01-DEC-1998;
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Heisler, L.M., Fors, L. and Brow, M.Ann.D.
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Sequence 2 from patent US 5985557
ARO86117
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                        Patent: US 5994069-A 2 30-NOV-1999;
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                                                  Hall, J.G., Lyamichev, V.I., Mast, A.L. and Brow, M. Ann.D. Detection of nucleic acids by multiple sequential inva
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Prudent,J.R., Hall,J.G., Lyamichev,V.I., Brow,M.Ann.D. and
Dahlberg,J.E.
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Detection of nucleic acid sequences by invader-directed cleavage Patent: US 6001567-A 2 14-DEC-1999;
                                                                 Invasive cleavage of nucleic acids Patent: US 6348314-A 2 19-FEB-2002;
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Brow,M.Ann.D., Hall,J.Steven.Grotelueschen., Lyamichov,V.,
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US-09-823-649A-4 (1-11) x AR193571 (1-2496)
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                                                                                                                                                                                                                                                                                                                                 Sequence 154 from Patent Woo190337.
                                                                                     Patent: WO 0190337-A 154 29-NOV-2001; THIRD WAVE TECHNOLOGIES, INC. (US)
                                                                                                                                  Allawi, H., Bartholomay, C.T., Chehak, L., Curtis, M.L., Bis, P.S., Hall, J.G., Ip, H.S., Kaiser, M., Kwłatkowski, R.W., Lukowiak, A.A., Lyamichev, V. Ma, W., Olson Munoz, M.C., Olson, S.M., Scheeler, J.J., Skrzypczynski, Z., Takova, T.Y., Vedvik, K.L. and Lyamichev, N.E.
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Dahlberg,J.E., Lyanichev,V.I. and Brow,M.Ann.D.
5' nucleases derived from thermostable DNA polymerase
Patent: US 5614402-A 2 25-MAR-1997;
Location/Qualifiers
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Sequence 2 from patent US 5614402.
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Dahlberg, J.E., Lyamichev, V.I. and Brow, M.Ann. D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          polymerase. These motifs represent a conserved region which affects the DNA polymerase's ability to incorporate dideoxynucleotides labelled with fluorescein and cyanine family dyes. The method of the invention is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Reverse transcribing an RNA, comprises performing a reverse transcriptase polymerase chain reaction amplification of a mixture using a mutant thermoactive DNA polymerase
                               Disclosure; Page 7; 23pp; English.
                                                                                       transcriptase polymerase chain reaction amplification of a mixture using a mutant thermoactive DNA polymerase
                                                                                                                                                                                                                                  WPI; 2002-076891/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-APR-2001; 2001EP-0109341
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            dye; amplification
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Native DNA polymerase motif #9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAM48260;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 4; Page 4; 23pp; English
                                                                                                                                                         Reverse transcribing an RNA, comprises performing a reverse
                                                                                                                                                                                                                                                                                              Schoenbrunner NJ, Wang AM;
                                                                                                                                                                                                                                                                                                                                                                                                   (HOFF ) HOFFMANN LA ROCHE & CO AG F.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           transverse transcription reaction; fluorescein; cyanine; thermoactive;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 48;
Pred. No.
                                                                                                                                                                                                                                                                                                                                 Higuchi RG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 23;
0.0051;
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RESULT 3
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                                                                                                                                                                                Reverse transcribing an RNA, comprises performing a reverse transcriptase polymerase chain reaction amplification of a rusing a mutant thermoactive DNA polymerase \, -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA polymerase's ability to incorporate dideoxynucleotides labelled with fluorescein and cyanine family dyes. The method of the invention is useful in reverse transcription/amplification reactions. The method provides improved reverse transcription efficiency at lower enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The sequences given in AAB47791-97 and AAM48259-AAM48270 repartive forms of motifs derived from DNA polymerases used in
                                                                                                                                                                                                                                                      WPI; 2002-076891/11.
                                                                                                                                                                                                                                                                                      Schoenbrunner NJ, Wang AM;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                dye; amplification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA polymerase; reverse transcription; primer; divalent cation; mutant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Native DNA polymerase motif #12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-MAR-2002 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  polymerase. These motifs represent a conserved region which affects the
                                                                                                                                                                                                                                                                                                                                    (HOFF ) HOFFMANN LA ROCHE & CO AG F.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            transverse transcription reaction; fluorescein; cyanine; thermoactive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     needed for the reaction.
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                                                                                                                                                                                                                                                                                                   Higuchi RG,
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                                                                                                                                                                                                                                                                                                   Myers TW;
                                                                                                                                                                                                      of a mixture
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The sequences given in AAB47791-97 and AAM48259-AAM48270 represent the native forms of motifs derived from DNA polymerases used in the method of the invention. The method for reverse transcribing an RNA, comprises

Disclosure; Page 7; 23pp; English.

DNA polymerase's ability to incorporate dideoxynucleotides labelled fluorescein and cyanine family dyes. The method of the invention is useful in reverse transcription/amplification reactions. The method

polymerase. These motifs represent a conserved region which affects the RNA, a primer, a divalent cation, and a mutant thermoactive DNA treating a transverse transcription reaction mixture which comprises the

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Best Local Similarity
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                                                                   useful in reverse transcription/amplification reactions. The method provides improved reverse transcription efficiency at lower enzyme concentrations relative to previous high temperature reverse transcription methods, and provide a wider range of usable salt concentrations. The use of the mutant DNA polymerase provides faster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          transcription methods, and provide a wider range of usable salt concentrations. The use of the mutant DNA polymerase provides faster reverse transcription extension rates, and consequently less time is
                                    needed for the reaction.
                                                                                                                                                           RNA, a primer, a divalent cation, and a mutant thermoactive DNA polymerase. These motifs represent a conserved region which affects the DNA polymerase's ability to incorporate dideoxygucleotides labelled with fluorescein and cyanine family dyes. The method of the invention is
                                                                                                                                                                                                                                  of the invention. The method for reverse transcribing an RNA, comprises treating a transverse transcription reaction mixture which comprises the
                                                                                                                                                                                                                                                                     The sequences given in AAB47791-97 and AAM48259-AAM48270 represent the native forms of motifs derived from DNA polymerases used in the method
                                                                                                                                                                                                                                                                                                                                                           Reverse transcribing an RNA, comprises performing a reverse transcriptase polymerase chain reaction amplification of a mixture using a mutant thermoactive DNA polymerase
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                                                     reverse transcription extension rates, and consequently less time
                                                                                                                                                                                                                                                                                                                             Disclosure; Page 7; 23pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-076891/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Smith ES,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Schoenbrunner
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wang AM;
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90.9%;
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Pred. No. 0.0051;
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Matches Query Match Best Local :

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Conservative

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Score 48; DB 1: Pred. No. 0.45; 0; Mismatches

DB 13; Length 545;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 96.0%;
Best Local Similarity 90.9%;
                                                                                          The sequence is that of a mutant of Thermus species sps17 polymerase mutant MET-ALA 288 Tsps17, having a different amt. of 5'-3' exonuclease activity than the native enzyme. Thermostable DNA polymerases are useful in many recombinant DNA techniques, esp. nucleic acid amplification by PCR, self-sustained sequence replication (SSR) and high temp. DNA sequencing. The absence of 5'-3' nuclease activity may be desirable in enzymes used in 5'-3' exonuclease activity may be desirable in enzymes used in homogeneous assays for the amplification and detection of a larget
                                                                                                                                                                                                                                                           Claim 11; Page 59; 185pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mutant thermostable DNA polymerase enzyme MET-ALA 288 Tsps17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR23157 standard; Protein; 545 AA
Sequence
                                                                                                                                                                                                                                                                                                   Thermostable DNA polymerases with altered 5'-3' exo nuclease activity - having conserved regions mutated or deleted, for a
                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAQ24010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-APR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Thermus species SPS17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5'-3'; exonuclease; PCR; amplification; SSR; sequencing; PLCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR23157;
                          See also AAR23140-79 and AAR23722.
                                                    regions of the enzymes can be used to prepare a range of recombin
proteins having 5'-3' exonuclease activity to a complete lack of
                                                                                 nucleic acid sequence.
                                                                                                                                                                                                                                                                                                                                                              WPI; 1992-150885/18.
                                                                                                                                                                                                                                                                                                                                                                                           Abramson RD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-SEP-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-SEP-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Misc-difference 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-0CT-1992 (first entry)
                                                                                                                                                                                                                                                                                     in e.g. PCk, sequencing and detection assays
                                                                                                                                                                                                                                                                                                                                                                                                                     (CETU ) CETUS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-SEP-1991;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10;
545 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                           Gelfand DH;
                                                                                                                                                                                                                                                                                                                                                                                                                                               9005-0590490
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               90US-0590213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note- *residues 2-287 deleted from the native
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                              Mutation of the DNA encoding particular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence"

 Mismatches

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 0.0051;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                   for use
                                                                   recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                exonuclease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
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RESULT 6
AAR23156
ID AAR23156
AAR23156
AAR23156
AAR23156
AAR23156
AAR23156
AAR2
AXX Muta
XXX 5'-3
XXX W5'-3
XXX W092
XXX
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                                                                                                                       Matches
                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-SEP-1990;
28-SEP-1990;
28-SEP-1990;
                                                                                                                                                                                                                                                                                                                                                      and high temp. DNA sequencing. The absence of 5'-3' nuclease activity may facilitate higher sensitivity allelic discrimination in a combined polymerase ligase chain reaction (PLCR) assay. An enhanced amt. of 5'-3' exonuclease activity may be desirable in enzymes used in homogeneous assays for the amplification and detection of a target nucleic acid sequence. Mutation of the DNA encoding particular regions of the enzymes can be used to prepare a range of recombinant proteins having 5'-3' exonuclease activity to a complete lack of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The sequence is that of a mutant of Thermus species sps17 polymerase mutant MET-THR 200 Tsps17, having a different amt. of 5'-3' exonucleas activity than the native enzyme. Thermostable DNA polymerases are useful in many recombinant DNA techniques, esp. nucleic acid amplification by PCR, self-sustained sequence replication (SSR) and high temp. DNA sequencing. The absence of 5'-3' nuclease activity
                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 11; Page 59; 185pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          in e.g. PCR, sequencing and detection assays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Thermostable DNA polymerases with altered 5'-3' exo nuclease activity - having conserved regions mutated or deleted, for use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAQ24009
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5'-3'; exonuclease; PCR; amplification; SSR; sequencing; PLCR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mutant thermostable DNA polymerase enzyme MET-THR 200 Tsps17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR23156 standard; Protein; 632 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1992-150885/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Abramson RD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9206200-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Misc-d fc ence 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-OCT-1992 (first entry)
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                                                                                                                                                                                                                                                                                                     See also AAR23140-79 and AAR23722.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (CETU ) CETUS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-SEP-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-APR-1992
478 LSQELSIPYEE 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              390 LSQELSIPYEE 400
                                                                                                                                                    Local
                                                      1 LSXELSIPYEE 11
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                                                                                                                    l Similarity
10; Conserv
                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gelfand DH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                90US-0590490
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                                                                                                                                              96.0%;
                                                                                                                    0
                                                                                                                                              Score 48; DB 1
Pred. No. 0.53;
                                                                                                                    Mismatches
                                                                                                                                                                              DB 13; Length 632;
                                                                                                                    1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  exonuclease
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AAR23154
ID AAR2
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ID AAR
XX
                                                                    dd.
                            RESULT 8
                                                                                                 Qy
                                                                                                                                                                                          RESULT 7
                                                                                                                                Matches
                                                                                                                                              Best Local Similarity
                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-SEP-1990;
28-SEP-1990;
28-SEP-1990;
                                                                                                                                                                                                                                         may facilitate higher sensitivity allelic discrimination in a combined polymerase figase chain reaction (PLCR) assay. An enhanced ant. of 5'-3' exonuclease activity may be desirable in enzymes used in homogeneous assays for the amplification and detection of a target nucleic acid sequence. Mutation of the DNA encoding particular regions of the enzymes can be used to prepare a range of recombinant proteins having 5'-3' exonuclease activity to a complete lack of
                                                                                                                                                                                                                                                                                                                                                                                            The sequence is that of a mutant of Thermus species sps17 polymerase mutant MET-LNU 152 Tsps17, having a different amt. of 5'-3' exonuclease activity than the native enzyme. Thermostable DNA polymerases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Thermostable DNA polymerases with altered 5'-3' exo nuclease activity - having conserved regions mutated or deleted, for use in e.g. PCR, sequencing and detection assays
                                                                                                                                                                                                                                                                                                                                                  amplitication by M'R, self sustained sequence replication (SSR) and high temp. UNA sequencing. The absence of 5'-3' nuclease activity
                                                                                                                                                                                                                                                                                                                                                                               activity than the native enzyme. Thermostable DNA are useful in many recombinant DNA techniques, esp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAQ24008
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5'-3'; exonuclease; PCR; amplification; SSR; sequencing; PLCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-OCT-1992 (first entry)
                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                    See also AAR23140-79 and AAR23722.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 11; Page 59; 185pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1992-150885/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Abramson RD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (CETU ) CETUS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-SEP-1991;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mutant thermostable DNA polymerase enzyme MET-LEU 152 Tsps17.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-APR-1992
                                                                    526 LSQELSIPYEE 536
                                                                                                  1 LSXELSIPYEE 11
                                                                                                                                10;
                                                                                                                                                                                        680 AA;
                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gelfand DH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      90US-0590490
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                           96.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence*
                                                                                                                              0
                                                                                                                                           Score 48; I
                                                                                                                                Mismatches
                                                                                                                                                         DB 13; Length 680;
                                                                                                                                            .58;
                                                                                                                                                                                                                                                                                                                                                                                 nucleic
                                                                                                                                                                                                                                                                                                                                                                                  acid
                                                                                                                              0;
                                                                                                                           Gaps
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AAR23154 standard; Protein; 758 AA

0;

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The sequence is that of a mutant of Thermus species sps17 polymerase mutant MET-ALA 74 Tsps17, having a different amt. of 5'-3' exonuclease activity than the native enzyme. Thermostable DNA polymerases are useful in many recombinant DNA techniques, esp. nucleic acid amplification by PCR, self-sustained sequence replication (SSR) and high temp. DNA sequencing. The absence of 5'-3' nuclease activity and high temp. DNA sequencing. The absence of 5'-3' nuclease activity and fight temp. DNA sequencing. The absence of 5'-3' nuclease activity and fight temp. DNA sequencing. The absence of 5'-3' nuclease activity and properties of the sequence of 5'-3' nuclease activity and properties of the sequence of 5'-3' nuclease activity and properties of 5'-3' nuclease activity and 5'-3' exponence of 5
        22-OCT-1992 (first entry)
                                                                       AAR23153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       polymerase ligase chain reaction (PLCR) assay. An enhanced amt. o. 5'-3' exonuclease activity may be desirable in enzymes used in homogeneous assays for the amplification and detection of a target
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Thermostable DNA polymerases with altered 5^{\prime}-3^{\prime} exo nuclease activity - having conserved regions mutated or deleted, for use
                                                                                                                             AAR23153 standard; Protein; 788 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         regions of the enzymes can be used to prepare a range of recombinant proteins having 5'-3' exonuclease activity to a complete lack of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nucleic acid sequence. Mutation of the DNA encoding particular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 11; Page 59; 185pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAQ24007.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Thermus species SPS17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5'-3'; exonuclease; PCR; amplification; SSR; sequencing; PLCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mutant thermostable DNA polymerase enzyme MET-ALA 74 Tsps17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   See also AAR23140-79 and AAR23722.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          in e.g. PCR, sequencing and detection assays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Abramson RD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (CETU ) CETUS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-SEP-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-SEP-1990;
28-SEP-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-SEP-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-APR-1992
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                                                                                                                                                                                                                                                                                                                         1 LSXELSIPYEE 11
                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                      LSQELSIPYEE 614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1992-150885/18
                                                                                                                                                                                                                                                                                                                                                                                  10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                758 AA;
                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gelfand DH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      90US-0590213.
90US-0590466.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              90US-0590490
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                             90.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                        96.0%;
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                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                             Score 48;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                             0.66;
                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 13; Length 758;
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                                                                                                                                                                                                                                                                                                                                                                                  0;
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                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                               0,
           KW XX DT AC XX
                                                                                                                                                                                                                                   RESULT 10
AAR23152
ID AAR23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-SEP-1990;
28-SEP-1990;
28-SEP-1990;
5'-3'; exonuclease; PCR; amplification; SSR; sequencing; PLCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    activity than the native enzyme. Thermostable DNA polymerases are useful in many recombinant DNA techniques, esp. nucleic acid amplification by PCR, self-sustained sequence replication (SSR) and high temp. DNA sequencing. The absence of 5'-3' nuclease activity may facilitate higher sensitivity allelic discrimination in a combined polymerase ligase chain reaction (PLCR) assay. An enhanced amt. of 5'-3' exonuclease activity may be desirable in enzymes used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The sequence is that of a mutant of Thermus species sps17 polymerase mutant MET-PHE 43 Tsps17, having a different amt. of 5'-3' exonuclease activity than the native enzyme. Thermostable DNA polymerases
                                                        Mutant thermostable DNA polymerase enzyme ASP43 Tsps17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nucleic acid sequence. Mulation of the DNA encoding particular regions of the enzymes can be used to prepare a range of recombinant proteins having 5'-3' exonuclease activity to a complete lack of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 11; Page 59; 185pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Thermostable DNA polymerases with altered 5'-3' exo nuclease activity - having conserved regions mutated or deleted, for use in e.g. PCR, sequencing and detection assays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Thermus species SPS17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mutant thermostable DNA polymerase enzyme MET-PHE 43 Tsps17.
                                                                                                                 22-OCT-1992 (first entry)
                                                                                                                                                                                AAR23152;
                                                                                                                                                                                                                                     AAR23152 standard; Protein; 830 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               See also AAR23140-79 and AAR23722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               homogeneous assays for the amplification and detection of a target
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Abramson RD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CETU ) CETUS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-SEP-1991;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5'-3'; exonuclease; PCR; amplification; SSR; sequencing; PLCR.
                                                                                                                                                                                                                                                                                                                                                                            634 LSQELSIPYEE 644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
                                                                                                                                                                                                                                                                                                                                                                                                                                  1 LSXELSIPYEE 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1992-150885/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       l Similarity
10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAQ24006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            788 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gelfand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      90US-0590490
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96.0<del>%</del>;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 48; DB 13; Length 788; Pred. No. 0.69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0.69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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AAR23153 ID AAR2

RESULT 9

B γΩ

604

Matches

Caps

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RESULT 11
AAR76060
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                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                   Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                       are useful in many recombinant DNA techniques, esp. nucleic acid amplification by PCR, self-sustained sequence replication (SSR) and high temp. DNA sequencing. The absence of 5'-3' nuclease activity may facilitate higher sensitivity allelic discrimination in a combined polymerase ligase chain reaction (PLCR) assay. An enhanced amt. of 5'-3' exonuclease activity may be desirable in enzymes used in homogeneous assays for the amplification and detection of a target
           W09514770-A
                                                               DNA-polymerase; Tfil; thermostable enzyme.
                                                                                         Tfil DNA-polymerase
                                                                                                                                                                                                                                                                                                                                                                                                                nucleic acid sequence. Mutation of the DNA encoding particular regions of the enzymes can be used to prepare a range of recombi proteins having 5'-3' exonuclease activity to a complete lack of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The sequence is that of a mutant of Thermus species sps17 polymerase mutant ASP43 Tsps17, having a different amt. of 5'-3' exonuclease activity than the native enzyme. Thermostable DNA polymerases
                                      Thermus filiformis
                                                                                                                        28-OCT-1995
                                                                                                                                                    AAR76060;
                                                                                                                                                                            AAR76060 standard; Protein; 830 AA
                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                         See also AAR23140-79 and AAR23722.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 11; Page 59; 185pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Thermostable DNA polymerases with altered 5'-3' exo nuclease activity - having conserved regions mutated or deleted, for use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAQ24005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Abramson RD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-SEP-1990;
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28-SEP-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-SEP-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9206200-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Misc-difference 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          in e.g. PCR, sequencing and detection assays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (CETU ) CETUS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-APR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Thermus species sps17
                                                                                                                                                                                                                                                   676 LSQELSIPYEE 686
                                                                                                                                                                                                                                                                             1 LSXELSIPYEE 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1992-150885/18.
                                                                                                                                                                                                                                                                                                        10;
                                                                                                                                                                                                                                                                                                                                                             830 AA;
                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gelfand DH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              90US-0590213.
90US-0590466.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "Gly in native sequence"
                                                                                                                                                                                                                                                                                                                     96.0%;
                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                     Score 48; DB 13; Length 830; Pred. No. 0.73;
                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                        0
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                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR64273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
                              5' Nuclease(s) derived from thermostable DNA polymerase(s) - have cleavage activity with reduced synthetic ability, used for detection of specific target sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             presence of Mg2+. The enzyme is a versatile DNA-polymerase suitable for use in DNA synthesis from DNA and RNA templates, and for automated JNA sequencing. Both of these reactions are performed in the same buffer. The enzyme has a high salt tolerance and is also suitable for use in cycled fluorescent
        Disclosure; Page 83-86; 159pp; English
                                                                                                                                                                                                                                                                                                                                         T. flavus DNA polymerase
                                                                                                                                                                                  04-JUN-1993;
                                                                                                                                                                                                                                                                                                             DNA-polymerase; DNAP; Tfl; DNA cleavage; KNA cleavage; 5' nuclease
                                                                                                                                                                                                                                                                                                                                                                    19-JUL-1995
                                                                                                                                                                                                                                                                                                                                                                                                                      AAR64273 standard; Protein; 831 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA sequencing using dye-primers and dye-terminators.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA-directed enzyme) has reverse-transcriptase activity in the presence of Mg2+. The enzyme is a versatile DNA-polymerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 4; Fig 2; 40pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-NOV-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-NOV-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-1995
                                                                                       N-PSDB; AAQ80750.
                                                                                                                             Brow MAD, Dahlberg JE,
                                                                                                                                                                                                            06-JUN-1994;
                                                                                                                                                                                                                                      22-DEC-1994
                                                                                                                                                                                                                                                               W09429482-A
                                                                                                                                                                                                                                                                                       Thermus flavus AT-62.
                                                                                                                                                                                                                                                                                                                                                                                               AAR64273;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Thermostable DNA-polymerase Tfil (DNA nucleotidyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   transcriptase activity in the presence of magnesium ions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New heat-stable DNA polymerase from Thermus filiformis - has reverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAQ92369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bergquist PL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (PACI-) PACIFIC ENZYMES 1993 LTD.
                                                                                                     WPI; 1995-036504/05
                                                                                                                                                       (THIR-) THIRD WAVE TECHNOLOGIES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       676 LSQELSIPYEE 686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 LSXELSIPYEE 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               830 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Day DJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93NZ-0250288
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                                                                                                                                                                                   93US-0073384.
                                                                                                                                                                                                            94WO-US06253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       90.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gibbs MD,
                                                                                                                             Lyamichev VI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 48; DB 1
Pred. No. 0.73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Reeves RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 16; Length 830;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Saul DJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The DNA and amino acid sequences of T. flavus AT-62 thermostable DNA-polymerase (DNAP) are given in AAQ80750 and AAR64273, respectively. 5' Nucleases, such as those given in AAQ80742-45, derived from thermostable DNAPs show reduced synthetic activity whilst retaining structure-specific cleavage activity.
for the detection of non-target cleavage products via the formation of a complete and activated protein binding region, and methods for the detection of nucleic acid from various viruses (e.g. human cytomegalovirus) in a sample. The method amplifies the detection molecule rather than the target itself, is less subject to contamination than exponential amplification processes, and allows many targets to be analysed in a single reaction.
                                                                                                                           AAV65783-86). Cleavage of the cleavage structure by the nuclease indicates the presence of specific nucleic acid sequences or specific variants. The invention further relates to methods for the separation of nucleic acid molecules based on charge, methods the separation of nucleic acid molecules based on charge, methods
                                                                                                                                                                                                    preferably using a thermostable structure-specific nuclease such as a modified Thermus DNAP that has reduced synthetic activity (see
                                                                                                                                                                                                                                         methods for forming a nucleic acid cleavage structure on a target sequence and cleaving this structure in a site-specific manner,
                                                                                                                                                                                                                                                                          and variations in nucleic acid sequences.
                                                                                                                                                                                                                                                                                                            This is the amino acid sequence of the thermostable DNA polymerase (DNAP) of Thermus flavus (Tfl). The invention relates to means
                                                                                                                                                                                                                                                                                                                                                                                                       cytomegalovirus DNA
                                                                                                                                                                                                                                                                                                                                                                                                                      Detecting target nucleic acid by sequence-specific cleavage of complex with two specific oligonucleotides - used to detect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (THIR-) THIRD WAVE TECHNOLOGIES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-1998.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Thermus flavus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA polymerase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acid detection; multiple sequential invasive cleavage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Thermus flavus DNA polymerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02-FEB-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW79961;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW79961 standard; Protein; 831 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                    Example 2; Page 266-268; 524pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24-MAR-1997;
                                                                                                                                                                                                                                                                                           for the detection and characterisation of nucleic acid sequences,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     677 LSGELSIPYEE 687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FOCUL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 LSXELSIPYEE 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAV65780.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hall JG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      831 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97US-0823516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98WO-US05809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 48; DB 1
Pred. No. 0.73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lyamichev VI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 16; Length 831;
                                                                                                                                                                                                                                                                          It also relates to
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AAW80428
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-DEC-1992;
04-JUN-1993;
06-JUN-1995;
                                     sequences, via a cleavage-based procedure, but without the need for amplification of target sequences. Thermostable polymerases, altered to have nuclease, but not polymerase activity are preferably used due to their specificity. The cleavage product specifically formed is detected, preferably by the use of radioactively labelled oligonucleotides. These
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                describes a method for detecting the presence of a nucleic acid molecule. The method uses a thermostable 5' nuclease derived from thermostable polymerase modified to have reduced synthetic activity where the 5' nuclease is capable of cleaving a linear nucleic acid
                                                                                                                                                                                                                                                                                                       Detection of target nucleic acid molecules - uses modified thermostable enzymes with specific cleavage activity to create specific detection products from oligo:nucleotide(s) and target
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Thermostable DNA polymerase; nucleic acid detection; thermostable 5' nuclease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW80428 standard; Protein; 831 AA
                                                                                                                                                                                                             The present sequence represents a thermostable DNA polymerase enzyme. The sequence is used in the course of the invention. The specification
                                                                                                                                                                                                                                                             Disclosure; Fig 3; 91pp; English.
                                                                                                                                                                                                                                                                                            hybridisation
                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAV63401.
                                                                                                                                                                                                                                                                                                                                                                                                                       Brow MAD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-JUN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US5837450-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Thermus flavus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA polymerase enzyme
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW80428;
                        can be used in e.g. forensic testing or paternity determination
                                                                                                                    duplex structure to create a single, single-stranded cleavage product. The methods are used for the specific detection of nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                  (THIR-) THIRD WAVE TECHNOLOGIES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-NOV-1998
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                                                                                                                                                                                                                                                                                                                                                                                     1999-023438/02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10;
                                                                                                                                                                                                                                                                                                                                                                                                                    Dahlberg JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     831 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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90.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                    Lyamichev VI;
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Pred. No. 0.73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 19; Length 831;
                                                                                                                                                                  synthetic activity,
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Query Match Matches

Local 10;

Similarity

96.0%;

Score 48; DB 2 Pred. No. 0.73;

DB 20; Length 831;

0;

Mismatches

0;

Gaps

0;

Sequence

831 AA;

QΨ

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RESULT 15
AAR722
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AAR722
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AC AAR72
XX
DT 05-DEC
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POlyme
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POlyme
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POlyme
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POLyme
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PF 22-AU
PR 12-JU
PR 13-JU

Search completed: January 15, 2003, 11:20:16 Job time : 30.2857 secs
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Best Local S
Matches 10
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22-AUG-1986;
17-JUN-1987;
12-JAN-1988;
15-MAY-1990;
28-SEP-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence is the thermostable polymerase of Thermus species \operatorname{sps17}. The Gly residue at position 43 may be substituted for an Asp residue. This substitution is shown to result in a 100 lold decrease in the 5'-3' exonuclease activity with no change to the polymerase activity of the enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Columns 7-12; 26pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA for Thermus species sps17 DNA polymerase - modified to encode an N-terminal deletion to reduce 5'-3' exo:nuclease activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US5405774-A.
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                                                                                                                                                                                                                                                                                                                                                                             Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1995-154582/20.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Polymerase; Thermus; enzyme; thermostable; exonuclease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tsps17 polymerase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-DEC-1995 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Abramson RD, Gelfand DH, Greenfield IL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HOFF ) HOFFMANN LA ROCHE INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22-AUG-1986;
                                                                                                                                 691 LSQELSIPYEE 701
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                                                                                                                                                                                                                                                  y Match 96.0%;
Local Similarity 90.9%;
hes 10; Conservative
                                                                                                                                                                                         1 LSXELSIPYEE 11
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                                                                                                                                                                                                                                                                                                                                                                             845 AA;
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86US-0899241.
87US-0063509.
88US-0143441.
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90US-0590213.
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                                                                                                                                                                                                                                                  Score 48; DB 16; Length 845; Pred. No. 0.74; 0; Mismatches 1; Indels
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OM protein - protein search, using sw model

CATB_PSEPU SUCC_AQUAE EMRA_HAEIN THTR_CORGL YDDR_ECOLI HIS4_THEET ILVE_ARCFU

067546 P44928

aquifex aeo

haemophilus

pseudomonas escherichia corynebacte

P08310

Q9rpq5 thermoanaer O29329 archaeoglob

archaeoglob

GenCore version 5.1.3 Compugen Ltd

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is the number of results predicted by chance to have a sater than or equal to the score of the result being printed, rived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  January 15, 2003, 09:04:22; Search time 6.28571 Seconds (without alignments) 72.584 Million cell updates/sec
              Q10518
Q9jyz2
Q91835
Q01835
P13092
Q9hja4
P71397
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P48534
Q9zjj4
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Q9h583
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I-51234
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                                                                                                                                                                                                                                                                                                                         Q06336 saccharomyc
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              thermoplasm
haemophilus
                                                                                                                                                                                                synechocyst
  aquifex aec
                                     wound tumor
                                                listeria gr
                                                              neisseria m
                                                                        mycobacteri
                                                                                       escherichia
                                                                                                  helicobacte
                                                                                                                         pisum sativ
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                                                                                                                                                                                                                                                                                                                                                             escherichia
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RESULT 2
ANGT_RAT
ID ANGT
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Best Local
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01-NOV-1997
01-NOV-1997
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Hypothetical 39.9 kDa protein y40x.
 P01015;
21-JUL-1986 (Rel. 01, Created)
                                                                                                                                                                                               Pfam; PF01408; GP0_IDH_MocA; 1.

Pfam; PF02894; GF0_IDH_MocA_C; 1.

Hypothetical protein; Plasmid; Oxidoreductase; NAD.

NP_BIND

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22
NAD (BY SINILARITY).
                                                                                                                                                                                                                                                                                                          the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial cutifities requires a license agreement (See http://www.isb-sib.ch/announce/
                          ANGT_RAT
                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                              InterPro; IPR000583; GFO_IDH_MocA_C. InterPro; IPR004104; GFO_IDH_MocA_C.
                                                                                                                                                                                                                                                                                              or send an email to licensesisb sib.ch).
                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the FMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                         "Molecular basis of symbiosis between Rhizobium and legumes.";
Nature 387:394-401(197).
-i- FUNCTION: COULD BE A NAD-DEPENDENT OXIDOREDUCTASE.
-i- SIMILARITY: LOW, TO R.MELILOTI RHIZOPINE CATABOLISM PROTEIN MOCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDLINE=97305956; PubMed=9163424;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=394;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plasmid sym pNGR234a.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rhizobium sp. (strain NGR234).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P55609;
                                                                                                                                                                                                                                                                        EMBL; AE000089; AAB91810.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Perret X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Freiberg C.A., Fellay R., Bairoch A., Broughton W.J., Rosenthal A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rhizobiaceae; Rhizobium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Y40X_RHISN
                                                                                     337 SVRLGQPVK 345
                                                                                                            2 SVRLGXPVK 10
                                                                                                                                                                                                                                                                                                                                                                                                AND S.GRISEUS STREPTOMYCIN BIOSYNTHESIS PROTEIN STRI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
8; Conserv
                                                                                                                                                                                     360 AA;
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                          STANDARD;
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                                                                                                                                                                                     39853 MW;
                                                                                                                                                 88.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last annotation
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DNLI_PYRHO
DNLI_PYRFU
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                                                                                                                                               Score 38; DB 1; Length 360; Pred. No. 1.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                     59998F5082DE26CA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALIGNMENTS
                                                                                                                                    Mismatches
                        477 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           update)
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059288
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pyrococcus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               homo sapien
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Result

Score

Match

Length

В

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SUMMARIES

Y40X_RHISN

77.6 73.5 73.5

OTSB_RHISN

GGA1_YEAST

APE_PIG

RECA_THEMA RM03_CAEEL

YNHG_ECOL:

HEAD_BPPH8 RNFC_BUCAI

Query

964 1034 12265 1223 123 155 249 259 259 259 302 313 313 451 511 520 759 819

MURB_HELPJ MURB_HELPY CHEW_CAUCR APX1_PEA

YCAN_ECOLI

P60_LISGR
VP7_WTV
PURL_THEAC
RNFC_HAEIN

COBD_MYCTU EX7L_NEIMB

CAPP_SYNY3
RPC2_SCHPO

LON2_MAIZE FEOB_ECOLI FEOB_SALTY PCL1_ARATH

GALA_BOVIN

0

DSRA_HUMAN

Database

SwissProt_40:*

and is derived by Pred. No. Post-processing: Minimum Match 0%

Maximum Match 100% Listing first 45 summaries

Maximum DB

seq length: 0 seq length: 2000000000

Total number of hits satisfying chosen parameters:

112892 segs, 41476328 residues

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext

Perfect score:

US-09-823-649A-5 49

LSVRLGXPVKE 11

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                                                                                                                           멂
                                                              Matches
                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Comparative studies on any poly poly method."; angiotensin and its identification by DNS method."; Chem. Pharm. Bull. 20:1579-1581(1972).

-I- FUNCTION: IN RESPONSE TO LOWERED BLOOD PRESSURE, THE ENZYME RE-
                                                                                                                                                                         PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                 EMBL; L00094; AAA98779.1; -
EMBL; L00091; AAA98779.1; JOINED.
EMBL; L00092; AAA98779.1; JOINED.
EMBL; L00093; AAA98779.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMB outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                            CARBOHYD
                                                                                                                                                                                                                          CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=83169849; PubMed=6572971;
Ohkubo H., Kageyama R., Ujihara M., Hirose T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Kattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Angiotensinogen precursor [Contains: Angiotensin I (Ang I); Angiotensin II (Ang II); Angiotensin III (Ang III) (Des-Asp[1]-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-JUL-1986 (Rel. 01, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                           CARBOHYD
                                                                                                                                                                                                           HILLARA
                                                                                                                                                                                                                                        SIGNAL
                                                                                                                                                                                                                                                       Vasoconstrictor; Glycoprotein; Plasma; Serpin; Signal.
                                                                                                                                                                                                                                                                                                     PRINTS;
                                                                                                                                                                                                                                                                                                                    Pfam; PF00079; serpin;
                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000227; Anglotensngn
                                                                                                                                                                                                                                                                                                                                                                     PIR; A01251; ANRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                entities requires a license agreement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nakayama T., Nakajima T., Sokabe H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=73060322; PubMed=4344907;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 25-34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Cloning and sequence analysis of cDNA for rat angiotensinogen.";
Proc. Natl. Acad. Sci. U.S.A. 80:2196-2200(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rattus norvegicus (Rat).
 148
                                                                              Local
                                1 LSVRLGXPVKE 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLEAVES ANGIOTENSIN I, FROM ANGIOTENSINOGEN. ACE (ANGIOTENSIN CONVERTING ENZYME) THEN REMOVES A DIPEPTIDE TO YIELD THE PHYSIOLOGICALLY ACTIVE PEPTIDE ANGIOTENSIN II. THE MOST POTENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE SPECIFICITY: Synthesized by the liver and secreted in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION: Secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRESSOR SUBSTANCE KNOWN, WHICH HELPS REGULATE VOLUME AND MINERAL BALANCE OF BODY FLUIDS.
LQVLLGVPVKE 158
                                                                                                                                                                                                                                                                                       SM00093; SERPIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SERPINA8
                                                              Similarity
8; Conser
                                                                                                                                                                                                                                                                                                       PR00654;
                                                                                                                                                                                                                                                                        PS00284; SERPIN; FALSE_NEG
                                                                                                                                                                                                                                                                                                                                   IPR000215; Serpin.
                                                                                                                          295
319
477 AA;
                                                              Conservative
                                                                                                                                                                                                                                                                                                       ANGIOTENSNON.
                                                                                                                                                        477
34
32
32
32
295
                                                                                                                           51981 MW;
                                                                          73.5%;
72.7%;
                                                              0;
                                                                              Score 36;
Pred. No.
                                                                                                                                                                       ANGIOTENSINOGEN.
ANGIOTENSIN I.
ANGIOTENSIN II.
ANGIOTENSIN III.
                                                                                                                        N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
689051A5788D593D CRC64;
                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (See http://www.isb~sib.ch/announce/
                                                                                         DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Usage by and for commercial

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                                                                                         Length 477;
                                                                                                                                           (POTENTIAL)
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                                                              Gaps
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                                                             Matches
                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S., Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K., Zamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y., Ninomiya K., Iwayanagi T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09H583; 09NW23;
16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HUMAN
                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                       modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "NEDO human cDNA sequencing project."; Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
Wagatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara
                                                                                                                                                      VARIANT
                                                                                                                                                                                     VARIANT
                                                                                                                                                                                                                   VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                  between the Swiss institute of Bioinformatics and the the European Bioinformatics Institute. There are no re
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bougueleret I., Chumakov I., Barry C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID-9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Melazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein BAP28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BP28_HUMAN
                                                                                                                                                                                                                                                 VARIANT
                                                                                                                                                                                                                                                                   REPEAT
                                                                                                                                                                                                                                                                             Polymorphism
                                                                                                                                                                                                                                                                                                                             EMBL; AK001221;
                                                                                                                                                                                                                                                                                                                                            EMBL; AL
                                                                                                                                                                                                                                                                                                                                                         EMBL; AX067150; CAC26776.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SIMILARITY: CONTAINS 1 HEAT REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SIMILARITY: BELONGS TO THE BAP28 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 1777-2144 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 1534-2144 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "A novel BAP28 gene and protein.";
Patent number WOOl00669, 04-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A., AND VARIANTS S-1694; A-1854; D-1967 AND G-2017
                                                                                                                                                                                                                                                                                               PROSITE; PS50077; HEAT_REPEAT; FALSE_NEG
                                                                                                                                                                                                                                                                                                           (nterPro; IPR000357;
923 LLINLGSPVKE 933
                                                                        Local
                            1 LSVRLGXPVKE 11
                                                         Similarity
7; Conserv
                                                                                                                                                                                                                                                                                                                                            136105;
                                                                                                                                                                                                                                                                                                                                                                                                                                     non-profit institutions as long
                                                                                                                                                                                  1967
                                                                                                                                                      2017
                                                                                                                                                                                                                   1854
                                                                                                                                                                                                                                                 1694
                                                                                                                       2144 AA;
                                                                                                                                                                                                                                                                   2106
                                                           Conservative
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                                                                                                                                                                                                                                                                                                           BAA91564.1; ALT_INIT.
0357; HEAT_repeat.
                                                                                                                                                                                                                                                                                                                                            CAC15948.1;
                                                                                                                                                      2017
                                                                                                                                                                                    1967
                                                                                                                                                                                                                 1854
                                                                                                                                                                                                                                                 1694
                                                                                                                                                                                                                                                                2142
                                                                        63.6%;
                                                                                                                       242355 MW; D66816EE78D8C9B7 CRC64;
                                                                                       73.5%;
                                                                                  Score 36; DB 1; Length 2144;
                                                      Pred. No. 31;
1; Mismatches
                                                                                                                                                                                                                 /FTId-VAR_010939
V -> A
                                                                                                                                    /FTId=VAR_010942
                                                                                                                                                                 /FTId=VAR_010941
                                                                                                                                                                                                 /FTId-VAR_010940
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cohen-Akenine A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                   as its content
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RESULT 4 YNHG_ECOLI

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                                                                                                                                                                                                                                                                                                                                                 RECA_THEMA
                                                                                                           RESULT 5
                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                      Query Match
                                           RECA_THEMA
P36203;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Itoh T., Kasai H., Kashimoto K., Kimura S., Kitakawa M., Kitagawa M., Makibo K., Mki T., Mizobuchi K., Mori H., Mori T., Motomura K., Nakade S., Nakamura Y., Nashimoto H., Nishio Y., Oshima T., Saito N., Sampei G., Seki Y., Sivasundaram S., Tanana T., Saito N., Sampei G., Seki Y., Sivasundaram S.,
  01-JUN-1994
                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR002482; LysM.

Pfam; PP01476; LysM; 1.

SMART; SM00257; LysM; 1.

Hypothetical protein; Periplasmic; Signal; Complete proteome.

SIGNAL 1 23 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Blattner F.R., Plunkett G. [II, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                      01-JUN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the Eurogian Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "A 570-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 28.0-40.1 min region on the linkage map.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oshima T., Saito N., S
Tagami H., Takeda J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical protein ynhG precursor.
                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; D90811; BAA15458.1; -.
EMBL; D90812; BAA15464.1; ALT_SEQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AE000263; AAC74748.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWTSS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA Res.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=97251357; PubMed=9097039;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=97426617; PubMed=9278503;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P76193; P76899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EcoGene; EG14015; ynhG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SIMILARITY: BELONGS TO THE ERFK/YBIS/YCFS/YNHG FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 1-233 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YNHG OR B1678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YNHG_ECOLI
                                                                                                                                                                             223 SVRTGTPVK 231
                                                                                                                                                                                                                                                             Local Similarity es 7; Conser
                                                                                                                                                                                                                    2 SYRLGXPVK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Res. 3:363-377(1996).
SUBCELLULAR LOCATION: Periplasmic (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complete genome sequence of Escherichia coli K-12.";
nce 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the Swiss Institute of Bioinformatics and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                / MG1655;
                                                                                                                                                                                                                                                                                                                                                 334 AA;
(Rel. 29, Created)
(Rel. 29, Last sequence update)
                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Horiuchi T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P76900
                                                                                                                                                                                                                                                                                                                                                 36082 MW;
                                                                                                                                                                                                                                                                                 69.48;
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                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                 Pred. No.
                                                                                                                                                                                                                                                                                                      Score 34;
                                                                                                                                                                                                                                                                                                                                                                      HYPOTHETICAL PROTEIN YNHG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                 25078BB429389D5F CRC64;
                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     334 AA
                                                                  356 AA
                                                                                                                                                                                                                                                                                                      DB 1; Length 334;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Usage
                                                                                                                                                                                                                                                               2;
                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL outstation -
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                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                    Best
RM03_CAEEL
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RM03_CAEEL
                             RESULT 6
                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nelson K.E. Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A., McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M., Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D., Stewart A.M., Sutton G.G., Pleischmann R.D., Elsen J.A., White O., Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
"Evidence for lateral gene transfer between Archaea and Bacteria from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-95014407; PubMed=7929298; Wetmur J.G., Wong D.M., Ortiz B., Tong J., Reichert F., Gelfand D.H.; "Cloning, sequencing, and expression of RecA proteins from three distantly related thermophilic eubacteria.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               genome sequence of Thermotoga maritima.";
Nature 399:323-329(1999).
-!- FUNCTION: CAN CATALYZE THE HYDROLYSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      J. Biol. Chem. 269:25928-25935(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Thermotogaceae; Thermotoga.
                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                               Complete proteome. NP_BIND 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AE001823; AAD36921.1; -. HSSP; P26345; 1G19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; L23425; AAA27417.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or send an email to licensewisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Thermotogae; Thermotogae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Thermotoga maritima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RECA OR TM1859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Reca protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA damage; DNA recombination; SOS response; ATP-binding; DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS50162; RECA_2; 1.
PROSITE; PS50163; RECA_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00321; RECA_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART; SM00382; AAA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ProDom;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PROUISZ; RECA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00154; recA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR003593; AAA_ATPase
InterPro; IPR001553; RecA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TIGE; TM1859;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE~99287316; PubMed~10360571;
                                                                                                                225 MEVRRGEPIKE 235
                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                              1 LSVRLGXPVKE 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FUNCTION: CAN CATALYZE THE HYDROLYSIS OF ATP IN THE PRESENCE OF SINGLE-STRANDED DNA, THE ATP-DEPENDENT UPTAKE OF SINGLE-STRANDED DNA BY DUPLEX DNA, AND THE ATP-DEPENDENT HYBRIDIZATION OF HOMOLOGOUS SINGLE-STRANDED DNAS. IT INTERACTS WITH LEXA CAUSING ITS ACCIVATION AND LEADING TO ITS AUTOCATALYTIC CLEAVAGE. SUBCELLULAR LOCATION: CYCOPIASMIC (By Similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PD000229;
                                                                                                                                                                                                                                                                                                                                                               356 AA; 38797 MW;
                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Recombinase A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Reca; i.
                                                                                                                                                                                                                                                                 69.4%;
54.5%;
                                                                                                                                                                                                                                        2; Mismatches
                                                                                                                                                                                                                                                                                                  Score 34;
                                                                                                                                                                                                                                                                                                                                                                                            ATP (BY SIMILARITY)
                                                                                                                                                                                                                                                                        Pred. No.
                                                                                                                                                                                                                                                                                                                                                               A2B70853C26C95FD CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       There are no
                                                                                                                                                                                                                                                                                                     DB 1;
                                                                                                                                                                                                                                                                                                  Length 356,
                                                                                                                                                                                                                                        Indels
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                                                                                                                                                                                                                                        Gaps
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STANDARD;

PRT;

381 AA.

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RESULT 7
GGA1_YEAS
В
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                         STRAIN=S288C / AB972;
Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Du Z.,
Favello A., Fulton L., Gattung S., Greco T., Kirsten J., Kucaba T.,
Hallsworth K., Hawkins J., Hillier L., Jier M., Johnson D.,
Johnston L., Langston Y., Latreille P., Le T., Mardis B., Menezes S.,
Miller N., Nhan M., Pauley A., Peluso D., Rifken L., Riles L.,
Trevaskis B., Vignati D., Wilcox L., Wohldman P., Vaudin M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (JUN-2001) to the EMBL/GenBank/DDbJ databases.
-!- SUBCELLULAR LOCATION: Mitochondrial (By Similarity).
-!- SIMILARITY: BBLONGS TO THE L3P FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                        ear-containing, ARF-binding protein 1). GGA1 OR YDR358W OR D9476.2.
                                                                                                                                                                                                                                                                                         16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
ADP-ribosylation factor binding protein GGAl (Golgi-localized, gamma
                                                                                                                                                                                                                                                                                                                                           GGA1_YEAST STANDARD;
Q06336;
16-OCT-2001 (Rel. 40, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00297; Ribosomal_L3; 1.
ProDom; PD001374; Ribosomal_L3; 1.
PROSITE; PS00474; RIBOSOMAL_L3; RALSE_NEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; U13875; AAA21160.2; -. WormPep; C26E6.6; CE26871.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-JUN-2002 (Rel. 41, Last annotation update) Putative mitochondrial 60S ribosomal protein L3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-FEB-1996 (Rel. 33, Creat
15-JUN-2002 (Rel. 41, Last
15-JUN-2002 (Rel. 41, Last
Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                       SEQUENCE FROM N.A
                                                                                                                                                                                                       Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                        Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                                 YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitten (NOV-1994) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P49404;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ribosomal protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000597; Ribosomal_L3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REVISIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   164 VRAGIPVKE 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
nes 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 VRLGXPVKE 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           381 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mitochondrion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           42288 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      69.48;
77.88;
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 Mismatches

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 34;
                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3F57FBC8C6F2B667 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                 557 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 381;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and for commercial
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QΥ
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                                                                                                                                                                                                                   RESULT 8
                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                        01-NOV-1997
01-NOV-1997
01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=21064505; PubMed-11124697;
Zhdankina O., Strand N.L., Redmond J.M., Boman A.L.;
Zhdankina O., Strand N.L., Redmond J.M., Boman A.L.;
"Yeast GGA proteins interact with GTP-bound Arf and facilitate transport through the Golgi.";
Yeast 18:1-18(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        facilitate trafficking between the trans-Golgi network and the vacuole/lysosome.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 [2] CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00790; VHS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=20211637; PubMed=10747088;
NCBI_TaxID-394;
                            Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
                                         Rhizobium sp. (strain NGR234).
Plasmid sym pNGR234a.
                                                                          OTSB OR Y4PB.
                                                                                                   Probable trehalose-phosphatase (EC
                                                                                                                                                                       P55611;
                                                                                                                                                                                    OTSB_RHISN
                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF02883; Alpha_adaptinC2;
Pfam; PF03127; GAT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SGD; S0002766; GGA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U28372; AAB64793.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -1- SIMILARITY: CONTAINS 1 GAMMA-ADAPTIN C-TERMINAL DOMAIN.
-1- SIMILARITY: CONTAINS 1 VHS DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           J. Cell Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "A family of proteins with gamma-adaptin and VHS domains that
             Rhizobiaceae; Rhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein transport; Golgi stack; Coiled coil.
DOMAIN 29 165 VHS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ProDom;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ProDom; PD003686; HRS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; 1Pk001121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR004152; GAT_dom
                                                                                       phosphatase) (TPP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR002014; HRS.
                                                                                                                                                                                                                                                                  523 ISVNLGKPIK 532
                                                                                                                                                                                                                                                                                                 1 LSVRLGXPVK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; PD021457; Gamma_adaptin_C;
SM00288; VHS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PD021457;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       non-profit
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                                                                                                                                                                                                                                                                                                                                                                                         442
557 AA;
                                                                               (Rel. 35, Created)
(Rel. 35, Last sequence update)
(Rel. 35, Last annotation update)
(Rel. 35, Last annotation update)
(Rel. 35, Last annotation update)
                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         149:67-80(2000).
                                                                                                                                                                                    STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                          62319 MW;
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Pred. No. 21;
                                                                                                                                                                                                                                                                                                                                                                                                                     COILED COIL (POTENTIAL)
COILED COIL (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                        GAMMA-ADAPTIN
                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                          DBA76787E998DBD7 CRC64;
                                                                                                                                                                                    265 AA
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                                                                                                                                                                                                                                                                                                                                                         Length 557;
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                                                                                                                                                                                                                                                                                                                             Caps
                                                                                                                                                                                                                                                                                                                             0;
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Freiberg C.A., Fellay R.,

[1] SEQUENCE FROM N.A.

MEDLINE=97305956;

PubMed=9163424;

Bairoch A., Broughton W.J., Rosenthal A.,

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111 LSIRIGHPI 119

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RESULT 9
YCXB_PORPU
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                                         Query Match
Best Local
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16-OCT-2001 (Rel. 40
Hypothetical 73.8 kD
(ORF621).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                       P51234;
01-OCT-1996 (
01-OCT-1996 (
16-OCT-2001 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                  Hypothetical SEQUENCE 67
                                                                                                                                         entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                       genome."
                                                                                                                                                                                                                                                                                                                                                                   Chloroplast.
Eukaryota; Rhodophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TIGRFAMS; TIGRO0685; otsB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AE000090; AAB91812.1;
InterPro; IPR003337; Trehalc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               phosphate.
-!- SIMILARITY: TO THE E.COLI (OTSB) AND YEAST ENZYME (TPS2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature 387:394-401(1997)
                                                                                                               EMBL; U38804; AAC08120.1; -
                                                                                                                                                                                                                                                       Plant Mol. Biol. Rep. 13:333-335(1995).
                                                                                                                                                                                                                                                                                               Reith M.E., Munholland J.;
                                                                                                                                                                                                                                                                                                              STRAIN-Avonport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -i- CATALYTIC ACTIVITY: Trehalose 6-phosphate + H(2)0 = trehalose
                                                                                                                                                                                                                                                                                    "Complete nucleotide sequence of the Porphyra
                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=2787;
                                                                                                                                                                                                                                                                                                                                                                                               Porphyra purpurea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YCXB_PORPU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      230 LSIRIGPPV 238
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  1 LSVRLGXPV 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PF02358; Trehalose_PPase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6;
                             υı
                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ar basis of symbiosis between Rhizobium and legumes.";
                                                                                  621 AA; 73754 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Plasmid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    265 AA;
                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                           34,
34,
40,
kDa
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                                         67.3%;
55.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Trehalose_PPase.
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Last annotation update)
protein in YCF10-PSBI i
                                                                                                 Chloroplast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
                                                                                                                                                                                                                                                                                                                                                                      Bangiophyceae; Bangiales; Bangiaceae; Porphyra.
                                         Score 33;
Pred. No.
                               ω
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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                                                                                    36BAF5EBE64F4FBC CRC64;
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                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 621 AA
                                             ДВ
37;
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                                                                                                                                                                                                                                                                                                                                                                                                                           intergenic region
                                                                                                                                                                                                                                                                                    purpurea chloroplast
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B/E) RECEPTOR AND FOR THE SPECIFIC APO-E RECEPTOR (CHYLOMICKON REMNANT) OF BEPATIC TISSUES.
-(- SUBCELLULAR LOCATION: Extracellular.
-i- TISSUE SPECIFICITY: SECRETED IN PLASMA.
-i- SIMILARITY: BELONGS TO THE APOA1 / APOE FAMILY.

OF LIPOPROTEIN PARTICLES. IT CAN SERVE AS A LIGAND FOR THE LDL (APO

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RESULT 10

APE_PIG

COC APER

APE BIG

APE 
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P18650;
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01-FEB-1994 (Rel. 28, Last sequence up
15-JUL-1999 (Rel. 38, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Weisgraber K.H., Troxler R.F., Rall S.C., Mahley R.W.;
"Comparison of the human, cantine and swine E approteins.";
"Comparison of the human, cantine and swine E approteins.";
Biochem. Biophys. Res. Commun. 95-374-380(1980).
-I--FUNCTION: APO-E MEDIATES BINDING, INTERNALIZATION, AND CATABOLISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Grimm D.R., Lunney J.K., Schook L.B., Piedrahita J.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=98347372; PubMed=9682450; Ramsoondar J.J., Rucker E.B., Vasquez J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Brzozowska A.M., Grim
Submitted (MAY-1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9823;
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sus scrofa (Pig).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Apolipoprotein E precursor (Apo-E).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY SEQUENCE OF 19-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Anim. Genet. 29:43-47(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Isolation and genetic characterization of the porcine apolipoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-81021043;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 019099;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PubMed=7417263;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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DOMAIN REPEAT REPEAT REPEAT Pfam; PF01442; Apolipoprotein; 1. Glycoprotein; Plasma; Lipid transport; HDL; PIR; A05312; A05312. PIR; S33450; S33450. EMBL; X72835; CAA51356.1; -. EMBL; U70240; AAC29512.1; -. modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-slb.ch/announce/ This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -REPEAT DOMAIN HSSP; P02649; 10EF. or send an email to licensewisb-sib.ch). the European DOMAIN DOMAIN CHAIN Heparin-binding; Repeat; InterPro; IPR000074; Apolipoprotein. non-profit 19 157 161 228 79 79 101 Bioinformatics Institute. 18 317 167 164 2354 254 1100 122 144 166 188 rmatics Institute. There are no restrictions on institutions as long as its content is in no Signal. LDL RECEPTOR BINDING (POTENTIAL).
HEBPARIN-BINDING (BY SIMILARITY).
HEPARIN-BUDING (BY SIMILARITY).
8 x 22 AA APPROXIMATE TANDEM REPE APOLIPOPROTEIN E. VLDL; Chylomicron; TANDEM REPEATS Ou

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Query Match
Best Local Similarity
""atches 6; Conserv
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HEAD_BPPH8
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      use k_f non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL cutstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Nucleotide sequence from bacteriophage phi 80 with high homology to the major coat protein gene of lambda."; Nucleic Acids Res. 16:764-764(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOY-1988 (Rel. 09, Created)
01-NOY-1988 (Rel. 09, Last sequence update)
01-JUN-1994 (Rel. 29, Last annotation updat
15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                  P57215;
                                                                                   RNFC_BUCAI
                                                                                                           BUCAI
                                                                                                                                                                                                                                                                                                                                                                      Coat protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     or send an email to licensewisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kitao S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10713;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;
Lambda-like viruses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteriophage phi-80.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HEAD_BPPH8
                                                                                                                                                                                      309 VQLGDPVRE 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    212 LSTRAGQPLRE 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 LSVRLGXPVKE 11
                                                                                                                                                                                                                             3 VRLGXPVKE 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: STRONG, TO MAJOR HEAD PROTEIN OF LAMBDA AND P21.
                                                                                                                                                                                                                                                                                                                                                                                           S03314; VHBP80.
                                                                                                                                                                                                                                                                                                                                                                                                               X06751; CAA29926.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nakano E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          211
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                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PubMed=3267214;
                                                                                                                                                                                                                                                                                                                                                   38054 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     36599 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         65.3%;
54.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NV -> KI (IN REF. 2).
V -> L (IN REF. 2).
DE -> EQ (IN REF. 2).
A -> G (IN REF. 2).
Q -> H (IN REF. 2).
R -> L (IN REF. 2).
M -> I (IN REF. 2).
M -> G (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2;
                                                                                                                                                                                                                                                                     2;
                                                                                                                                                                                                                                                                                         Score 32; DB
Pred. No. 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 32; DB 1; Length 317; Pred. No. 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -> P (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                     BCDAE15ED85785E2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     83E7F51A07785055 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                     Mismatches
                                                                                     473 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      341 AA
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                                                                                                                                                                                                                                                                                                          DB 1; Length 341;
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    SEQUENCE FROM N.A
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RESULTA 13
PCLL_ANA
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Best Local Similarity
Triches 5; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Electron transport; 37 33 METAL 340 34 METAL 347 34 METAL 347 34 METAL 376 37 METAL 376 37 METAL 379 37 METAL 379 37 METAL 382 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       METAL
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa H.; "Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp. APS.";
                                                                                                                                                                     Putative prenylcysteine lyase precursor (EC 4.4.1.18).
AT563910 OR MGI19.4 OR MGI19.11.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-Tokyo 1998;
                                                                                                      Spermatophyta; Magnoliophyta; eudicotyledons; core eurosids II; Brassicales; Brassicaceae; Arabidopsis
                                                                                                                                                                                                                                                                                                                  16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                P57681;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AP001118; BAB12833.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SUBCELLULAR LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SUBUNIT: Composed of at least six subunits; rnfA, rnfB, rnfC, rnfD, rnfE and rnfG (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -:- COFACTOR: Binds 2 4FE-4S clusters (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 407:81-86(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-20445173; PubMed=10993077;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       symbiotic bacterium)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RNFC OR BUll5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Electron transport complex protein rnfC
                                                                      NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PCL1_ARATH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ptam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR001450; 4Fe4S_ferredoxin.
InterPro; IPR001949; Complex1_51K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -1- SIMILARITY: BELONGS TO THE 4FE4S BACTERIAL-TYPE FERREDOXIN FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -:- FUNCTION: May be part of a membrane complex involved in electron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=118099;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria; gamma subdivision; Buchnera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        272 VRIGTPIK 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 VRLGXPVK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RNFC SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   transport (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PF00037; fer4; 2.
PF01512; Complex1_51K; 1.
TE; PS00198; 4FE4S_FERREDOXIN; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Iron-sulfur; 4Fe-4S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     65.38;
62.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           54563 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Membrane-associated (By similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ifur; 4Fe-4S; Complete p
IRON-SULFUR (4FE-4S)
IRON-SULFUR (4FE-4S)
IRON-SULFUR (4FE-4S)
IRON-SULFUR (4FE-4S)
IRON-SULFUR (4FE-4S)
IRON-SULFUR (4FE-4S)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 32; DB
Pred. No. 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IRON-SULFUR (4FE-4S)
IRON-SULFUR (4FE-4S)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           04E64102F1315AEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            рв 1;
                                                                                                                                         core eudicots; Rosidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 473;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (POTENTIAL). (POTENTIAL). (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 proteome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (POTENTIAL).
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Matches
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Best Local
SEQUENCE OF 33-330 FROM N.A. STRAIN=ATCC 14028; MEDLINE=97045140; PubMed=8890205;
                                                                                                                                                                        McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA Res. 4:401-414(1997).

-IF FUNCTION: INVOLVED IN THE DEGRADATION OF PRENYLATED PROTEINS.
-ICLEAVES THE THIOETHER BOND OF PRENYL-L-CYSTEINES, SUCH AS
FARNESYLCYSTEINE AND GERANYLGERANYLCYSTEINE (BY SIMILARITY).
-I- CATALYTIC ACTIVITY: A prenyl-L-cysteine + H(2)0 = a prenol + L-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Structural analysis of Arabidopsis thaliana chromosome 5. III. Sequence features of the regions of 1,191,918 bp covered by seventeen physically assigned Pl clones.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AB007646; BAB11039.1; EMBL; AB019227; BAB11039.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                             Waterston R., Wilson R.K.;
                                                                                                                                                                                                                                                                  STRAIN=LT2 / SGSC1412 / ATCC 700720;
MEDLINE=21534948; PubMed=11677609;
                                                                                                                                                                                                                                                                                                                                                                                                                               Salmonella typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tabata
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                                                                                         Nature 413:852-856(2001).
                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=602;
                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEOB OR STM3506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEOB_SALTY
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                                                                                                                                     "Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 114 LTVRLPTPIEE 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 LSVRLGXPVKE 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COFACTOR: FAD (BY SIMILARITY)
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500 AA;
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56
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54.5%;
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N-LINKED (GLCNAC. . ) (POTENTIAL).

N-LINKED (GLCNAC. . ) (POTENTIAL).

N-LINKED (GLCNAC. . ) (POTENTIAL).

N-LINKED (GLCNAC. . ) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Signal; Glycoprotein; Lysosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       772 AA.
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NP_BIND 16
NP_BIND 56
TRANSMEM 102
TRANSMEM 382
TRANSMEM 309
TRANSMEM 334
                                                                                      01-FEB-1994
01-FEB-1994
16-OCT-2001
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CONFLICT
CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entities requires a license agreement (for send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF02421; FeoB; TIGRFAMS; TIGRO0231;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Infect. Immun. 64:4549-4556(1996).
-I- FUNCTION: PROBABLE GTP-DRIVEN TRANSPORTER OF FERROUS ION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Contribution of TonB- and Feo-mediated iron uptake to growth of Salmonella typhimurium in the mouse.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         StyGene; SG10640; feoB.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         modified and this statement is not removed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tsolis R.M., Baumler A.J., Heffron F., Stojiljkovic I.;
SEQUENCE FROM N.A.
                                                                FEOB OR B3409.
                                                                                                                         FEOB_ECOLI
P33650;
                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                   CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the European
                     NCBI_TaxID=562;
                                          Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae
                                                      Escherichia coli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IPR005225;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IPR003373; FeoB.
IPR005289; GTP-bindding_dom.
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(Rel.
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28, Last sequence update)
40, Last annotation update)
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77.8%;
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D -> N (IN REF.
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N -> Y (IN REF. 2).
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                                                                                                                                   773 AA.
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Search completed: January 15, 2003, 11:21:28 Job time: 11.2857 secs
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PIR; A5693; A36932;
ECOGENE; BG12102; feoB.
InterPro; IPR003373; FeoB.
InterPro; IPR005289; GTP-bindding_dom.
InterPro; IPR005289; GTP-bindding_dom.
InterPro; IPR005281; FeoB.
Pfam; PF02421; FeoB; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
-I- FUNCTION: PROBABLE GTP-DRIVEN TRANSPORTER OF FERROUS ION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=94012482; PubMed=8407793;
Kammler M., Schoen C., Hantke K.;
"Characterization of the ferrous iron uptake system of Escherichia coli.";
                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                TRANSMEM
                                                                                                                                                                                             TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                    TIGRFAMS; TIGRO0650; MG442;
                                                                                                                                                                                                                                                                                                                                                                                                                                 TIGRFAMs; TIGRO0437; feoB;
                                                                                                                                                                                                                                                                                                                                                                                                                                               TIGRFAMs; TIGRO0231; small_GTP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; X71063; CAA50387.1; -. EMBL; U18997; AAA58207.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=K12 / MG1655;
MEDLINE=97426617; PubMed=9278503;
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                                                                                                                                                                                                                                                                                                                                                                                                      Iron transport; Transport; Transmembrane; Inner membrane; GTP-binding;
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137 LSARLGCPV 145
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                                                                                                            65.3%; Score 32; DB 1; Length 773; 77.8%; Pred. No. 75; tive 0; Mismatches 2; Indels
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Result
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Maximum Match 100%
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                                                                                                                                                                   Score
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Match Length DB
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sp_bacteria:*
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Q9RTNZ
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P82673
Q9AF18
7 Q9YE62
6 Q51771
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Q9K138
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                                                                                   09x134 thermotoga
09x138 neisseria m
09y138 neisseria m
09y120 neisseria m
08ybv0 bruceila me-
09wy86 thermotoga
09h044 homo sapien
P82673 homo sapien
                          Q9w4r4 drosophila
Q9rbf8 alcaligenes
Q8tdv3 homo sapien
                                                                           Q9af18 agrobacteri
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                                                        Q9ye62 aeropyrum p
O51771 borrelia bu
        Q9rtn2 deinococcus
Q8rbh7 thermoanaer
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16	N	10	16	10	15	5	N	0	σ		0	S	w	ω			7	Q	σ		9		\vdash		\circ	σ	16	σ,
Q8UG88	Q8RLH6	Q9M835	Q9RS42	Q9FPH3	Q9YLQ1	Q8YBY5	Q8RL00	Q94BB9	Q9CLS3	Q9x556	Q98RT1	Q71221	P79922	Q918 S4	Q9K110	Q45308	Q9UY43	Q92T00	Q8Y0V5	6AOM8D	Q9PEA2	075162	Q62688	Q15111	Q94JA1	Q97NC0	Q983E2	Q981G4
		Q9m835 arabidopsis		arabid		Q8yby5 brucella me	Q8r100 providencia	Q94bb9 plinthus cr	Q9cls3 pasteurella	Q9x556 enterococcu	Q98rt1 guillardia	=	xenopus	xenopus		σ		rh	Q8y0v5 ralstonia s	aphrocall	2 xylella	homo sap	⊈.	homo sapie	ijal ory	7nc0 streptococ	83e2 rhizob	rhizobium

ALIGNMENTS

DR DR	尿모	DR DR	DR	DR DR	DR DR	DR	2 Z	RT	RA	RA A	RA	RA.	RA S	Z 73	RP	RΝ	0 X	3 6	GN	DE	DT	ם בו	AC	ID	RESULT Q9X1V4
	Pro; IPR003584; Pr01612; 3_5_ex		InterPro; IPR001098; DNA_pol.	002562; 3	HSSP; P00582; 1KLN. TIGR; TM1619;	EMBL; AE001805; AAD36686.1;		"Evidence for lateral gene transfer between Archaea and Bacteria from	Salzberg S.L., Smith H.O., Venter J.C., Fraser C.W.	Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D., Heidelberg J., Sutton G.G., Fleischmann R.D., Bisen J.A., White O.,	McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,	Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,	Nelson K.E. (lavion R.A. Gill S.B. Gwinn K.E. Dodgon D.T.	STRAIN-MSH8 / DSM 3109;	SEQUENCE FROM N.A.	[1]	NCBI_TaxID-2336;	Thornoton and Thornoton		d DNA polymerase I.	(TrEMBLrel, 21, Last annotation	01-NOV-1999 (Tremblrel 12, Created)		Q9X1V4 PRELIMINARY; PRT; 893 AA.	ULT 1 1V4

Q8x604 escherichia

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RESULT 2
Q9K138
ID Q9K1
                                                                                             RESULT 3
Q9JSU2
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Best Local :
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     Q9JSU2;
01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E., Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J., Nelson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey E.K., Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A., Mason T., Ciecko A., Parksey D.S., Blair E., Cittone H., Clark E.B., Cotton M.D., Utterback T.R., Khouri H., Qin H., Vamathevan J., Gill J., Scarlato V., Masignani V., Pizza M., Grandi G., Sun L., Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C., "Complete genome sequence of Neisseria meningitidis serogroup B strain "Complete genome sequence of Neisseria meningitidis serogroup B strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART; SMU4904; Function of TIGREAMS; TIGRO593; pola; 1.

DNA-directed DNA polymerase; Complete proteome.

DNA-directed DNA polymerase; Complete proteome.

102160 MW; 669EE226DBBB39F3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART; SM00474; 35EXOC; 1.
SMART; SM00475; 53EXOC; 1.
SMART; SM00279; HhH2; 1.
SMART; SM00482; POLAC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation updat
Hypothetical protein NMA2135.
                                                                                Q9JSU2
                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00571; CBS; 2. Pfam; PF01380; SIS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=MC58 / SEROGROUP B;
MEDLINE=20175755; PubMed=10710307;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Neisseria meningitidis (serogroup B)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sugar isomerase, KpsF/GutQ family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9K138;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   TIGE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Science 287:1809-1815(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=491;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria;
                                                                                                                                                                                                                                                                                                      Isomerase;
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                                                                                                                                                                                                                                                                                                                                                                                  InterPro;
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                                                                                                                                                             213 AVRLGTPLKE 222
                                                                                                                                                                                                                       Local Similarity
nes 7; Conserv
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                                                                                                                                                                                         2 SYRLGXPYKE 11
                                                                                                                                                                                                                                                                                                                                                                                                                                 NMB0352;
                                                                                                                                                                                                                                                                                                                                                                                                                                               AE002392; AAF40795.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10;
                                                                                                                                                                                                                                                                                                                                     SM00116;
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                                                                                                                                                                                                                                                                                                                                                                                 IPR004800; KpsF
IPR001347; SIS.
                                                                                                                                                                                                                                                                                                                                                                                                                  IPR000644; CBS_domain
                                                                                                                                                                                                                                                                                       Complete proteome. 324 AA; 34155 MW;
                                                                                                                                                                                                                       Conservative
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                                                                                PRELIMINARY;
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90.9%;
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70.0%;
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Pred. No. 0.35;
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Pred. No. 9.8;
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                                                                                324 AA
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                                                                                                                                                                                                                                                       DB 16; Length 324;
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RESULT 4
Q8Y8WO
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                                                                                                                                    InterPro; IPR001327; FAD pyr_redox.
Pfam; PF00070; pyr_redox; 1.
Oxidoreductase; Complete proteome.
SEQUENCE 441 AA; 48477 MW; E9D8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=16M / ATCC 23456 / BIOTYPE 1;
MEDLINE-20020109; PubMed=11756688;
DelVecchio V.G., Kapatral V., Redkar R.J., Patra G., Mujer C., Los Ivanova N., Anderson I., Bhattacharya A., Lykidis A., Reznik G., Colteman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00571; CBS; 2.
Pfam; PF01380; SIS; 1.
SMART; SM00116; CBS; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-2002 (TrEMBLrel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TIGRFAMS; TIGR00393; kpsF; 1. Hypothetical protein; Complete proteome
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MEDLINE-20222556; PubMed=10761919;
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                                                                                                                                                                                                                                                                                                                 Brucella melitensis.";
Proc. Natl. Acad. Sci. U.S.A. 99:443-448(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                        Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J., Haselkorn R., Kyrpides N., Overbeek R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Brucellaceae; Brucella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Brucella melitensis.
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InterPro; IPR004800; KpsF.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               meningitidis Z2491.
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                                                                                                                                                                                                                                                                                    EMBL; AE009713; AAL54028.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goltsman K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID-29459;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Complete DNA sequence of a serogroup A strain of Neisseria
                                                                                                                                                                                                                                                                                                                                                                                    "The genome sequence of the facultative intracellular pathogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              213 AVRLGTPLKE 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
nes 7; Conserv
                                    Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    dehydrogenase (EC 1.6.99.3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              324 AA;
       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
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                                    75.5%;
63.6%;
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       2;
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                                                                  Score 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 38; DB
Pred. No. 9.8;
                                        Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              U5989FBC97FF4876 CRC64;
       Mismatches
                                                                                                                                           E9D846904C6CB5D7 CRC64;
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                                                                     DB
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                                                                     16;
                                                                  Length 441;
   Indels
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Gaps
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1 LSVRLGXPVKE 11

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RESULT PROPERTY OF THE PROPERT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       멍
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALD DATE OF REAL REPORTS OF SOLUTION OF SO
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                              Submitted (DEC-2000) to the EM EMBL; AL512733; CAC21665.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09H044;
01-MAR-2001 (TrEMBLrel. 15, Created)
01-MAR-2001 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 15, Last annotation update)
Hypothetical 32.0 kDa protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A., McDonald L., Utterback T.R., Malek J.A., Linher K.D., Gazrett M.M., Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D., Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O., Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-99287316; PubMed=10360571;

Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9WY86;
01-NOV-1999
                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; V
Mammalia; Eutheria; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001949; Complex1_51K,
Pfam; PF01512; Complex1_51K; 1.
Pfam; PF00037; fer4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   genome sequence of Thermotoga maritima.";
Nature 399:323-329(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09WY86
                                                                                                                                                                    Hypothetical protein.
NON_TER 1
                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DKFZP762P093.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9H044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TIGR; TM0244;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AE001708; AAD35335.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=2336;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Thermotoga maritima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TM0244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Electron transport complex protein, putative
                                                                                                                                                                                                                                                                                                                                                                       TISSUE-MELANOMA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00198; 4FE4S_FERREDOXIN; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001450; 4Fe4S_ferredoxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           [ron-sulfur;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       313 LIVRIGTPVKD 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               247 VEVRLGIPVKD 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 LSVRLGXPVKE 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Thermotogae; Thermotogales; Thermotogaceae; Thermotoga
                                                                                                                             277 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    451 AA;
                                                                                                                                                                                                                                                                                                                                Beyer A., Mewes H.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Complete proteome. 51 AA; 49515 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      / DSM 3109;
                                                                                                                         31950 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  75.5%;
63.6%;
    73.5%;
                                                                                                                                                                                                                                                                                         to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
Score 36; DE
Pred. No. 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 37; DB Pred. No. 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7B2D7272CFC6E418 CRC64;
                                                                                                                             778CCFFC20D1A2E3 CRC64;
                                                                                                                                                                                                                                                                                                                            Weil B., Wiemann S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           451 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                277 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB
                                       DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 451;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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A CONTROL OF THE CONT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Addms M.D., Kerlavage A.R., Fleischmann R.D., Fuldner R.A., Bult C.J., Lee N., Kirkness E.F., Weinstock K.G., Gocayne J.D., White C., Sutton G., Elake J.A., Brandon R.C., Chiu M.-W., Clayton R.A., Cline R.T., Coulton M.D., Earle-Hughes J., Fine L.D., FilzGerald L.M., Fritzhugh W.M., Fritchman J.L., Geoghagen N.S.M., Glodek A., Gnehm C.L., Hanna M.C., Hedblom E., Hinkloyf P.S., Kelley J.M., Klimek K.M., Kelley J.C., Liu L.-I., Marmaros S.M., Merrick J.M., Moreno-Palanques R.F., McDonald L.A., Nguyen D.T., Pellegrino S.M., Moreno-Palanques R.F., McDonald L.A., Nguyen D.T., Pellegrino S.M., Small K.V., Spriqgs T.A., Utterback T.R., Weidman J.F., Li Y., Bednarik D.P., Cao L., Cepeda M.A., Coleman T.A., Colins E.-J., Bednarik D.P., Cao L., Cepeda M.A., Coleman T.A., Colins E.-J., Pellegrino B. M., Martinos G.A., He W.-W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dimke D., Feng P., Ferrie A., Fischer C., Hastings G.A., He W.-W., Hu J.-S., Greene J.M., Gruber J., Hudson, Kim A., Kozak D.L., Kunsch C., Ji H., Li H., Meissner P.S., Olsen H., Raymond L., Wei Y.-F., Wind J., Xu C., Yu G.-L., Ruben S.M., Dillon P.J., Francon M.R., Rosen C.A., Haseline W.A., Fields C., Fraser C.M.,
                                                                                                                                                                                                                                                                           "Identification of four proteins from the small subunit of the mammalian mitochondrial ribosome using a proteomics approach.", Submitted (JUL-2000) to the SWISS-PROT data bank.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hillier L., Clark N., Dubuque T., Elliston K., Hawkins M., Holman M., Hultman M., Kucaba T., Le M., Lennon G., Marra M., Parsons J., Rifkin L., Hohlfing T., Soares M., Tan F., Trevaskis E., Waterston R., Williamson A., Wohldmann P., Wilson R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 1-23 FROM N.A.
Wei Y., Tsang Y.T.M., Mei G., Ku J.M., Ali-Osman F.R. Jr.,
Bouck J., Gibbs R.A., Margolin J.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-007-2000 (TrEMBLITE). 15, Created)
01-007-2000 (TrEMBLITE). 15, Last sequence update)
01-007-2000 (TrEMBLITE). 15, Last annotation update)
SEQUENCE
                                                                                                    EMBL; AA314022; -; NOT_ANNOTATED_CDS EMBL; N24248; -; NOT_ANNOTATED_CDS.
                                                                                                                                                                       EMBL; BE242647; -; NOT_ANNOTATED_CDS.
EMBL; AI096645; -; NOT_ANNOTATED_CDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 221-323 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Based upon 84 million basepairs of cDNA sequence."; Nature 377:3-174(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Venter J.C. ... Venter J.C. ... Year of human gene diversity and expression patterns
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mitochondrial 28S ribosomal protein S28 (MRP-S28).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-0CT-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P82673
                                                                  Ribosomal protein; Mitochondrion
                                                                                                                                                                                                                                                                                                                                                                                           Spremulli L.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=96026280; PubMed=7566098;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 8-212 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DENTIFICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 LSVRLGXPVKE 11
                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: MITOCHONDRIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LPVRMGYPVKK 47
                                                                                                                                                                                                                                                                                                                                                                                                                        ., Burkhart W., Blackburn K., Moseley A., Koc H.,
   323 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
   36844 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2;
                                 POLY-ALA.
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   B29F819E914F2B49 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A
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RESULT 9
Q9YE62
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Q9AF18
ID Q9AF
  ID DATE OF THE PROPERTY OF THE
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                              Kawarabayasi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Y., Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankai A., Kosug Hosoyama A., Fukui S., Nagai Y., Sishijima K., Nakazawa H., Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Kubota K., Nakamura Y., Nomura N., Sako Y., Kikuchi H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J. Bacteriol. 100.002
EMBL; AY026066; AAK13016.1; -
EMBL; AY02603662; sub_transporter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-CCT-2001 (TrEMBLrel. 18, Last annotation update)
753AA long hypothetical aldehyde oxidoreductase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation updat
                                                   DNA Res.
                                                                             crenarchaeon,
                                                                                                                                                                                                                                                                                                                          STRAIN-K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APE0708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9YE62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "The Agrobacterium tumefaciens rnd Homolog Is Required for Trar-
Mediated Quorum-Dependent Activation of Ti Plasmid tra Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. MEDLINE=21289077;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9AF18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9AF18
                                                                                                    "Complete genome sequence of an aerobic hyper-thermophilic
                                                                                                                                                                                                                                                                                             MEDLINE=99310339; PubMed=10382966;
                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Desulfurococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Archaea; Crenarchaeota; Thermoprotei; Desulfurococcales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Aeropyrum pernix.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9YE62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Agrobacterium tumefaciens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Putative transport protein Mep.
InterPro; IPR000674; Aldxan_dh_C
                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=56636;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Luo 2.Q.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rhizobiaceae; Rhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           375 LQVRVGVPVEE 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity hes 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        83 LPVRMGYPVKK 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
nes 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 LSVRLGXPVKE 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 LSVRLGXPVKE 11
                            AP000060; BAA79684.1; -
                                                aeon, Aeropyrum pernix K1.";
6:83-101(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Farrand S.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          430 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sugar_tr; 1.
AA; 46176 MW; 313B2FF3D08A1E28 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PubMed=11395455;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         73.5%;
63.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Aeropyrum
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63.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alpha subdivision; Rhizobiaceae group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 36;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      430 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   753 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2; Length 430;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 4; Length 323;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                            Kosugi H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
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RESULT 10
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                                                                                                                                                                                                       Q9W4R4
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                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                          01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Praser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A., lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwinn M., Dougherty B., Tomb J.-F., Felschmann R.D., Richardson D., Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., Hanson M., van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman J., Utterback T., Watthey L., McDonald L., Artiach P., Bowman C., Garland S., Fuji C., Cotton M.D., Horst K., Roberts K., Hatch H., Smith H.O., Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ol-JUN-1998 ("FEMFITE). 06, Created)
Ol-JUN-1998 ("FEMFITE). 06, Last sequence update)
Ol-JUN-2002 (TrEMBETel. 21, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               051771
051771;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Complete proteome. SEQUENCE 753 AA;
                         Ephydroidea; Drosophilidae; NCBI_TaxID-7227;
                                  Eukaryota; Metazoa; Arthropoda; Tidoneda, Diptera; Brachycera; Muscomorpha; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF01315; Ald_xan_dh_C; 1 Pfam; PF02738; Ald_xan_dh_C2;
                                                                                  Drosophila melanogaster (Fruit fly)
                                                                                                                                                                         Q9W4R4;
                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-ATCC 35210 / B31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_Tax1D=139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Borrelia burgdorferi (lyme disease spirochete).
Bacteria; Spirochaetales; Spirochaetaceae; Borrelia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Xylose operon regulatory protein (XYLR-2)
                                                                                                               CG13021 protein (AT30881p).
                                                                                                                                                                                           Q9W4R4
                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00480; ROK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  TIGE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            нмв.; анооптат; амс67180.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 390:580-586(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             purgdorieri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=98065943; PubMed=9403685;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BB0831
                                                                                                                                                                                                                                                                                                                                                                                                 Complete proteome
                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000600; ROK_family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       252 LAMRLGRPVK 26
                                                                                                                                                                                                                                                                  190 VAMRLGKPIKE 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genomic sequence of a Lyme disease spirochaete, Borrelia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
nes 7; Conser
                                                                                                                                                                                                                                                                                               1 LSVRLGXPVKE 11
                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 LSVRLGXPVK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                               BB0831
                                                                                                                                                                                                                                                                                                                             σ,
                                                                                                                                                                                                                                                                                                                                                                                      315 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           753 AA;
                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         82419 MW;
                                                                                                                                                                                                                                                                                                                                                                                      34455 MW; C132BA0030D54B75 CRC64;
                                                                                                                                                                                                                                                                                                                                           71.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           73.5%;
                                                                                                                                                                                                                                                                                                                             4; Mismalches
                                                                                                                                                                                                                                                                                                                                          Score 35; DE
Pred. No. 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6836618422F1322D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              annotation update)
                                                                                                                                                                                        110 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         315 AA.
                                                                                                                                                                                                                                                                                                                                                        DB 16; Length 315;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 17; Length 753;
                                                                                                                          update)
                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0,
                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0,
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SEQUENCE FROM N.A.

STRAIN-BERKELEY;

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Q9RBF8
ID QS
AC QS
DT 01
DT 01
DT 01
DT 01
OC Be
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RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Wan K.H., Doyle C., Baxer R.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Borkova D., Botchan M.R., Bouck J., Broxstein P., Brottler P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dorster G., Cahriellan A.F. (Garra N.S. Galbart W. Classer V.)
RA Posler C., Cahriellan A.F. (Garra N.S. Calbart W. Classer V.)
RA Posler C., Cahriellan A.F. (Garra N.S. Calbart W. Classer V.)
                                                                                                                                                                                                                                                                                                                            RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local
                                                                                                             Q9RBF8;
01-MAY-2000
01-MAY-2000
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng Y., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhu X., Smith H.O.,
Zhong X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Smith H.O.,
Gibbs R ^\, Myers E.W., Rubin G.M., Venter J.C.;
"The gen we sequence of Drosophila melanogaster.";
Science 407:2185-2195(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
Hastin D., Houston K.A., Howland T.J., Wel M.-H., Ibewamm C.,
Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.
Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
Liasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
Liasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
Mount S.M., Moly M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.
Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
Reinert K., Schen E., Schen M. C., Scheeler F., Shen H.,
Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
Reinert K., Remington R., Saunders R.D.C., Scheeler F., Shen H.,
Reinert K., Remington R., Scheeler F., Shen H.,
Reinert K., Remington R., Saunders R.D.C., Scheeler F., 
01-MAY-2000 (TREMBLrel. 13, Created)
01-WAY-2000 (TREMBLrel. 13, Last sequence update)
01-UN-2002 (TREMBLrel. 21, Last annotation update)
10-JUN-2002 (TREMBLrel. 21, Last annotation update)
Hypothetical 13.7 Kba protein (Fragment).
Alcaligenes eutrophus (Ralstonia eutropha).
Bacteria; Proteobacteria; beta subdivision; Ralstonia group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases. EMBL; A8003427; AAF45879.1; -. EMBL; AV075295; AAL68162.1; -. EMBL; AV075295; AAL68162.1; -. EMBL; AV075295; CG13021.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Kromiller B., Li P., Liao G., Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S., Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
                                                                                                                                                                                                                                                    Q9RBF8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Stapleton M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=20196006; PubMed=10731132;
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5; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    110
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                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Brokstein P., Hong L., Agbayani A., avez C., Dorsett V., Dresnek D., Far
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11901 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   69.4%;
50.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4;
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                                                                                                                                                                                                                                                                124
                                                                                                                                                                                                                                                                AA
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QRIDVA
ID QRIDV
AC QRIDV
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT PUTAT
GN GPCR.
COS HOMO
OC ELMMAR
OX MCBI_
RN [1]
RP SEQUE
RA TEAKOD
RT GEORG
RT G
       RESULT
Q9RTN2
ID Q9RTN2
ID O1
DT 01
DT 01
DT 01
DT 01
DT 05
DE Hy
GN DH
OC Ba
OC Ba
OC DC
RN | 11
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Best Local
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9RTN2
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           SEQUENCE FROM N.A
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Q9RTN2;
01-MAY-2000
01-MAY-2000
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                   "Identification of G genome sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q8TDV3;
01-JUN-2002 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seibert V., Schloemann M.;
"Characterization of a Gene Cluster Encoding the Maleylacetato
Reductase from Raistonia eutropha 335, an Enzyme Recruited for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ralstonia.
NCBI_TaxID=510;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelo
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical protein.
NON_TER 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF03466; LysR_substrate; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      with 4-Fluorobenzoate.";
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                                                        Hypothetical DR1728.
                                                                                                                                                                                                                                                                                                                                                       Submitted (APR-2002) to the EMBL; AB083587; BAB89300.1;
                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID-9606
             Bacteria; Thermus/Deinococcus
Deinococcaceae; Deinococcus.
                                          Deinococcus radiodurans.
NCBI_TaxID-1299;
                                                                                                                                                                                                                180 VRLGNPFKE 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11 LSVRLGSP 18
                                                                                                                                                                                                                                           3 VRLGXPYKE 11
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                                                                                                                                                                                                                                                                    Similarity
7; Conserv
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7; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            G-protein
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                                                                                 O (TrEMBLrel. 13,
O (TrEMBLrel. 13,
2 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                             235 AA;
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                                                                    protein DR1728
                                                                                                                                           PRELIMINARY;
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Lrel. 21, Last sequence update)
Lrel. 21, Last annotation update)
coupled receptor.
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87.5%;
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77.8%;
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                                                                                    Last annotation
                                                                                              Last sequence update)
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                                                                                                                                                                                                                                                                                   Score 34; DB
Pred. No. 49;
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                          group; Deinococci; Deinococcales;
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pled receptor genes
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                                                                                                                                           277 AA
                                                                                                                                                                                                                                                                                                 DB 4;
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                                                                                  update
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                                                                                                                                                                                                                                                                     Indels
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                                                                                                                                                                                                                                                                                                                                                                                                   human
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Q8RBH 28RBH AC Q8RBH DT 01-JU DT 01-JU DT 01-JU DT Therm OC Therm OC Therm OC THERM (1) RN [1] RP SEQUE RC STRAI RX MEDLI RA Bao Q RA Tan H RT TAN H RA TAN H RA TAN H RA CEMBL! SQ SEQUE
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Best Local Similarity
Thehes 7; Conserva
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Search completed: January 15, 2003, 12:35:56
Job time: 33.5714 secs
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                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

STRAIN-MB4T / JCM1007;

MEDLINE=21992316; PubMed=11997336;

BAO Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J.,

BAO Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J.,

Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling L.,

Tan H., Chen R., Wang J., Yu J., Yang H.;

Tan Complete sequence of T. tengcongensis genome.";

Genome Res. 12:689-700(2002).

EMBL; AE011050; AAM24098.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q8RBH7;
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Pfam; PF03618; DUF299; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 277 AA; 30170 MW; FB133B533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WEDLINE=20036896; PubMed=10567266;
White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D., Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L., Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M., Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C., Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D., Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
                                                                                                                                                                                                                                                               Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Thermoanaerobacter tengcongensis.
Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Membrane proteins related to metalloendopeptidases. NLPD2 OR TTE0841.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          radiodurans R1.";
Science 286:1571-1577(1999).
EMBL; AE002014; AAF11284.1; ..
                                                                                                                                                                                                                                                SEQUENCE
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                                                                                 205 ISVHIGTPVK 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Thermoanaerobacteriales; Thermoanaerobacteriaceae; Thermoanaerobacter.
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                                                                                                                     1 LSVRLGXPVK 10
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-MODEL=frame+_p2n.model -DEV=xlh
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed. is derived by analysis of the total score distribution.

SUMMARIES

Query

0 0 00 0000 No. Score Match 11716 11716 11716 11716 11717 11737 11737 11833 Length DB AC102022 AC102022 AC102022 AP003544 AP004731 AC027747 AE001805 AC069419_0 AC069419_1 AC112132 AR094386 AR094389 AR094390 AR094373 AR098587 AR094371 AR094377 AR094382 AR094384 I12096 I15436 AR149833 AR173616 AR098596 AR098598 AR098585 AR098591 Ħ AR094366 AK072494 AR023935 AR098620 AR098605 AR072499 AC069258 AC078857 E31690 AR098580 AR098604 AR098603 AR098600 AR098593 AR094379 AR094391 AR094392 AC069258 Homo sapi AC102022 Mus muscu AC102022 Mus muscu AP003544 Oryza sat AP004731 Oryza sat AC027747 Homo sapi AE001805 Thermotog AC069419 Homo sapi Continuation (2 of AC112132 Homo sapi AC078857 Homo sapi AR098596 Sequence AR098598 Sequence AR098600 Sequence AR098603 Sequence AR098604 Sequence AR098625935 Sequence AR098585 AR098591 AR094379 Sequence AR094382 Sequence AR094384 Sequence AR072494 Sequence AR094366 Sequence I15436 Sequence 3 141266 Sequence 1 AE001805 Thermotos E31690 Denatured I12096 Sequence 1 AR149833 Sequence AR173616 Sequence AR098580 Sequence AR098593 AR094390 AR094389 AR094386 AR094377 AR094371 AR094373 Sequence AR098587 Sequence AR098605 AR094391 AR098606 Sequence AR094392 AR072499 Sequence Description Sequence 1 Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence

ALIGNMENTS

RESULT 1

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                                                                                                                 1 LeuSerValArgLeuGly***ProValLysGlu 11
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         Sequence 38 from patent US 6077664.
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                                                                                                                                                                                                                                                                                                                                           Slater,M.R., Huang,F. and Hartnett,J.R. Thermophilic DNA polymerases from thermotoga neapolitana Patent: US 6001645-A 38 [14-DBC-1999;
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AR094392
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AR098606.1 GI:12808372
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Slater, M.R., Huang, F., Hartnett, J.R., Bolchakova, E., Storts, D.R.,
otto, P., Miller, K.M., Novikov, A. and Velikodvorskaya, G.A.
Thermophilic DNA polymerases from Thermotoga neapolitana
Patent: US 6077664-A 36 20-JUN-2000;
\label{eq:otto_problem} Otto, \texttt{P., Miller, K.M., Novikov, A. and Velikodvorskaya, G.A.} \\ Thermophilic DNA polymerases from Thermotoga ncapolitana
                1 (bases 1 to 1737)
Slater, M.R., Huang, F., Hartnett, J.R., Bolchakova, E., Storts, D.R., Otto, P., Miller, K.M., Novikov, A. and Velikodvorskaya, G.A.
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Thermophilic DNA polymerases from thermotoga neapolitana
Patent: US 6001645-A 10 14-DEC-1999;
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                                                 1 (bases 1 to 1833)
Slator, M.R., Huang, F. and Hartnett, J.R.
Thermophilic DNA polymerases from thermotoga neapolitana
Patent: US 6001645-A 15 14-DEC-1999;
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Thermophilic DNA polymerases from thermotoga neapolitana
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Thermophilic DNA polymerases from thermotoga neapolitana
Patent: US 6001645-A 28 14-DEC-1999;
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Slater,M.R., Huang,F. and Hartnett,J.R.
Thermophilic DNA polymerases from thermotoga neapolitana
Patent: US 6001645-A 25 14-DEC-1999;
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Slatter, M.R., Huang, F. and Hartnett, J.R.
Thermophilic DNA polymerases from thermotoge neapolitane
Patent: US 6001645-A 34 14-DEC-1999;
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Slater, M.R., Huang, F. and Hartnett, J.R.
Thermophilic DNA polymerases from thermotoga neapolitana
Patent: US 6001645-A 32 14-DEC-1999;
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AR094389
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Search completed: January 16, 2003, 11:02:34 Job time: 1532.14 secs

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Copyright (c) 1993 - 2003 Compugen Ltd.
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RESULY 1
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ID ART31
XX ART3
AC ART3XX 15-AI
AC IN-AI
AC ART3XX IN-AI
AC A

Thermotoga neapolitana strain DSM 5068

/*tag= a

Location/Qualifiers

thermostable enzyme; ss.

DNA polymerase; Tne; DNA sequencing; amplification;

The DNA polymerase C-terminal region DNA.

15-AUG-1996 (first entry)

AAT30049;

AAT30049 standard; DNA; 694 BP.

ALIGNMENTS

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    08-SEP 1995;
                                                                     06-SEP-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequencing and amplification reactions. It can be obtd. by obtd. from transformed host cells, e.g. E. coli, carrying the DNA polymerase gene. Mutants having improved enzymatic properties may be produced (see also AAR98144-47).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A DNA fragment (AAR30049) codes for the C-terminal portion (AAR98144) of the 100 kDa thermostable DNA polymerase (AAR98145) of Thermotoga neapolitana (Tne), including the O helical region. Tna polymerase is a thermostable enzyme suitable for use in DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02-OCT-1995;
                            14-AUG-1996;
                                                                                                                                                            WO9709451-A1
                                                                                                                                                                                                     Thermotoga neapolitana strain DSM 5068
                                                                                                                                                                                                                                                                      DNA polymerase; Tne; exonuclease; DNA amplification; DNA sequencing;
                                                                                                                                                                                                                                                                                                                      Thermotoga neapolitana DNA polymerase C-terminal region DNA
                                                                                                                                                                                                                                                                                                                                                             09-JUN-1997 (first entry)
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30-SEP-1994;
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                                                                                                                                                                                                                                                   enzyme engineering; protein engineering; mutagenesis;
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/transl_except= (671..673, aa:Ser)
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02-OCT-1995;
21-DEC-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A DNA sequence (AAT60031) encodes the C-terminal region, including the O-helix, of the Thermologa neapolitana (The) DNA polymerase. It was obta from a genomic DNA expression library by screening E. coli transformants for thermostable DNA polymerase activity. When the sequence is translated it does not produce the entire amino acid sequence of The polymerase due to frameshift errors generated during sequencing. However, an amino acid sequence was obta, by translating all 3 reading frames (AAW13862-64), comparing these with known sequences, and splicing the The sequence together to form the sequence given in AAW13863. A complete coding sequence for The
                        06-SEP-1996;
                                                                                                                                                                                                                                                                                              Thermotoga neapolitana.
                                                                                                                                                                                                                                                                                                                                                                                                             T. neapolitana Tne polymerase C-terminal cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA%88767;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 694 BP; 230 A; 136 C; 178 G; 150 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            polymerase is given in AAT60032.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 5; Fig 5; 120pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mutant DNA polymerase, esp. from Thermotoga - has reduced exonuclease activity or dideoxynucleotide discrimination, useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1997-192925/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chatterjee DK,
                                                                     18-JAN-2000
                                                                                                              US6015668-A
                                                                                                                                                                                                                                                                                                                                         thermostability; The; ss.
                                                                                                                                                                                                                                                                                                                                                               DNA polymerase; Poil; O-helix; DNA sequencing; amplification; mutant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-MAY-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAZ88767 standard; cDNA; 694 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P-PSDB; AAW13862, AAW13863, AAW13864.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (HUGH/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CHAT/) CHATTERJEE D K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           for DNA amplification, synthesis and sequencing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             233 CTTTCTCTCAGACTTGGAATACCGGTTAAAGAA 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 LeuSerValArgLeuGly***ProValLysGlu 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HUGHES A J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95US-0537397.
95US-0537400.
95US-0576759.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hughes AJ;
                        9608-0706706
                                                                                                                                                     /product= "Tne"
/note= "partial sequence, no start codon given"
                                                                                                                                                                                                       /*tag=
                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0.495
47.00
90.91%
90.91%
90.91%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
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Otto P;

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US-09-823-649A-5 (1-11) x AAZ88767 (1-694)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09-JAN-1995;
08-SEP-1995;
02-OCT-1995;
21-DEC-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence more than 500 bases; reduce false stops in the sequence ladder; reduce template requirements 10-fold (when using 355 labeling); and also requirements for primer and labeled terminator. They increase sequencing efficiency with structure-containing or GC-rich templates; reduce film
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  methods, also for DNA labeling and for synthesis of cDNA from mRNA templates. (I) have higher thermostability than known enzymes (e.g. 50% retention of activity after 60 min at 90 plusoC), and may be free of exonuclease activity and/or ability to discriminate against dideoxynucleotides (ddNTP). They permit sequencing at high temperature, provide strong, clear sequences (increased signal-to-noise ratio); can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This invention describes novel methods for sequencing DNA, amplifying double-stranded DNA or synthesizing DNA which use a mutant Thermotoga neapolitana DNA polymerase (I) or its fragments. (I) are used for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             exposure times; do not generate sequencing artefacts with homopolymeric sequences and allow quantitation of bases in heterologous mixtures. This sequence encodes the Thermotoga neapolitana The polymerase carboxyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of Thermotoga neapolitana polymerase with reduced exonuclease activity or reduced discrimination against dideoxynucleotides
  WO9641014-A1
                                          Synthetic.
                                                                                 polymerase chain
                                                                                                     DNA polymerase; Tne; thermostable enzyme; protein engineering; thermostability; DNA sequencing; amplification; PCR;
                                                                                                                                                                  Thermotoga neapolitana DNA polymerase Tne M284 delB gene
                                                                                                                                                                                                                                                          AAT58155;
                                                                                                                                                                                                                                                                                                   AAT58155 standard; DNA; 1485 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 694 BP; 229 A; 136 C; 179 G; 150 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequencing, amplification and synthesis of DNA by essentially
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 5; Column 51-54; 65pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA sequencing, amplification and synthesis methods, using mutant forms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hughes AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (LIFE-) LIFE TECHNOLOGIES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02-OCT-1995;
30-SEP-1994;
                                                                                                                                                                                                                 15-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  terminal which is described in the method of the invertion.
                                                                                                                                                                                                                                                                                                                                                                                      233 CTTTCTGTGAGACTTGGAATACCGGTTAAAGAA 265
                                                                                                                                                                                                                                                                                                                                                                                                                            1 LeuSerValArgLeuGly***ProValLysGlu 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2000-181138/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chatterjee DK;
                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95US-0525057.
95US-0537400.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95US-0537397.
94US-0316423.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96US-0689818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95US-0576759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95US-0370190.
                                                                                 reaction; exonuclease; Thermotoga neapolitana; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0.495
47.00
90.91%
90.91%
95.92%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 694
10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       00-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       standard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAT58145
ID AAT5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-823-649A-5 (1-11) x AAT58155 (1-1485)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A DNA sequence (AAW158155) encodes deletion mutant The M284 delB (AAW1525) of the DNA polymerase (see also AAW1531) of Thermotoga neapolitana. The deletion mutant lacks the N-terminal 283 amino acids from the 5' exonuclease domain of the native enzyme and also has amino acid residues 309-424 of the 3' exonuclease domain deleted. The DNA construct was obtd by restriction digestion of pw284-derived DNA (see also AAT58135), when expressed in E. coli, "The M884 delB showed no detectable polymerase activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31-MAY-1996;
07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1024 CTFTCTCTGAGACTTGGAATACCGGTTAAAGAA 1056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1485 BP; 490 A; 312 C; 365 G; 318 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Thermostable DNA polymerase from Thermotoga neapolitana – useful in DNA sequencing or for amplification of double stranded DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1997-052374/05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bolchakova E,
                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                                                                                              DNA polymerase; The; thermostable enzyme; protein engineering; thermostability; DNA sequencing; amplification; PCR;
                                                                                                                                                                                                                                                                                                                                                             Thermotoga neapolitana DNA polymerase Tne M323 gene
                                                                                                                                                                                                                                                                                                                                                                                                          15-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAT 58145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 4; Page 174-175; 200pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P-PSDB; AAW11525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Slater MR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (PROM-) PROMEGA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19-DEC-1996
(PROM-) PROMEGA CORP
                                          07-JUN-1995;
                                                          31-MAY-1996;
                                                                                                       07-JUN-1996;
                                                                                                                                                                                           W09641014-A1
                                                                                                                                                                                                                                                                          polymerase chain reaction; exonuclease; Thermotoga neapolitana; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAT58145 standard; DNA; 1719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        In contrast, a Tne M284 mutant (see also AAW11514) was active.
                                                                                                                                                19-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 LeuSerValArqLeuGly***ProValLysGlu 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Storts DR;
                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hartnett JR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95US-0484661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96WO-US09641.
                                        96US-0656664
95US-0484661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96US-0656664
                                                                                                     96WO-US09641.
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47.00
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95.92%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Miller KM,
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AAT58155
AAT58157
XX
AC AATT
XX
DT 15-2
DT 15-2
DT Theil
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Theil
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COS Syntax
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RESULT 6
AAT58144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A DNA sequence (AAT58145) encodes deletion mutant The M323 (AAW11524) of the DNA polymerase (see also AAW11513) of Thermotoga neapolitana. The M323 has an artificially created methionine at amino acid position 323 as the initiator methionine in the 3' exonuclease domain of the enzyme. When expressed in E. coli, The M323 showed
                  Thermostable DNA polymerase from Thermotoga neapolitana - useful in DNA sequencing or for amplification of double stranded DNA
                                                                                                                                           31-MAY-1996;
07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                        1255 CTTTCTGTGAGACTTGGAATACCGGTTAAAGAA 1287
Example 3; Page 133-135; 200pp; English.
                                                      P-PSDB; AAW11523
                                                                                     Slater MR,
                                                                                                Bolchakova E,
                                                                                                                                                                           07-JUN-1996;
                                                                                                                                                                                                                        WO9641014-Al
                                                                                                                                                                                                                                             Synthetic.
                                                                                                                                                                                                                                                                                        DNA polymerase; The;
                                                                                                                                                                                                                                                                                                             Thermotoga neapolitana DNA polymerase Tne M316 gene.
                                                                                                                                                                                                                                                                                                                                   15-APR-1997
                                                                                                                                                                                                                                                                                                                                                         AAT58144;
                                                                                                                                                                                                                                                                                                                                                                               AAT58144 standard; DNA; 1737 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1719 BP; 553 A; 367 C; 413 G; 386 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             no detectable polymerase activity. In contrast, a Tne M284 mutant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 4; Page 169-172; 200pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA sequencing or for amplification of double stranded DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Thermostable DNA polymerase from Thermotoga neapolitana - useful in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P-PSDB; AAW11524.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1997-052374/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Slater MR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bolchakova E,
                                                                                                                      (PROM-) PROMEGA CORP.
                                                                                                                                                                                                 19-DEC-1996
                                                                                                                                                                                                                                                                 polymerase chain reaction; exonuclease; Thermotoga neapolitana; ss.
                                                                                                                                                                                                                                                                             thermostability; DNA sequencing; amplification; PCR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (see also AAW11514) was active.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                No. :
                                                                                                                                                                                                                                                                                                                                                                                                                                               1 LeuSerValArgLeuGly***ProValLysGlu 11
                                                                 1997-052374/05.
                                                                                      Storts DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Storts DR;
                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hartnett JR,
                                                                                                Hartnett JR,
                                                                                                                                          96US-0656664
95US-0484661
                                                                                                                                                                            96WO-US09641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.38
47.00
90.91%
90.91%
95.92%
                                                                                                                                                                                                                                                                                     thermostable enzyme; protein engineering;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Huang F,
                                                                                                Huang F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Miller KM,
                                                                                                  Miller KM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1719
10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Otto P;
                                                                                                  Otto P;
                                                                                                                                                                                                                                CCCCCCCX PX PHX DR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAT58135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
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US-09-823-649A-5 (1-11) x AAT58144 (1-1737)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           %888888888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of the DNA polymerase (see also AAWI1513) of Thermotoga neapolitana. The M316 has an artificially created methionize at amino acid position 316 as the initiator methionine. It was created by introducing a Met residue at position 316 (and a corresponding NCOI site) via site-directed mutagenesis of the native The gene (see also AATS8134). When expressed in E. coli from a T7 or tro
                    A DNA sequence (AAT58135) in plasmid pM284 codes for modified DNA polymerase The M284 (AAW11514) in which amino acids 1-283 of the native Thermotoga neapoiltana enzyme (see also AAW11513) are deleted and the naturally occurring Met-284 residue becomes the initiating methionine. It was obtd. by restriction digestion of the native gene (AAT58134). The deleteion results in elimination of 5' exonuclease activity. Further modification of the DNA in pM284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1276 CTTTCTGTGAGACTTGGAATACCGGTTAAAGAA 1308
                                                                                                                                                                                                                                                Claim 20; Page 128-131; 200pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31-MAY-1996;
07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-JUN-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA polymerase: The: thermostable enzyme; protein engineering; thermostability; DNA sequencing; amplification; PCR; polymerase chain reaction; exonuclease; Thermotoga neapolitana;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAT58135 standard; DNA; 1833 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1737 BP; 553 A; 374 C; 417 G; 393 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A DNA sequence (AAT58144) encodes deletion mutant The M316 (AAW11523)
                                                                                                                                                                                                                                                                                                                                                                                           P-PSDB; AAW11514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Slater MR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19-DEC-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Thermotoga neapolitana DNA polymerase Tne M284 gene
exonuclease activity. Further modification of the DNA in pM284 (see also AAT58136-43) yield mutant enzymes (AAW11515-22) that also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bolchakova E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (PROM-) PROMEGA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-APR-1997
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                                                                                                                                                                                                                                                                                                        DNA sequencing or for amplification of double stranded DNA
                                                                                                                                                                                                                                                                                                                                   Thermostable DNA polymerase from Thermotoga neapolitana - useful in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        romoter, The M316 produced no detectable polymerase activity. The M284 mutant (see also AAW11514) was active.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     l LeuSerValArgLeuGly***ProValLySGlu 11
                                                                                                                                                                                                                                                                                                                                                                                                                      1997-052374/05
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9505-0484661
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47.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches:
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RESULT 8
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                                               A DNA sequence (AAT58136) codes for mutant thermostable DNA polymerase The M284(D323B) (AAW1515) in which amino acids 1-283 of the native Thermotoga neapolitana enzyme (see also AAW1513) are deleted and amino acid residue 323 (Asp) of native The is substd. by Glu. It was obtd. by site-directed mutagenesis of pM284 DNA (see also AAT58135). The mutated gene can be incorporated into a vector and used for prodn. of The M284(D323E) in transformed host cells. The mutant enzyme has no significant 5' or 3' exonuclease activity and
e.g. PCR.
                                                                                                                                                                                                                                                                                           Claim 20; Page 138-140; 200pp; English.
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07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1372 CTTTCTGTGAGACTTGGAATACCGGTTAAAGAA 1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Slater MR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA polymerase; Tne; thermostable enzyme; protein engineering; thermostability; DNA sequencing; amplification; PCR; polymerase chain reaction; exonuclease; Thermotoga neapolitana; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-APR-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amplifications, esp. PCR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              are useful in DNA sequencing reactions and nucleic acid
                           is suitable for use in DNA sequencing and amplification reactions,
                                                                                                                                                                                                                                                                                                                                               DNA sequencing or for amplification of double stranded DNA
                                                                                                                                                                                                                                                                                                                                                                        Thermostable DNA polymerase from Thermotoga neapolitana - useful in
                                                                                                                                                                                                                                                                                                                                                                                                                             P-PSDB; AAW11515
                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1997-052374/05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bolchakova E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-JUN-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Thermotoga neapolitana DNA polymerase Tne M284(D323E) gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (PROM-) PROMEGA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19-DEC-1996
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                                                                                                A DNA sequence (AART58137) codes for mutant thermostable DNA polymcrase Tne M284(E3250) (AAWIL516) in which amino acids 1-283 of the native Thermotoga neapoliticana enzyme (see also AAWIL513) are deleted and amino acid residue 325 (Glu) of native Tne is substd. by Asp. It was obtd. by site-directed mutagenesis of pM284 DNA (see also AMEGERS 25)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1372 CTTTCTGTGAGACTTGGAATACCGGTTAAAGAA 1404
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                           e.g. PCR
                                      ANY58135). The mutated geno can be incorporated into a vector and used for prodn. of The M284(B232b) in transformed host cells. The mutant enzyme has no significant 5' or 3' exonuclease activity and is suitable for use in DNA sequencing and amplification reactions.
                                                                                                                                                                                           Claim 20; Page 142-144; 200pp; English.
                                                                                                                                                                                                                                                                                                                                                                                          07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAT58137;
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                                                                                                                                                                                                                      DNA sequencing or for amplification of double stranded DNA
                                                                                                                                                                                                                                      Thermostable DNA polymerase from Thermotoga neapolitana - useful in
                                                                                                                                                                                                                                                                      P-PSDB; AAW11516.
                                                                                                                                                                                                                                                                                      WPI; 1997-052374/05
                                                                                                                                                                                                                                                                                                                 Slater MR,
                                                                                                                                                                                                                                                                                                                                  Bolchakova E,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag= a /note= "base 126 (C) is A in the native The gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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Sequence 1833 BP; 590 A; 395 C; 440 G; 408 T; 0 other;

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AAT58138

AAC AAT5

XX AAT58138

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XX DAA AC AAT5

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                           Pred. No.:
                                                      Alignment Scores:
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                                                                                                                                                                                                                                                                        A DNA sequence (AAT58138) codes for mutant thermostable DNA polymerase Tne M284(Y464F) (AAW11517) in which amino acids 1-283 of the native Thermotoga neapolitana enzyme (see also AAW11513) are deleted and amino acid residue 464 (Tyr) of native Tne is substd. by Phe. It was obtd. by site-directed mutagenesis of pM284 DNA (see also AAT58135). The mutated gene can be incorporated into a vector and AAT581351.
                                                                                                          Sequence 1833 BP;
                                                                                                                                                                    sequencing and amplification reactions, e.g. PCR.
                                                                                                                                                                                            used for prodn. of The M284(Y464F) in transformed host cells mutant enzyme has no significant 5' exonuclease activity and reduced 3' exonuclease activity. It is suitable for use in DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 20; Page 147-149; 200pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA sequencing or for amplification of double stranded DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mutation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Thermotoga neapolitana DNA polymerase Tne M284(Y464F) gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAT58138;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Thermostable DNA polymerase from Thermotoga neapolitana - useful in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1997-052374/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Slater MR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (PROM-) PROMEGA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             polymerase chain reaction; exonuclease; Thermotoga neapolitana; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           thermostability; DNA sequencing; amplification; PCR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA polymerase; Tne; thermostable enzyme; protein engineering;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-APR-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Storts DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hartnett JR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96US-0656664
95US-0484661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96WO-US09641
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /*tag--a*/note= "base 542 (T) is A in the native Tne gene"
                                                                                                             590 A; 393 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        90.91%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Huang F, Miller KM,
                                                                                                             440 G; 410 T;
   Matches:
                        Length:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative:
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                                                                                                          0 other;
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Query Match:

Best Local Similarity: Percent Similarity:

47.00 90.91% 90.91% 95.92% 1.49

Mismatches:

1833 10

Indels: Conservative: Matches: Pred. No.: Alignment Scores:

Sequence 1833 BP; 591 A; 394 C; 439 G; 409 T; 0 other;

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DT
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Best Local Similarity:
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                     AAMT58135). The mutated gene can be incorporated into a vector and used for prodn. of The M284(D468N) in transformed host cells. The mutant enzyme has no significant 5' exonuclease activity and reduced 3' exonuclease activity. It is suitable for use in DNA
                                                                                                                                 A DNA sequence (AATS8139) codes for mutant thermostable DNA polymerase Tne M284(Y464F) (AAW11518) in which amino acids 1-283 of the native
         sequencing and amplification reactions, e.g. PCR.
                                                                                                  Thermologa neapolitana enzyme (see also AAW11513) are deleted and amino acid residue 468 (Asp) of native The is substd. by Asn. It
                                                                                                                                                                              Claim 20; Page 151-154; 200pp; English.
                                                                                                                                                                                                           DNA sequencing or for amplification of double stranded DNA
                                                                                                                                                                                                                                                                                                        Slater MR,
                                                                                                                                                                                                                                                                                                                                                                                                                                07-JUN-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mutation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA polymerase; The; thermostable enzyme; protein engineering; thermostability; DNA sequencing; amplification; PCR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAT58139 standard; DNA; 1833 BP
                                                                                    was obtd. by site-directed mutagenesis of pM284 DNA (see also
                                                                                                                                                                                                                        Thermostable DNA polymerase from Thermotoga neapolitana - useful in
                                                                                                                                                                                                                                                            P-PSDB;
                                                                                                                                                                                                                                                                                                                   Bolchakova E,
                                                                                                                                                                                                                                                                                                                                                   (PROM-) PROMEGA CORP
                                                                                                                                                                                                                                                                                                                                                                                 07-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               polymerase chain reaction; exonuclease; Thermotoga neapolitana; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Thermotoga neapolitana DNA polymerase Tne M284(D468N) gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAT58139;
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                                                                                                                                                                                                                                                                      1997:0523/4/05.
                                                                                                                                                                                                                                                            AAWII'S B.
                                                                                                                                                                                                                                                                                                      Storts DR;
                                                                                                                                                                                                                                                                                                                     Hartmett JR,
                                                                                                                                                                                                                                                                                                                                                                                  96US-0656664
95US-0484661
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "base 553 (A) is G in the mative The gene"
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                                                                                                                                                                                                                                                                                                                     Huand F, Miller KM,
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Indels:
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                                                                                                                                                                                                                                                                                                                     Otto P;
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AAT58140
ID AATS
                                                                                                                                                                                                     US-09-823-649A-5 (1-11) x AAT58139 (1-1833)
                                              Query Match:
                                                                   Percent Similarity:
Best Local Similarity:
                                                                                                                                      Alignment Scores: Pred. No.:
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                                                                                                                                                                                                                                                                                                                              A DNA sequence (AAT58140) codes for mutant thermostable DNA polymerase Tne M284(D3218) (AAW11519) in which amino acids 1-283 of the native Thermotoga neapolitana enzyme (see also AMV1513) are deleted and amino acid residue 323 (Asp) of native Tne is substd. by Ala. It was obtd. by site-directed mutagenesis of pM284 DNA (see also AMV1513) are deleted and according to the substd. by Site-directed mutagenesis of pM284 DNA (see also AMV1513) are directed mutagenesis of pM284 DNA (see also AMV1513) are directed mutagenesis of pM284 DNA (see also AMV1513) are directed mutagenesis of pM284 DNA (see also AMV1513) are directed mutagenesis of pM284 DNA (see also AMV1513) are directed mutagenesis of pM284 DNA (see also AMV1513) are directed mutagenesis of pM284 DNA (see also AMV1513) are directed mutagenesis of pM284 DNA (see also AMV1513) are directed mutagenesis of pM284 DNA (see also AMV1513) are directed mutagenesis of pM284 DNA (see also AMV1513) are directed mutagenesis of pM284 DNA (see also AMV1513) are directed mutagenesis of pM284 DNA (see also AMV1513) are directed mutagenesis of pM284 DNA (see also AMV1513) are directed mutagenesis of pM284 DNA (see also AMV1513) are directed mutagenesis of pM284 DNA (see also AMV1513) are directed mutagenesis of pM284 DNA (see also AMV1513) are directed mutagenesis of pM284 DNA (see also AMV1513) are directed mutagenesis of pM284 DNA (see also AMV1513) are directed mutagenesis of pM284 DNA (see also AMV1513) are directed mutagenesis of pM284 DNA (see also AMV1513) are directed mutagenesis of pM284 DNA (see also AMV1513) are directed mutagenesis of pM284 DNA (see also AMV1513) are directed mutagenesis of pM284 DNA (see also AMV1513) are directed mutagenesis of pM284 DNA (see also AMV1513) are directed mutagenesis of pM284 DNA (see also AMV1513) are directed mutagenesis of pM284 DNA (see also AMV1513) are directed mutagenesis of pM284 DNA (see also AMV1513) are directed mutagenesis of pM284 DNA (see also AMV1513) are directed mutagenesis of pM284 DNA (see also AMV1513) are dire
                                                                                                                                    No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Thermostable DNA polymerase from Thermotoga neapolitana - useful DNA sequencing or for amplification of double stranded DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Slater MR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bolchakova E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31-MAY-1996;
07-JUN-1995;
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                                                                                                                                                                                                   Sequence 1833 BP; 590 A; 395
                                                                                                                                                                                                                                            amplification reactions, e.g. PCR.
                                                                                                                                                                                                                                                                      mutant enzyme is suitable for use in DNA sequencing and
                                                                                                                                                                                                                                                                                         AAT58135). The mutated gene can be incorporated into a vector used for prodn. of The M284(D323A) in transformed host cells.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20; Page 156-158; 200pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  neapolitana DNA polymerase Tne M284(D323A) gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Storts DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hartnett JR,
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95US-0484661.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "base 119 (C) is
                         1.49
47.00
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18
                                                                                                                                                                                                   C; 440 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Huang
                                                                   Mismatches:
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                                                Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Miller KM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A in the native Tne gene"
                                                                                                                                                                                                       Τ;
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ID AAT58

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DR AT5

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PR 07--

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δā.
                                                                                                                                                                              Score:
                                                                                                                                                                                                                       Alignment Scores:
                                                                                                               Query Match:
                                                                                                                                                           Percent Similarity:
                                                                                                                                                                                                       Pred.
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07-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAT58141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P-PSDB; AAW11520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1997-052374/05.
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                                                                                                                                                                                                       No.:
                                                                                                                                    Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Storts DR;
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1372 CTTTCTGTGAGACTTGGAATACCGGTTAAAGAA 1404
                                                                   1 LeuSerValArgLeuGly***ProValLysGlu 11
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AAT58141 standard; DNA; 1833 ВP

(first entry)

DNA polymerase; The; thermostable enzyme; protein engineering; thermostability; DNA sequencing; amplification; PCR; polymerase chain reaction; exonuclease; Thermotoga neapolitana; ss

gene

Location/Qualifiers 317..318
/*tag=_a

/note= "bases 317-318 (CG) are gene" AC in the native Tne

96WO-US09641

96US-0656664 95US-0484661

JR, Huang F, Miller XX. Otto

٦,

Thermostable DNA polymerase from Thermotoga neapolitana - ${\tt DNA}$ sequencing or for amplification of double stranded DNA useful

Claim 20; Page 161-163; 200pp; English.

The M284(D323E) (AAW11520) in which amino acids 1-283 of the native Thermotoga meapolitana enzyme (see also AAW11513) are deleted and amino acid residue 389 (Asp) of native The is substd. by Ala. It was obtd. by site-directed mutagenesis of pM284 DNA (see also AAT58135). The mutated gene can be incorporated into a vector and used for prodn. of The M284(D389A) in transformed host cells. The amplification reactions, e.g. mutant enzyme is suitable for use in DNA sequencing and A DNA sequence (AAT58141) codes for mutant thermostable DNA polymerase

Sequence 1833 BP; 590 A; 394 C; 441 G; 408 T; 0 other;

1.49 47.00 90.91% 90.91% 95.92% 18 Gaps: Conservative: Mismatches: Indels: Matches: 1833 10 0 1

US-09-823-649A-5 (1-11) x AAT58141 (1-1833)

g 1372 CTTTCTGTGAGACTTGGAATACCGGTTAAAGAA 1404 LeuSerValArgLeuGly***ProValLysGlu 11

US-09-823-649A-5 (1-11)

x AAT58140 (1-1833)

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RESULT 14
AAT58142
                                                                                                         Query Match:
                                                                 Alignment Scores: Pred. No.:
                           Best Local Similarity:
                                       Percent Similarity:
                                                                                                                                        A DNA sequence (AAT58142) codes for mutant thermostable DNA polymerase Tne M284(D323E,D389A) (AAM1521) in which amino acids 1-283 of the native Thermotoga neapolitana enzyme (see also AAM1513) are deleted and amino acid residue 323 (Asp) of native Tne is substd. by Ala, and Asp-389 by Ala. It was obtd. by site-directed mutagenesis of pM284 DNA (see also AAT58135). The mutated gene can be incorporated into a vector and used for prodn. of the triple mutant in transformed host cells. The triple mutant has no significant 5' or 3' exonuclease activity and a half-life at 97.5 deg C of 22 min compared with 5 min for native Tne and 8 min for native Taq. It is suitable for use in DNA sequencing and amplification reactions,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31-MAY-1996;
07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA polymerase; Tne; thermostable enzyme; protein engineering; thermosta: lity; DNA sequencing; amplification; PCR; polymerase chain reaction; exonuclease; Thermotoga neapolitana; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                07-JUN-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Thermotoga neapolitana DNA polymerase Tne M284(D323A,D389A) gene.
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                                                                                                       Sequence 1833
                                                                                                                                                                                                                                                                                                     Claim 20; Page 165-167; 200pp; English.
                                                                                                                                                                                                                                                                                                                            Thermostable DNA polymerase from Thermotoga neapolitana - useful in DNA sequencing or for amplification of double stranded DNA
                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1997-052374/05.
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                                                                                                                                                                                                                                                                                                                                                                                                                                               (PROM-) PROMEGA CORP
                                                                                                                                                                                                                                                                                                                                                                                                           Storts DR;
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                                                                                                       BP;
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95US-0484661
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                                                                                                         589
 1.49
47.00
90.91%
90.91%
95.92%
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                                                                                                       395 C;
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                                                                                                                                                                                                                                                                                                                                                                                                                      Huang F,
                                                                                                       441 G; 408
            Conservative: Mismatches: Indels:
                                                     Matches:
                                                                Length:
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                                                                                                         0 other;
1833
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US-09-823-649A-5 (1-11) x AAT58142 (1-1833)

Percent Similarity: Best Local Similarity:

1.49 47.00 90.91% 90.91%

Length:
Matches:
Conservative:
Mismatches:

1833 10 0

No.:

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Alignment Scores
                                                  mease in the 3' exonuclease domain of the enzyme. It was obtd.] site-directed mutagenesis of DNA (AATS8142) coding for a triple mutant. The mutated gene can be incorporated into a vector and used for prodn. of The Quad in transformed host cells for use in DNA amplification reactions and esp. for radioactive sequenci reactions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1372
                                                                                                       A DNA sequence (AAT58143) codes for mutant thermostable DNA polymerase The Quad (AAW11522) in which amino acids 1-283 of the native Thermotoga neapolitana enzyme (see also AAW11513) are deleted and amino acid residue 3 amino acid substims. (D323A, D389A, F730Y) are made in the 3' exonuclease domain of the enzyme. It was obtd. by
                                                                                                                                                                                Claim 20; Page 180-182; 200pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA polymerase; "Inc; Quad polymerase; thermostable enz protein engineering; thermostability; DNA sequencing; polymerase chain reaction; amplification; exonuclease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAT58143 standard; DNA; 1833
                                                                                                                                                                                                       Thermostable DNA polymerase from Thermotoga neapolitana - useful in DNA sequencing or for amplification of double stranded DNA
                                                                                                                                                                                                                                                                                                                                            31-MAY-1996;
07-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tne Quad polymerase gene
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                         Sequence 1833
                                                 reactions.
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                                                                                                                                                                                                                                                                                                                   (PROM-) PROMEGA CORP
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95US-0484661
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317..318
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /*t.ag=
                      590 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "base 119 (C) is A in the native Tne gene"
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                      395 C;
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                                                                                                                                                                                                                                                                                          Huang F,
                        440
                        <u>.</u>
                      408 T;
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                        0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    the native Tne gene'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      in the native "ne
                                                                                                                                                                                                                                                                                             Otto P;
                                                          sequencing
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Search completed: January 15, 2003, 12:55:39 Job time : 137.143 secs US-09-823-649A-5 (1-11) x AAT58143 (1-1833) Query Match: DB: 95.92**%** 18 Indels: Gaps: 00

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15, 18,

28, Appl
34, Appl
7, Appl
15, Appl
16, Appl
22, Appl
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O
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                  Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq
 4444447777477744477774477777
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length: 2000000000
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Ygapop 10.0 , 1
Fgapop 6.0 , 1
Delop 6.0 , 1
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49
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Maximum Match 100%
Listing first 45 summaries
 LSVRLGXPVKE 11
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                                                                                                                                                                                                                                                                                                                                                                 /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/Dackfiles1.seq:*
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 1485
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US-08-537-400-15

US-08-706-702-17

US-08-706-706-17

US-08-484-661A-38

US-08-656-664-38

PCT-US96-09641-38

US-08-484-661A-36

US-08-656-664-36

US-08-656-664-10

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 Sequence
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 RESULT 1
US-08-537-400-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
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TITLE OF INVENTION: C
TITLE OF INVENTION: C
NUMBER OF SEQUENCES:
                                                                                                                                                   CLASSIFICATION: 435
PRIOR APPLICATION DATA:
US
                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
     REFERENCE/DOCKET NUMBER: 09
TELECOMMUNICATION INFORMATION
                                                  ATTORNEY/AGENT INFORMATION: NAME: Esmond, Robert W.
                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                         COUNTRY:
ZIP: 200
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                                                                                                                                   APPLICATION NUMBER: US 01 FILING DATE: 30-SEP-1994
                                                                                                                                                                                                                                                                                                                                                                          STATE:
                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: STERNE, KESSLER, COLDSTEIN & FOX P.L.L.C STREET: 1100 New York Avenue, N.W., Suite 600
                                 NAME: Esmond, Robert W. REGISTRATION NUMBER: 32,893
                                                                                    FILING DATE: 09-JAN-1995
                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                      OPERATING SYSTEM: PC-DOS/MS-DOS
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US-08-484-661A-34
US-08-484-661A-34
US-08-484-661A-34
US-08-656-664-15
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US-08-656-664-25
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US-08-656-664-25
US-08-656-664-25
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PCT-US96-09641-34
PCT-US96-09641-34
US-07-971-819A-1
US-07-977-434-3
US-08-475-231-1
US-08-458-819-3
US-08-706-702-2
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US-09-823-649A-5 (1-11) x US-08-537-400-15 (1-694)
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Patent No. 5948614
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                                                                                                                                             APPLICATION NUMBER: US 08/537,397 FILING DATE: 02-OCT-1995 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Rel-
CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
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TELECOMMUNICATION INFORMATION: TELEPHONE: 202-371-2600
                                                                                             ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                         FILING DATE: 14-AUG-
PRIOR APPLICATION DATA:
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: C
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                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 08/537,400 FILING DATE: 02-OCT-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 694 base pairs TYPE: nucleic acid STRANDEDNESS: double
                                                       NAME: Esmond, Robert W. REGISTRATION NUMBER: 32,893
                                          REFERENCE/DOCKET NUMBER:
                                                                                                             APPLICATION NUMBER: US 0 FILING DATE: 08-SEP-1995
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NVENTION: Cloned DNA Polymerases from Thermotoga
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                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08
FILING DATE: 01-JAN-1995
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APPLICANT: Chatterjee, Deb K.
Thermotoga and
                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/537,397
FILING DATE: 02-OCT-1995
                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/576,759
FILING DATE: 21-DEC-1995
                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/316,423
FILING DATE: 30-SEP-1994
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CORRESPONDENCE ADDRESS:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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APPLICATION NUMBER:
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APPLICATION NUMBER: 1
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                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM IN OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 1100 New CITY: Washington
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                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
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SYSTEM: PC DOS/MS-DOS
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US 08/525,057
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Matches:
Conservative:
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08-SEP-1995

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RACCIONALIA

NAME: INCOLIA, DIANE E.

REGISTRATION NUMBER: 40,027

REFERENCE/DOCKET NUMBER: PRMG-01175

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 705-8410

TELEPAX: (415) 397-8338

INFORMATION FOR SEQ ID NO: 38:

SEQUENCE CHARACTERISTICS:

LENGTH: 1485 base pairs

TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-823-649A-5 (1-11) x US-08-706-706-17 (1-694)
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APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,661A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 694 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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REFERENCE/DOCKET NUMBER: 0942.2800005
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: MODIFIED THERMOPHILIC DNA POLYMERASES TITLE OF INVENTION: FROM THERMOTOGA NEAPOLITANA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
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                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
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STREET: 220 MONTGOMERY STHEET, SUITE 2200
CITY: SAN FRANCISCO
                                                                                                                                                                                                                                                                                                                                                                                                        ZIP:
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   STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Application US/08484661A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BOLCHAKOVA, ELENA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SLATER, MICHAEL R. HARTNETT, JAMES R. HUANG, FEN
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Best Local Similarity:
Query Match:
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                           Alignment Scores:
                                                          US-08-656-664-38
                 Pred. No.:
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INFORMATION FOR SEQ ID NO:
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APPLICANT:
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TITLE OF INVENTION: THERMOPHILIC DNA POLYM
TITLE OF INVENTION: THERMOTOGA NEAPOLITANA
                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: PRITELECOMMUNICATION (NFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                 MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
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                                                                       NAME/KEY:
LOCATION:
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LOCATION: 1...]
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                                                                                                                                                                 TYPE:
                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 40,027
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                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
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Hartnett, James R.
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N: 435
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Length:
Matches:
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Best Local Similarity:
                                                           US-09-823-649A-5 (1-11) x PCT-US96-09641-38 (1-1485)
                                                                                                           Query Match:
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Best Local Similarity:
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SEQUENCE CHARACTERISTICS:
LENGTH: 1485 base pair
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                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: PRI
TELECOMMUNICATION INFORMATION:
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1024 CTTTCTGTGAGACTTGGAATACCGGTTAAAGAA 1056
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
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               1 LeuSerValArgLeuGly***ProValLysGlu 11
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220 Montgomery Street, Suite 2200
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Storts, Douglas R.
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415) 397-8338
                                                                                                                                                                                                                                                                                        DNA (genomic)
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Indels:
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                                                                                            Gaps:
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                                                                                                                                                                           length:
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Percent Similarity:
Best Local Similarity:
Query Match:
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                                                                                                                                    Patent No.
                                                                                                                                                    Sequence 36,
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                                                                              GENERAL INFORMATION:
APPLICANT: Slater,
APPLICANT: Huang,
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TITLE OF INVENTION: MODIFIED THERMOPHILIC DNA POLYMERASES
TITLE OF INVENTION: FROM THERMOTOGA NEAPOLITANA
                                                                                                                                                                                                                       1255 CTTTCTGTGAGACTTGGAATACCGGTTAAAGAA 1287
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LENGTH: 1716 base pairs
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TITLE OF INVENTION: THERMOPHILIC DNA POLYMERASES FROM
                                                                  APPLICANT:
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                   APPLICANT:
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TOPOLOGY: lin
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                                                                                                                                    6, Application US/08656664
6077664
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SAN FRANCISCO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CALIFORNIA
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                 Otto,
                            Bolchakova, Elena
Storts, Douglas R.
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                                                                                Slater, Michael R.
Huang, Fen
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                                                                Hartnett, James R.
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Conservative:
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PCT-US96-09641-36
; Sequence 36, Application PC/TUS9609641
; GENERAL INFORMATION:
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Best Local Similarity:
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ATTORNEY/AGENT INFORMATION:
NAME: Ingolia, Diane E.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                              APPLICANT:
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                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                      TITLE OF INVENTION: THERMOPHILIC DNA POLYMERASES FROM TITLE OF INVENTION: THERMOTOGA NEAPOLITANA NUMBER OF SEQUENCES: 57
                                                                                                                                                                                                              APPLICANT:
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REFERENCE/DOCKET NUMBER: PRITELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
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NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: 18M PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0
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CITY: San Francisco
                                                                                   ADDRESSEE: Medlen & Carroll
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
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                                                COUNTRY:
                                                                  STATE:
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                                 94104
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                                                California
United States Of America
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                                                                                                                                                                                                        Paul
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57
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Percent Similarity:
Best Local Similarity:
Query Match:
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                                                                                                                                       COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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LENGTH: 1716 base pair
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REFERENCE/DOCKET NUMBER: PR
TELECOMMUNICATION INFORMATION:
                                                                  CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: HOLCHAKOYA, ELENA
TITLE OF INVENTION: MODIFIED THERMOPHILIC DNA POLYMERASES
TITLE OF INVENTION: FROM THERMOTOGA NEAPOLITANA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: SLATER, MICHAEL R. APPLICANT: HARTNETT, JAMES R.
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                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
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CITY: SAN FRANCISCO
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                                                                                                       APPLICATION NUMBER: FILING DATE: 07-JUN
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                                 REGISTRATION NUMBER: 40,027
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                                                 INGOLIA, DIANE
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                                                                                      07-JUN-1995
N: 435
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                  PRMG-01175
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                                                                       TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 1737 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 10,
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                 TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
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LENGTH: 1737 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                         APPLICATION NUMBER: US/08
FILING DATE: 31-MAY-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSE: Medlen & Carroll
STREET: 220 Wontgomery Street, Suite 2200
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: THERMOPHILIC DNA POLYMERASES FROM TITLE OF INVENTION: THERMOTOGA NEAPOLITANA
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               MOLECULE TYPE:
                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Otto, Paul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         No.:
                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TOPOLOGY: li
                                                                                                                                                                            NAME: Ingolia, Diane E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: PR
                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Slater, Mic
Huang, Fen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hartnett, James R.
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                                                                                                                                                                                                                                                                                                                                                                                                           United States Of America
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             DNA (genomic)
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Percent Similarity:

Pest Local Similarity:

Query Match:
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                            Percent Similarity:
Best Local Similarity:
               Query Match:
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                                                                                       Alignment Scores:
                                                                                                                         PCT-US96-09641-10
                                                                           Pred. No.:
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TELEPHONE: (415) 705-8410
TELEPAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
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                                                                                                                                                                     FEATURE:
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LOCATION:
                                                                                                                                                                                                             LENGTH: 1737 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                                       NAME/KEY.
                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 40, REFERENCE/DOCKET NUMBER:
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                                                         Length:
Matches:
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Conservative:
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Indels:
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                                            Conservative:
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APPLICANT:

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US-08-484-661A-15; Sequence 15, Application US/08484661A; Patent No. 6001645
                                                                         RESULT 14
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                                                                                                                                                                                                                                           Query Match:
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                                                                                                                                                                                                                                                                                   Percent Similarity:
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TBLECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEPAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
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GENERAL INFORMATION:
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                                                                                                           1372 CTTTCTGTGAGACTTGGAATACCGGTTAAAGAA 1404
                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
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NAME: INGOLIA, DIANE E.
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TITLE OF INVENTION: MODIFIED THERMOPHILIC DNA POLYMERASES
TITLE OF INVENTION: PROM THERMOTOGA NEAPOLITANA
NUMBER OF SEQUENCES: 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: SLATER, MICHAEL R. APPLICANT: HARTNETT, JAMES R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: DNA (genomic)
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                                                                                                                                                                                                                                                                                                                         No . .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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                                                                                                                               1 LeuSerValArgLeuGly***ProValLysGlu 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
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Matches:
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Percent Similarity:
Best Local Similarity:
Query Match:
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Pred. No.:
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                                                                                                                                                                                                                                     ; Patent No. 6001645 ; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                            : Sequence 18, Application US/08484661A
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INFORMATION FOR SEQ ID NO: 15
SEQUENCE CHARACTERISTICS:
LENGTH: 1833 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                         1372 CTTTCTGTGAGACTTGGAATACCGGTTAAAGAA 1404
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NAME: INGOLIA, DIANE E.
REGISTRATION NUMBER: 40,027
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CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION: MODIFIED THERMOPHILIC DNA POLYMERASES
TITLE OF INVENTION: FROM THERMOTOGA NEAPOLITANA
                                                                                               TITLE OF INVENTION: MODIFIED THERMOPHILIC DNA POLYMERASES TITLE OF INVENTION: FROM THERMOTOGA NEAPOLITANA NUMBER OF SEQUENCES: 51
                                                                                                                                                                                           APPLICANT: SLATER, MICHAEL R. APPLICANT: HARTNETT, JAMES R.
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LOCATION:
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STATE: CALIFORNIA
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                      SAN FRANCISCO
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220 MONTGOMERY STREET,
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                                                                                                                                                      HUANG, FEN
BOLCHAKOVA, ELENA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HUANG, FEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA (genomic)
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47.00
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90.91%
95.92%
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                                       SUITE 2200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative: Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches:
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER TEM PC compatible
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: TEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: U5/08/484,661A
FILING DATE: 07-UN-1995
CLASSIFICATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: 40,027
REFERENCE/DOCKET NUMBER: PRMG-01175
TELECOMMUNICATION INDOMATION:
TELEPHONE: (415) 705-8410
TELEPHONE: (415) 397-8338
INFORMATION FOR SEO ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 1833 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
Search completed: January 15, 2003, 12:58:49 Job time : 29 secs
                                                                                                                                                                         Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                               ; NAME/KEY: CDS
; LOCATION: 1..1830
US-08-484-661A-18
                                                                                                                                        US-09-823-649A-5 (1-11) x US-08-484-661A-18 (1-1833)
                                                                                                                                                                                                                                                                Alignment Scores: Pred. No.:
                                                                                                                                                                                                                              Percent Similarity:
                                                                                                                                                                                                                                             Score:
                                                                    COUNTRY: UNITED STATES OF AMERICA ZIP: 94104
                                                                                                                                                                                          0.256
47.400
90.91%
90.91%
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Matches:
Conservative:
Mismatches:
Indels:
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10
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Result
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Maximum DB seq
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                         Scoring table:
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                                                                                                                                                                                                                                                                                                                     Database
                                                                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                        Score
 protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                               length: 0
length: 2000000000
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49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     January 15, 2003, 11:15:24; Search time 12.1429 Seconds (without alignments) 87.086 Million cell updates/sec
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PIR_73:*
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pir2:*
pir3:*.
pir4:*
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D81785
G81207
AI3607
E72398
                                                          T00362
C82721
                                     C75016
S73155
JC5145
                                                                                A98114
I54390
                                                                                                      C88445
S61154
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A99927
E85775
                       в90092
AF3603
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inositol 1,4,5-tri
              hypothetical prote oxidoreductase (EC appolipoprotein E
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protein C26E6.6 [i
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RESULT 2 D81785 conserved hypothetica C; Species: Neisseria C; Date: 05-May-2000 # C; Accession: D81785 R; Parkhill, J.; Achtm ; Holroyd, S.; Jagels Nature 404, 502-506, A; Title: Complete DNA A; Reference number: A A; Accession: D81785 A; Status: preliminary A; Molecule type: DNA	Query Mato Best Local Matches Qy 1 LS Db 741 LS	C.M. Nature 399, 323-329, 1999 A; Title: Evidence for lateral ge A; Reference number: A/2200; MUID A; Accession: E72232 A; Status: preliminary A; Molecule type: DNA A; Residues: 1-893 <arn> A; Residues: 1-893 <arn> A; Cross-references: GB:AE001805; A; Experimental source: strain MS C; Genetics: A; Gene: TM1619 C; Superfamily: DNA-directed DNA</arn></arn>	RESULT 1 E72222 DNA-directed DNA pol: C;Species: Thermotog: C;Date: 11-Jun-1999 C;Actession: E72232 R;Nelson, K.E.; Clay Garrett, M.M.; Stewa.		30 30 30 30 30 30 30 30 30 30 30 30 30 3
Neiss Neiss -May-2 5-May-2 n: D81 [/ J.; 50: J S: J Si J Si J Si D81 Si D81 Si D81 Si D81	Match Local Simi Local Simi LSVRLGX	9, 323 Eviden ce num on: E7 prelii e type s: 1-8 eferen eental: s: s: s: mily:	ed DN Theri -Jun- n: E7 K.E.;		3
hypothetical p : Neisseria men 5-May-2000 #seq n: D81785 1, J.; Achtman, 7, S.; Jagels, K. 4, 502-506, 200 Complete DNA se ce number: A817 n: D81785 preliminary s type: DNA	ilarit Conse XPVKE 	323-329, 1999 dence for latern number: A72200; E72232 elliminary ype: DNA- 1-893 CARN rences: GB:AE00 al source: stra 19 y: DNA-directed	ed DNA polymerase I Thermotoga maritima 1999 #sequence_ 1:E7232 K.E.; Clayton, R.A.;		& & & & & & & & & & & & & & & & & & &
rote ingi uenc M.; I,; I O quen	95. 90. tive	, 1999 A72200; MUII A72200; MUII ry ARNN GB:AE001805 ce: strain M	ymerase I - The a maritima #sequence_revis ton, R.A.; Gill rt, A.M.; Cotto		429 429 473 684 688 773 773 773 773 1034 11165 11226 11226 11284
ein NMA2 itidis ce_revis ; James, Leather, nce of a	***	gene JID:9 J5; G MSB8	re re		00000000000000000000000000000000000000
135 [imported] - ion 05-May-2000 # K.D.; Bentley, S S.; Moule, S.; M serogroup A stra 222556; PMID:1076	Score 47; DB 2; Length Pred. No. 0.17; 0; Mismatches 1; Ind	al gene transfer between Archaea MUID:99287316; PMID:10360571 1805; GB:AE000512; NID:g4982180; in MSB8	rmotoga maritima (stri ion 11-Jun-1999 #text , S.R.; Gwinn, M.L.; I n, M.D.; Pratt, M.S.;	ALIGNMENTS	C97500 AG2718 AG84943 G90473 B90275 AH0997 AH0997 AH0997 AH0997 AF6666 B6606 B76134 S76134 S765593 AG2490
Neisseria meningitidis (strain Z2 text_change 02-Feb-2001 .D.; Churcher, C.; Klee, S.R.; Mo hungall, K.; Quail, M.A.; Rajandre in of Neisseria menigitidis Z2491	gth 893; Indels 0; Gaps 0;	eea and Bacteria from genome 30; PIDN:AAD36686.1; PID:g498	ain MSB8) _change 21-Jui-2000 _codson, R.J.; Haft, D.H.; Hic Phillips, C.A.; Richardson,		hypothetical prote MFS permease [impo membrane protein [hypothetical prote hypothetical prote ferrous iron trans iron [II] transport ferrous iron trans ferrous iron

A;Molecule type: DNA
A;Residues: 1-324 <PAR>
A;Coss-references: GB:AL162758; GB:AL157959; NID:g7380672; PIDN:CAB85347.1; PID:g738
A;Experimental source: serogroup A, strain 22491
C;Genetics:
A;Gene: NMA2135
A;Gene: NMA2135
C;Superfamily: probable ATP-binding protein gutQ; CBS homology

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R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougharty, B ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M. Science 287, 1809-1815, 2000
A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R. A;Tille: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A;Reference number: A81000; MUID:20175755; PMID:10710307
A;Accession: G81207
                                                                                                                                                                                               A; Map position: II
C; Superfamily: NADH dehydrogenase
C; Keywords: oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Residues: 1-324 <TET>
A;Residues: 1-324 <TET>
A;Cross-references: GB:AE002392; GB:AE002098; NID:g7225573; PIDN:AAF40795.1; PID:g722557
A:Experimental source: serogroup B, strain MC58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sugar isomerase, KpsF/GutQ family NMB0352 [imported] - Neisseria meningitidis (strain C;Species: Neisseria meningitidis
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
                        D,
                                                               Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                          .; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 03-Jun-2002
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C; Superfamily:
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                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-441 <KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                 A;Reference number: AD3252; PMID:11756688
A;Accession: AI3607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;DelVecchio, V.C.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, ; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NADH2 dehydrogenase (EC 1.6.99.3) [imported] - Brucella melitensis (strain 16M) C;Species: Brucella melitensis
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                                                                                                                                                                                                                                                               A; Gene: BMEII0786
                                                                                                                                                                                                                                                                                                                              A;Cross-references: GB:AE008918; PIDN:AAL54028.1; PID:g17984981; GSPDB:GN00191
                                                                                                                                                                                                                                                                                                                                                                                             A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Accession: AI3607
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                                                                                                            Matches
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                                                                                                                                  Similarity
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70.0%;
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Pred. No.
                                                                                                                                  Score 37;
Pred. No.
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Pred. No.
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Dougherty, B.A.
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Best Local
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                                                               Local
  1 LSVRLGXPVKE 11
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A;Cross-references: GB:L00094; GB:J00704; NID:g202912; PIDN:AAA98779.1; PID:g202914 R;Bouhnik, J.; Clauser, E.; Strosberg, D.; Frenoy, J.P.; Menard, J.; Corvol, P. Biochemistry 20, 7010-7015, 1911.
A;Title: Rat angiotensinogen and Des(antiotensinI)angiotensinogen: purification, char; A;Reference number: A90456; MUID:82091819; PMID:6797467
A;Accession: A90456
                                                                                                                                                                                                                                                                                                                                                                                                               A, Molecule type: protein
A, Rolecule type: protein
A; Residues: 25-41 <BOU>
C; Comment: Anglotensin I is released from angiotensinogen by renin, which is secreted
e I (angiotensin-converting enzyme), primarily in the lungs.
C; Comment: The release of the amino-terminal residue (Asp-25) from angiotensin I and
sp-1]angiotensin I is converted to angiotensin III by dipeptidyl carboxypeptidase I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N;Contains: angiotensin I; angiotensin II; angiotensin III
C;Species: Rattus norvegicus (Norway rat)
C;Date: 13-Jun-1983 #sequence_revision 13-Jun-1983 #text_change 18-Jun-1999
C;Accession: A93945; A90456; A01251
R;Ohkubo, H.; Kageyama, R.; Ujihara, M.; Hirose, T.; Inayama, S.; Nakanishi, Proc. Natl. Acad. Sci. U.S.A. 80, 2196-2200, 1983
A;Title: Cloning and sequenc analysis of cDNA for rat angiotensinogen.
A;Reference number: A93945; MUID:83169849; PMID:6572971
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C;Accession: E72398
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein TM0244 - Thermotoga maritima (strain MSB8)
C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
                                                                                                                      F;25-34/Product: angiotensin I *status experimental <PPI>F;25-32/Product: angiotensin II *status experimental <PPI>F;26-32/Product: angiotensin III *status experimental <PPI>F;26-32/Product: angiotensin III *status experimental <PPI>F;295,319/Binding site: carbohydrate (Asn) (covalent) *status experimental <PPI **
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Title: Evidence for lateral gene transfer between Archaea A;Reference number: A72200; MUID:99287316; PMID:10360571 A;Accession: E72398
                                                                                                                                                                                                                                                             F;1-24/Domain: signal sequence #status predicted <SIG>F;25-477/Product: angiotensinogen #status predicted <MPT>
                                                                                                                                                                                                                                                                                                                     C: Keywords: blood pressure control; glycoprotein; liver; plasma;
                                                                                                                                                                                                                                                                                                                                                                      C; Superfamily: antithrombin III
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
A; Residues: 1-477 < OHK>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local
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Similarity 63.6%;
7; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                323-329, 1999
Similarity
8; Conserv
                           73.5%;
                           Score 36;
Pred. No.
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Pred. No.
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                                                           DB 1;
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                                                           Length 477
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Conservative

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Mismatches

Indels

Gaps

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C;Accession: E75361
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J., M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
                                                                                                                      conserved hypothetical protein - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          probable aldehyde oxidoreductase APE0708 - Aeropyrum pernix (strain K1)
C;Species: Aeropyrum pernix
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 16-Jun-2000
                                                                                                                                                                                                                                                                                                  В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               xylose operon regulatory protein (xylR-2) homolog - Lyme disease spirochete
C;Species: Borrelia burgdorferi (Lyme disease spirochete)
C;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 08-Oct-1999
C;Accession: F70203
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C;Superfamily: glucose kinase; glucose kinase homology
F;61-188/Domain: glucose kinase homology <GKH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Authors: Smith, H.O.; Venter, J.C.
A; Title: Genomic sequence of a Lyme disease spirochaete,
A; Reference number: A70100; MUID:98065943; PMID:9403685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Superfamily: carbon-monoxide dehydrogenase large chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-753 < KAW>
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nes 7; Conserv
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va. M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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54.5%;
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Pred. No.
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27;
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Vugt,
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F64925
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gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; SHI DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: A99227
A;Accession: A99227
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                                                                                                                                                                                                                                                                                                                                C;Date: 18-Jul-2001 *sequence_revision 18-Jul-2001 *text_change 03-Aug-2001 C;Accession: A99927
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C;Superfamily: conserved hypothetical protein b0819
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A; Residues: 1-277 <WHI>
A; Gene: ECs2385
C; Superfamily: conserved hypothetical
                                                A; Experimental source: C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein ECs2385 [imported] - Escherichia coli (strain 0157:H7, substrain C;Species: Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Title: The complete genome sequence of Escherichia coli K-12 A; Reference number: A64720; MUID:97426617; PMID:9278503 A; Accession: F64925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Escherichia coli
C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002
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A;Experimental source: strain Rl
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                                                                                                                  A; Molecule type: DNA
A; Residues: 1-334 <HAY>
                                                                                                                                                                 A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Gene: DR1728
                                                                                               A;Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         223 SVRTGTPVK 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity les 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 SVRLGXPVK 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | ||| |||:
||EARLGLPVKD
                                                                                                                                                                                                                                                                               T.; Makino, K.; Ohnishi, M.; N.; Yasunaga, T.; Kuhara, S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1-334 <BLAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                 GB:BA000007; PIDN:BAB35808.1; PID:g13361852; GSPDB:CN00154ce: strain 0157:H7, substrain RIMD 0509952
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 69.48;
63.68;
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77.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 34;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                               Kurokawa, K.; Ishii, K.; Yokoyama,
Shiba, T.; Hattori, M.; Shinagawa,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 334;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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protein b0819

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R:Wetmur, J.G.: Wong, D.M.; Ortiz, B.; Tong, J.; Reichert, F.; Gelfand, D.H.
J. Biol. Chem. 269, 25928-25935, 1994
A:Title: Cloning, sequencing, and expression of RecA proteins from three distantly relat A:Reference number: A55020; MUID:95014407; PMID:7929298
A:Accession: D55020
C; Superfamily: recombination protein recA C; Superfamily: nucleotide binding; P-loop: C; Keywords: ATP; DNA binding; DNA recombination; DNA repair; nucleotide binding R; R0, R1, R2, R3, R3, R4, R5, R5
                                                                                                                                                                                                                                                                   A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-356 <ARN>
                                                                                                                                                                                                                                                                                                                                                               A;Title: Evidence for lateral gene transfer between Archaea A;Reference number: A72200; MUID:99287316; PMID:10360571 A;Accession: D72201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:L23425; NID:g385169; PIDN:AAA27417.1; PID:g385170 R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hi Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Qγ
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                                                                                                                                    A; Gene: TM1859
                                                                                                                                                                          C;Genetics:
                                                                                                                                                                                                  A;Cross-references: GB:AE001823; GB:AE000512; NID:g4982441; PIDN:AAD36921.1; PID:g498244
A;Experimental source: strain MSB8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Thermotoga maritima
C;Date: 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 02-Teb-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N; Alternate names: DNA repair protein;
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A;Experimental source: strain 0157:H7, substrain EDL933
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 409,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein ynhG [imported] - Escherichia coli (strain 0157:H7, substrain EDL93, C;Species: Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nature 399,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary
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Best Local
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milarity 77.8%;
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77.88;
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Pred. No. 31;
0; Mismatches
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      Search completed: January 15,
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R;anonymous, The C: elegans Sequencing Consortium.

Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating bio A:Reference number: A75000; MUID:99069613; PMID:9851916
A;Note: see websites genome.wustl.edu/9sc/C_elegans/ and www_sanger.ac.uk/Projects/C_A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; A;Accession: C88445
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-379 <STO>
A;Residues: 1-379 <STO>
A;Cross-references: GB:ch_III; PIDN:AAA21160.1; PID:9532807; GSPDB:GN00021; CESP:C26
A;Molec: similar to ribosomal protein L3
C;Genotics:
A;Gene: C2666.6
A;Map position: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                 N;Alternate names: hypothetical protein D9476.2

C;Species: Saccharomyces cerevisiae
C;Date: 23-Feb-1996 #sequence_revision 01-Mar-1996 #text_change 19-Apr-2002
C;Accession: S61154
                                                                                                                                        A; Map position: 4R
C; Superfamily: Schizosaccharomyces pombe hypothetical protein SPBC25H2.16c
                                                                                                                                                                                  A;Gene: SGD:GGA1; MIPS:YDR358w
A;Cross-references: SGD:S0002766
A;Map position: 4R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein C26E6.6 |imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
C;Accession: C88445
                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-557 < DUZ>
                                                                                                                                                                                                                                                                                                                                                                            submitted to the EMBL Data Library, June 1995
ArDescription: The sequence of S. cerevisiae
                                                                                                                                                                                                                                                                                                                                                    A:Reference number: S61148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F;74/Binding site: ATP (Lys) #status predicted
                                                                                                                                                                                                                                                     C; Genetics:
                                                                                                                                                                                                                                                                    A;Cross-references: EMBL:U28372; NID:g849170; PID:g849172; GSPDB:GN00004; MIPS:YDR358
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523 ISVNLGKPIK 532
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Pred. No. 51;
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2003, 12:37:23

Job time : 16.1429 secs

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49
1 LSVRLGXPVKE 11
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//SIDSZ/gogdata/geneseq/geneseqp-emb1/AA2000.DAT:

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  AAB47795
AAM48266
AAM48267
AAR98144
AAR98145
AAW13863
AAW11572
AAW11525
AAW11525
AAW11524
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(without alignments)
52.083 Million cell updates/sec
                                       The DNA polymerase
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Thermotoga neapoli
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neapoli
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ALIGNMENTS	AAW11515 AAW11516 AAW11518 AAW11519 AAW11521 AAW11521 AAW11521 AAW183977 AAW83969 AAW83969 AAW84000 AAW84000 AAW84000 AAW84000 AAW84000 AAW84000 AAW84001 AAW84002 AAW84003	15
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Smith ES, Elfstrom CM, Gelfand DH, Schoenbrunner NJ, Wang AM;
                                              12-APR-2001; 2001EP-0109341
                                                                                                                      dye; amplification
                                  18-APR-2000; 2000US-198336P.
                                                           07-NOV-2001
                                                                      EP1152062-A2
                                                                                         Misc-difference
                                                                                                          Thermotoga sp.
                     (HOFF ) HOFFMANN LA ROCHE & CO AG F.
                                                                                          Location/Qualifiers
                                                                                  /label= Val, Ile
         Higuchi RG,
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DNA polymerase; reverse transcription; primer; divalent cation; mutant; transverse transcription reaction; fluorescein; cyanine; thermoactive;

Native DNA polymerase motif #5

25-MAR-2002 AAB47795;

(first entry)

AAB47795 standard; peptide; 11 AA

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RESULT 2
AAM48266
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  polymerase. These motifs represent a conserved region which affects the polymerase's ability to incorporate dideoxynucleotides labelled with fluorescein and cyanine family dyes. The method of the invention is useful in reverse transcription/amplification reactions. The method provides improved reverse transcription efficiency at lower enzyme concentrations relative to previous high temperature reverse transcription methods, and provide a wider range of usable salt concentrations. The use of the mutant DNA polymerase provides faster reverse transcription extension rates, and consequently less time is needed for the reaction. This motif is derived from DNA polymerases from
          Disclosure; Page 7; 23pp; English
                               Reverse transcribing an RNA, comprises performing a reverse transcriptase polymerase chain reaction amplification of a mixture using a mutant thermoactive DNA polymerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           treating a transverse transcription reaction mixture which comprises the RNA, a primer, a divalent cation, and a mutant thermoactive DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of the invention. The method for reverse transcribing an RNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The sequences given in AAB47791-97 and AAM48259-AAM48270 represent the native forms of motifs derived from DNA polymerases used in the method
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 2; Page 4; 23pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Reverse transcribing an RNA, comprises performing a reverse transcriptase polymerase chain reaction amplification of a mixture using a mutant thermoactive DNA polymerase \,
                                                                                                       Smith ES, Elfstrom CM, Schoenbrunner NJ, Wang
                                                                                                                                                                                                                     07-NOV-2001
                                                                                                                                                                                                                                                                     Thermotoga maritima
                                                                                                                                                                                                                                                                                             dye;
                                                                                                                                                                                                                                                                                                                                             Native DNA polymerase motif #15
                                                                                                                                                                                                                                                                                                                                                                                              AAM48266;
                                                                                                                                                                                                                                                                                                                                                                                                                    AAM48266 standard; Peptide; 11 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Thermotoga species maritima and neopolitana.
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                                                                                WPI; 2002-076891/11.
                                                                                                                                                                     18-APR-2000; 2000US-198336P
                                                                                                                                                                                             12-APR-2001; 2001EP-0109341
                                                                                                                                                                                                                                               EP1152062-A2
                                                                                                                                                                                                                                                                                                                    DNA polymerase; reverse transcription; primer; divalent dation; mutant;
                                                                                                                                                                                                                                                                                                                                                                     25-MAR-2002
                                                                                                                                            (HOFF ) HOFFMANN LA ROCHE & CO AG F.
                                                                                                                                                                                                                                                                                                       transverse transcription reaction; fluorescein; cyanine; thermoactive;
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nes 11; Conserv
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                                                                                                                                                                                                                                                                                            amplification.
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100.0%;
                                                                                                                      Gelfand DH,
                                                                                                         AM;
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The sequences given in AAB47791-97 and AAM48259-AAM48270 represent the native forms of motifs derived from DNA polymerases used in the method of the invention. The method for reverse transcribing an RNA, comprises of the invention a transcription reaction mixture which comprises the treating a transverse transcription reaction mixture which comprises the

RNA, a primer, a divalent cation, and a mutant thermoactive DNA

polymerase. These motifs represent a conserved region which affects the

DNA polymerase's ability to incorporate dideoxynucleotides labelled with thuorescein and cyanine family dyes. The method of the invention is useful in reverse transcription/amplification reactions. The method

Reverse transcribing an RNA, comprises performing a reverse transcriptase polymerase chain reaction amplification of a mixture using a mutant thermoactive DNA polymerase

Smith ES, Elistrom CM, Ge Schoenbrunner NJ, Wang AM; WP1; 2002-076891/11.

(HOFF) HOFFMANN LA ROCHE & CO AG F.

Gelfand DH,

Higuchi RG,

Myers TW:

12-APR-2001; 2001EF 0109341 18-APR-2000; 2000BS 1983361

Disclosure; Page 7; 23pp; English.

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RESULT 3
AAM48267
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Matches 10; Conserv
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The sequences given in AAB47791-97 and AAM48259-AAM48270 represent the native forms of motifs derived from DNA polymerases used in the method of the invention. The method for reverse transcribing an RNA, comprises
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 fluorescein and cyanine family dyes. The method of the invention is useful in reverse transcription/amplification reactions. The method provides improved reverse transcription efficiency at lower enzyme
                                                                                  Thermotoga neapolitana
                                                                                                                              transverse transcription dye; amplification.
                                                                                                                                                                                                                                                                                                                                                                  AAM48267 standard; Peptide; 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     transcription methods, and provide a wider range of usable salt concentrations. The use of the mutant DNA polymerase provides taster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              treating a transverse transcription reaction mixture which comprises the
07-NOV-2001
                                           EP1152062-A2
                                                                                                                                                                              DNA polymerase; reverse transcription; primer; divalent cation; mutant;
                                                                                                                                                                                                                          Native DNA polymerase motif #16.
                                                                                                                                                                                                                                                                        25-MAR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         needed for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          reverse transcription extension rates, and consequently less time is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                concentrations relative to previous high temperature reverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 LSVRLGXPVKE 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LSVRLGVPVKE 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the reaction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95.98;
                                                                                                                                                      reaction; fluorescein; cyanine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 47; DB 23;
Pred. No. 0.0033;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                           thermoactive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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RESULT 4
AAR98144
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Best Local Similarity
Thehes 10; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       D,
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                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                concentrations relative to previous high temperature reverse transcription methods, and provide a wider range of usable salt concentrations. The use of the mutant DNA polymerase provides faster reverse transcription extension rates, and consequently less time is needed for the reaction.
                                                                                                                                                                                                                                                                                                                                        The C-terminal portion (AAR98144) of the 100 kDa thermostable DNA polymerase (AAR98143) of Thermotoga neapolitana (Tne) includes an O helical region. Tna polymerase is a thermostable enzyme suitable for use in DNA sequencing and amplification reactions. It can be obtd. from host cells, e.g. E. coli, carrying the DNA polymerase gene. Mutants having improved enzymatic properties may also be produced (see also AAR98144-47).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Thermotoga neopolitana DNA polymerase and thermostable mutants useful in DNA sequencing and amplification reactions % \left( 1\right) =\left( 1\right) +\left( 1\right)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAT30049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chatterjee DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-OCT-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Thermotoga neapolitana strain DSM 5068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA polymerase; Tne; DNA sequencing; amplification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tne DNA polymerase C-terminal region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-AUG-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR98144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR98144 standard; Protein; 230 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             provides improved reverse transcription efficiency at lower enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 10; Fig 5A-B; 67pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09-JAN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO961064≏-Al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 thermostable enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (LIFE-) LIFE TECHNOLOGIES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-APR-1596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 LSVRLGXPVKE 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 LSVRLGIPVKE 11
1 LSVRLGXPVKE 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1996-209362/21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10;
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                                                                                                                                                                                                                                                        230 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95US-0370190.
94US-0316423.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hughes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95WO-US12358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers 63..72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label= 0-helical_region
                                                                                                                            95.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                    0;
                                                                                    Score 47; DB 17; Length 230; Pred. No. 0.094; 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 47; DB 23;
Pred. No. 0.0033;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0,
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                                                                                    Gaps
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09-JUN-1997

(first entry)

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RRESULT 5
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                                                                                                                                                              RESULT
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Best Local
                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Site-directed mutagenesis was used to substitute a tyrosine residue for phenylalanine in the O-helical region of Thermotoga neapolitana (The) DNA polymerase. This residue corresponds to position 67 of a C-terminal fragment (see also AAR98144) of the enzyme. As a result of the mutation, the polymerase becomes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               non-discriminating against non-natural nucleotides such as dideoxynucleotides. The mutant enzyme, which may also incorporate a D233A mutation in the N-terminal portion (see AAR98146) or has the 5'-3' exonuclease domain deleted (see AAR98147), is active and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09-JAN-1995;
30-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA polymerase;
thermostable en:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR98145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 50; Fig5A-B; 67pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Thermotoga neopolitana DNA polymerase and thermostable mutants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chatterjee DK, Hughes AJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 02-OCT-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11-APR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         W09610640-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The DNA polymerase C-terminal region (F67Y mutant)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-AUG-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR98145 standard; Protein; 230 AA
                                                                                                     AAW13863 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 reactions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        heat stable, and can be used in DNA sequencing and amplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (LIFE-) LIFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                78 LSVRLGIPVKE 88
                                                                                                                                                                                                                                          78
                                                                                                                                                                                                                                                                                                1 LSVRLGXPVKE 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1996-209362/21
                                                                                                                                                                                                                                          LSVRLGIPVKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           in DNA sequencing and amplification reactions
                                                                                                                                                                                                                                                                                                                                                10;
                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                         230 AA;
                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     se; The; DNA sequencing; amplification; enzyme; protein engineering; mutagenesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TECHNOLOGIES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95US-0370190
94US-0316423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95WO-US12358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label- O-helical_region
                                                                                                     Protein;
                                                                                                                                                                                                                                                                                                                                                                            95.9%;
                                                                                                        230
                                                                                                                                                                                                                                                                                                                                                0,:
                                                                                                                                                                                                                                                                                                                                                                            Score 47; DB 17
Pred. No. 0.094;
                                                                                                     A
                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amplification;
                                                                                                                                                                                                                                                                                                                                                                                                   DB 17;
                                                                                                                                                                                                                                                                                                                                                                                                Length 230;
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PN XXX XXX DEXX
                                                                                                                                                                                                                                                           Matches
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Best Local :
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02-OCT-1995;
21-DEC-1995;
                                                                                                                                                                                                                                                                                                                               single reading frame. The 3 sequences were compared with known polymerase amino acid sequences and spliced to generate the The sequence given in AAW13863. A complete amino acid sequence for
                                                                                                                                                                                                                                                                                                                                                                Polypeptide sequences (AAW13862-64) were deduced for all 3 reading frames of a DNA sequence (AAT60031) encoding the C-terminal region, including the O-helix, of the Thermotoga neapolitana (Tne) DNA polymerase. Frameshift errors generated during sequencing of the DNA prevented the entire amino acid sequence being deduced from a
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mutant DNA polymerase, esp. from Thermotoga - has reduced exonuclease activity or dideoxynucleotide discrimination, useful for DNA amplification, synthesis and sequencing
                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chatterjee DK, Hughes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08-SEP-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14-AUG-15 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-SEP-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9709451-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Thermotoga neapolitana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA polymerase; Tne; exonuclease; DNA amplification; DNA sequencing;
18-JAN-2000
                    US6015668-A.
                                       Thermotoga neapolitana
                                                                                                                  18-MAY-2000
                                                                                                                                                           AAY51572 standard; Protein; 230 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                Example 5; Fig 5; 120pp; *English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAT60031.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (CHAT/) CHATTEI
(HUGH/) HUGHES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The DNA polymerase C-terminal region.
                                                                        DNA polymerase; PolI; O-helix; DNA sequencing; amplification; mutant;
                                                                                           T. neapolitana Tne polymerase C-terminal protein fragment.
                                                                                                                                                                                                                                                                                                                      polymerase is given in AAW13899.
                                                            thermostability; Tne
                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                 78 LSVRLGIPVKE 88
                                                                                                                                                                                                                                     1 LSVRLGXPVKE 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1997-192925/17
                                                                                                                                                                                                                                                           10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       engineering; protein engineering; mutagenesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHATTERJEE D K.
                                                                                                                                                                                                                                                                                                    230 AA;
                                                                                                                                                                                                                                                           Conservative
                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95US-0537397.
95US-0537400.
95US-0576759.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     АJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96US-0525057
95US-0525057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96WO-US14189
                                                                                                                                                                                                                                                                    95.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ΑJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 strain DSM 5068
                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                    Score 47; DB 18
Pred. No. 0.094;
                                                                                                                                                                                                                                                                                                                                   A complete amino acid sequence for "Ine
                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                DB 18;
                                                                                                                                                                                                                                                                              Length 230;
                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                           Caps
                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                              AAW11525
ID AAW1
B
                                                                                                                                                                                                                                               δÃ
                                                                                                                                                                                             RESULT 8
                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                          DNA polymerase; Tne; thermostable enzyme; protein engineering; thermostability; DNA sequencing; amplification; PCR; polymerase chain reaction; exonuclease; Thermotoga neapolitana
19-DEC-1996
                                                                                                      Thermotoga neapolitana DNA polymerase Tne M284 delB
                   W09641014-A1
                                        Synthetic.
                                                                                                                             15-APR-1997
                                                                                                                                                  AAW11525;
                                                                                                                                                                        AAW11525
                                                                                                                                                                                                                            78 LSVRLGIPVKE 88
                                                                                                                                                                                                                                                1 LSVRLGXPVKE 11
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QΥ

10;

Conservative

95.98;

Score 47; DB Pred. No. 0.09 0; Mismatches

DB 21; .094;

Length 230; Indels

0;

Gaps

0;

standard;

Protein;

494

(first entry)

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XX PR PR PR PR PR PR PR PR PR PR
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09-JAN-1995;
                                                    dideoxynucleotides (ddWTP). They permit sequencing at high temperature; provide strong, clear sequences (increased signal to-noise ratio); can sequence more than 500 bases; reduce false stops in the sequence ladder; reduce template requirements 10-fold (when using 350 labeling); and also requirements for primer and labeled terminator. They increase sequencing efficiency with structure-containing or GC-rich templates; reduce film exposure times; do not generate sequencing artefacts with homopolymeric sequences and allow quantitation of bases in heterologous mixtures. This sequence represents the Thermotoga neapolitana The polymerase carboxyl terminal which is described in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                   methods, also for DNA labeling and for synthesis of cDNA from mRNA templates. (1) have higher thermostability than known enzymes (e.g. 50% retention of activity after 60 min at 90 plusoC), and may be free
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA sequencing, amplification and synthesis methods, using mutant forms of Thermotoga neapolitana polymerase with reduced exonuclease activity or reduced discrimination against dideoxynucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              double-stranded DNA or synthesizing DNA which use a mutant Thermo neapolitana DNA polymerase (I) or its fragments. (I) are used for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 5; Column 53-54; 65pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAZ88767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (LIFE-) LIFE TECHNOLOGIES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08-SEP-1995;
02-OCT-1995;
Sequence
                                                                                                                                                                                                                                                                                                                                                                  of exonuclease activity and/or ability to discriminate against
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequencing, amplification and synthesis of DNA by essentially standard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This invention describes novel methods for sequencing DNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-181138/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hughes AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-DEC-1995;
14-AUG-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02-OCT-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-SEP-1996;
   230 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chatterjee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96US-0689818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96US-0706706
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95US-0537400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94US-0316423.
95US-0370190.
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В
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                                                                                                                                                                                                                                                                                                                       Best
                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                  Deletion mutant The M284 delB (AAW11525) of the The DNA polymerase (see also AAW11513) of Thermotoga neapolitana lacks the N-terminal 283 amino acids from the 5' exonuclease domain of the native enzyme and also has amino acid residues 309-424 of the 3' exonuclease domain deleted. It can be obtd. by expression of a DNA construct (AATS8155) created, by restriction digestion of pW284-derived DNA also AATS8135). When expressed in E. coli, The M284 delB showed no detectable polymerase activity. In contrast, a The M284 mutant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bolchakova E, Hartnet Slater MR, Storts DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31-MAY-1996;
07-JUN-1995;
        WPI; 1997-052374/05
N-PSDB; AAT58145.
                              Bolchakova E, Hartnet Slater MR, Storts DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Thermostable DNA polymerase from Thermotoga neapolitana - useful DNA sequencing or for amplification of double stranded DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAIF58155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-JUN-1996;
                                                                      31-MAY-1996;
07-JUN-1995;
                                                                                                                                                                                          Thermotoga neapolitana DNA polymerase The M323 mutant
                                                                                                                                                                                                                         AAW11524;
                                                                                                                                                                                                                                         AAW11524 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 4; Page 174-175; 200pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (PROM-) PROMEGA CORP
                                                      (PROM-) PROMEGA CORP
                                                                                              07-JUN-1996;
                                                                                                              19-DEC-1996
                                                                                                                            WO9641014-A1
                                                                                                                                           Synthetic
                                                                                                                                                           thermostability; DNA sequencing; amplification; PCR; polymerase chain reaction; exonuclease; Thermotoga neapolitana
                                                                                                                                                                            DNA polymerase; Tne;
                                                                                                                                                                                                          15-APR-1997
                                                                                                                                                                                                                                                                                342
                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                              (see also
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                                                                                                                                                                                                                                                                                                                      Local
                                                                                                                                                                                                                                                                                              1 LSVRLGXPVKE 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1997-052374/05
                                                                                                                                                                                                                                                                                LSVRLGIPVKE 352
                                                                                                                                                                                                                                                                                                               10;
                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                             AAW11514) was active.
                                                                                                                                                                                                                                                                                                                                             494 AA;
                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                          (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hartnett JR,
                                                                      96US-0656664
95US-0484661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96US-0656664
95US-0484661
                                       Hartnett
                                                                                              96WO-US09641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96WO-US09641
                                                                                                                                                                                                          entry)
                                                                                                                                                                            thermostable enzyme; protein engineering;
                                                                                                                                                                                                                                                                                                                      95.9%;
                                       JR,
                                                                                                                                                                                                                                         572
                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                     Score 47;
Pred. No. (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Huang
                                       Huang
                                                                                                                                                                                                                                         A
                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'n
                                       'n
                                                                                                                                                                                                                                                                                                                      No. 0.22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Miller KM,
                                        Miller KM,
                                                                                                                                                                                                                                                                                                                              DB 18;
                                                                                                                                                                                                                                                                                                                              Length 494;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Otto
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                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                               0;
Qy
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Query Match
Best Local Similarity
Matches 10; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Deletion mutant The M323 (AAW11524) of Thermotoga neapolitana DNA polymerase The (see also AAW11513) has an artificially created methionine at amino acid position 323 as the initiator methionine in the 3' exonuclease domain of the enzyme. It can be expressed in the 3' exonuclease domain of the enzyme.
mutagenesis. When expressed in E. coli from a T/ or The M316 produced no detectable polymerase activity. mutant (see also AAW11514) was active.
                                                     Deletion mutant Tne M316 (AAW11523) of Thermotoga neapolitana DNA polymerase Tne (see also AAW11513) has an artificially created methionine at amino acid position 316 as the initiator methionine. It can be expressed using a DNA construct (AAT58144) created by introducing a Met residue at position 316 (and a corresponding NcoI site) into the native gene (AAT58134) via site-directed mutagenesis. When expressed in E. coli from a T7 or trc promoter,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA polymerase; The; thermostable enzyme; protein engineering; thermostability; DNA sequencing; amplification; PCR; polymerase chain reaction; exonuclease; Thermotoga neapolitana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Thermotoga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW11523;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW11523 standard; Protein; 578 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA sequencing or for amplification of double stranded DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Thermostable DNA polymerase from Thermotoga neapolitana - useful in
                                                                                                                                                                                                                                                                               Example 3; Page 133-135;
                                                                                                                                                                                                                                                                                                                                  Thermostable DNA polymerase from Thermotoga neapolitana - DNA sequencing or for amplification of double stranded DNA
                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAT58144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bolchakova E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (PROM-) PROMEGA CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               W09641014-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                419 LSVRLGIPVKE 429
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                                                                                                                                                                                                                                                                                                                                                                                                                                             1997-052374/05
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 572 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Storts DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9505-0656664.
9505-0484661.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hartnett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96WO-US09641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JR,
                                                                                                                                                                                                                                                                            200pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          polymerase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 47;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Huang F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tne M316
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     . 26;
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                                 A Tne M284
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Best Local
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                                                                                                                                                                                          Sequences AAW83969 to AAW84011 represent The (Thermotoga neapolitana) DNA polymerase mutants which can be used in the method of the invention of identifying and analysing polymorphic DNA. The method comprises reacting a DNA sample with at least one DNA polymerase having reduced ability to add non-templated nucleotides to the 3'-terminus and amplifying the fragment, followed by analysis, identification or typing of the amplicons. The DNA polymerases used are thermostable and the
amplifying the fragment, followed by analysis, identification or typing of the amplicons. The DNA polymerases used are thermostable and the modification or mutation is in the O-helix of the The DNA polymerase. Analysis of polymorphic DNA is particularly used to establish relationships between individuals (forensic or paternity testing), particularly where the polymorphism is a mini- or micro-satellite or short tandem repeat. More generally the DNA polymerase and its mutant form are useful in any process that involves nucleic acid amplification, e.g. identification of pathogens, cancer or genetic diseases (cystic fibrosis, haemophilia, Alzheimer's disease), screening organs or tissues before transplanting, diagnosis, plant breeding, Note: This sequence is not provided in the specification. It has been created by modifying the wild-type Tne DNA polymerase sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tne; O-helix; DNA polymerase; polymorphic; amplicon; thermostable; mutant; forensic; paternity testing; nucleic acid amplification; cancer pathogen; genetic disease; cystic fibrosis; haemophilia; transplanting; Alzheimer's disease; screening; organ; diagnosis; plant breeding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-FEB-1999
                                                                                                                                                                                                                                                                                                                                     Claim 52;
                                                                                                                                                                                                                                                                                                                                                                New mutant polymerases that do not add non-templated 3 nucleotides - specifically for analysis of hypervariable polymorphisms e.g. for forensic and paternity testing, disease diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1998-447254/38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chatterjee DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-JAN-1998;
07-FEB-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-AUG-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Thermotoga neapolitana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tne DNA polymerase mutant N'del284, D323A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW83971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW83971 standard; Protein; 609 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (LIFE-) LIFE TECHNOLOGIES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         426 LSVRLGIPVKE 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 LSVRIGXPVKE 11
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                                                                                                                                                                                                                                                                                                                                   Page -; 187pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98US-0037393.
97US-0037393.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98WO-US02791
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Solus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note=_"wild-type Asp is replaced with Ala"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label= D323A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95.9%;
90.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ç
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Yang S;
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  . 26;
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                    DNA clone pM284 (AAT58135) produced by restriction enzyme digestion of the native gene (AAT58134). The N-terminal deletion eliminates the 5' exonuclease activity of the enzyme. The M284 has a half-life at 97.5 deg C of 18 min compared with 5 min for the native enzyme. Amino acid substns. in the 3' exonuclease domain of The M284 (see also AAW11516-22) yield enzymes esp. suitable for DNA M284 (see also AAW11516-22) yield enzymes esp. suitable for DNA
                                                                                                                                                                                                                                                                                                                                                            31-MAY-1996;
07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA polymerase; The; thermostable enzyme; protein engineering; thermostability; DNA sequencing; amplification; PCR; polymerase chain reaction; exonuclease; Thermotoga neapolitana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Thermotoga neapolitana DNA polymerase Tne M284 mutant.
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                                                                                                                                 DNA polymerase mutant Tne M284 (AAW11514) lacks the N-terminal 283 amino acid residues of the native enzyme (AAW11513) of Thermotoga
                                                                                                                                                                          Claim 11; Page 128-131; 200pp;
                                                                                                                                                                                                    Thermostable DNA polymerase from Thermotoga neapolitana - DNA sequencing or for amplification of double stranded DNA
                                                                                                                                                                                                                                                              WPI; 1997-052374/05
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        sequencing and amplification reactions, e.g.
                                                                                          DNA clone pM284 (AAT58135)
                                                                                                       initiating methionine.
                                                                                                                     neapolitana.
                                                                                                                                                                                                                                                 N-PSDB; AAT58135
                                                                                                                                                                                                                                                                                          Slater MR,
                                                                                                                                                                                                                                                                                                       Bolchakova E,
                                                                                                                                                                                                                                                                                                                                 (PROM-) PROMISIA CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                 19-DEC-1996
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                                                                                                                                                                                                                                                                                        Storts DR;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                  The natural
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                                                                                                                                                                                                                                                                                                     Hartnett JR,
                                                                                                                                                                                                                                                                                                                                                           96US-0656664
95US-0484661
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "residues 1-14 comprise the C-terminal
end of the Tne 5'-exonuclease domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label= Polymerisation_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label= 5'~Exonuclease_domain
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90.9%;
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                                                                                                     ally-occurring Met-284 residue becomes the The mutant enzyme is obtd. by expression of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
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Pred. No. 0.27;
                                                                                                                                                                                                                                                                                                     Huang F,
                                                                                                                                                                          English.
                                                                                                                                                                                                     of double stranded DNA
                                                                                                                                                                                                                                                                                                     Miller KM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 19;
           PCR.
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                                                                                                                                                                                                                    useful in
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Дb

Query Match

DB 18; Length 610;

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RESULT 13
AAW11515
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Best Local
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                       DNA polymerase mutant The M284(D323E) (AAW11515) lacks the N-terminal 283 amino acid residues of the native enzyme (AAW11513) of Thermotoga neapolitana and contains a D323E substn. In the 3' exonuclease domain (numbering according to the native enzyme). It is obtd. by expression of a DNA clone (AAT58136) created by site-directed mutagenesis of construct pM284 (see also AAT58135). The M284(D323E) has no significant 5' or 3' exonuclease activity and has a half-life at 97.5 deg c of 12.5 min compared with 5 min for native The and 8 min for native Taq. It can be used in DNA sequencing reactions and for the amplification of double stranded DNA.
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                                                                                                                                                                                                   Thermostable DNA polymerase from Thermotoga neapolitana - useful DNA sequencing or for amplification of double stranded DNA \,
                                                                                                                                                                                                                                                                                    Bolchakova E, Hartnett JR, Slater MR, Storts DR;
                                                                                                                                                                                                                                                                                                                                                                                            07-JUN-1996;
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07-JUL; 1995;
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Sequence
                                                                                                                                                                                                                                                                                                                          (PROM-) PROMEGA CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   458 LSVRLGIPVKE 468
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                                                                                                                                                                          Page 138-140; 200pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 chain
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95US-0484661.
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DNA sequencing; amplification; PCR;
reaction; exonuclease; Thermotoga neapolitana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "the D323E substn. corresponds to amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label= Polymerisation_domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .610
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      " 5'-Exonuclease_domain
"residues 1-14 comprise the C-terminal
end of the Tne 5'-exonuclease domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 acid position 40 in the mutant enzyme
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Pred. No. 0.27;
                                                                                                                                                                                                                                                                                                Huang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                hti
                                                                                                                                                                                                                                                                                                Miller KM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 610
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610 AA;

Sequence

610 AA;

XX Ld YX VG

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RESULT 14
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Matches
                               mutagenesis of construct pM284 (see also AAT58135). The M284 (H325D) has no significant 5' or 3' exonuclease activity and has a half-life at 97.5 deg C of 5 min (unchanged from the native enzyme).
                                                                                                 DNA polymerase mutant The M284(D325D) (AAW11516) lacks the N-torminal 283 amino acid residues of the native enzyme (AAW11513) of 'Phormotoga neapolitana and contains a E325D substn. in the 3' exonuclease domain (numbering according to the native enzyme). It is obtd. by expression of a DNA clone (AAW58137) created by site-directed
                                                                                                                                                                                                                               Claim 11; Page 142-144; 200pp; English.
                                                                                                                                                                                                                                                                                DNA
                                                                                                                                                                                                                                                                                                                                                                                                                          Bolchakova E,
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It can be used in DNA sequencing amplification of double stranded
                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAT58137
                                                                                                                                                                                                                                                                                                                                                                                                        Slater
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (PROME) PROMEGA CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                07-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Thermotoga neapolitana DNA polymerase Tne M284(E325D) mutant.
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                                                                                                                                                                                                                                                                                           Thermostable DNA polymerase from Thermotoga neapolitana - useful in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             thermostability;
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nes 10; Conserv
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                                                                                                                                                                                                                                                                            sequencing or for amplification of double
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                                                                                                                                                                                                                                                                                                                                                                                                        MR,
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                                                                                                                                                                                                                                                                                                                                                                                                      Storts DE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                            Barrnett Jk.
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95US-0484661
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label- 5'-Exonuclease_domain
/note= "residues 1-14 comprise the C-terminal end of the The 5'-exonuclease domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            200..610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label= Polymerisation_domain
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DNA sequencing; amplification; Pound
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "the E325D substn. corresponds to amino acid position 42 in the mutant enzyme"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3'-Exonuclease_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 47; DB Pred. No. 0.27 0; Mismatches
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reactions
DNA.
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RESULT 15
AAW11517
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Best Local Similarity
                        DNA polymerase mutant The M284(Y464F) (AAW11517) lacks the N-terminal 283 amino acid residues of the native enzyme (AAW11513) of Thermotoga neapolitana and contains a Y464F substn. in the 3' exonuclease domain (numbering according to the native enzyme). It is obtd. by expression of a DNA clone (AAF58138) created by site-directed mutagenesis of construct pM284 (see also AAM788135). The M284(Y464F) has no significant 5' exonuclease activity and only 1.9% of the native 3' exonuclease activity. Its half-life at 97.5 deg C is 16 min compared with 5 min for native The and 8 min for native Taq. It can be used in DNA sequencing reactions and for the amplification of double stranded DNA.
                                                                                                                                                                                                                                                                                                                                                                                          31-MAY-1996;
07-JUN-1995;
                                                                                                                                                                                                                                                                             WPI; 1997-052374/05.
N-PSDB; AAT58138.
                                                                                                                                                                                                                                                                                                                      Bolchakova E, Hartnet Slater MR, Storts DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW11517 standard; Protein; 610 AA
Sequence
                                                                                                                                                                                                    Claim 11; Page 147-149; 200pp; English.
                                                                                                                                                                                                                                 Thermostable DNA polymerase from Thermotoga neapolitana – useful DNA sequencing or for amplification of double stranded DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA polymerase; Tne; thermostable enzyme; protein engineering; thermostability; DNA sequencing; amplification; PCR;
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 610 AA;
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                                                                                                                                                                                                                                                                                                                                   Hartnett JR,
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95US-0484661.
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/note= "residues 1-14 comprise the C-terminal
end of the Tne 5'-exonuclease domain"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label= 3'-Exonuclease_domain
/note=."The Y464F substn. corresponds to amino
acid position 181 in the mutant enzyme"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label= Polymerisation_domain
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Query Match 95.9%; Score 47; DB 18; Length 610; Best Local Similarity 90.9%; Pred. No. 0.27; Matches 10; Conservative 0; Mismatches 1; Indels 0; Caps Oy 1 LSVRIGXPVKE 11
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Db 458 LSVRLGIPVKE 468

Search completed: January 15, 2003, 11:20:17 Job time: 29.2857 secs

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Perfect score:
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49
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110:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
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: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
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1: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
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/cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
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US-09-891-332A-3

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US-09-891-332A-6

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US-09-891-332A-9

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                                  US-09-741-664-2

US-10-053-632-4

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US-09-823-649A-15
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Sequence 5, Appli
sequence 16, Appl
sequence 17, Appli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 5, Application US/09823649A Patent No. US20020012970A1
                                                                                                                                   Matches
                                                                                                                                                     Query Match
Best Local
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APPLICANT: Gelfand, David
APPLICANT: Higuchi, Russell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
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                                                                                                                                                                                                                                 NAME/KEY: VARIANT LOCATION: (7)...(7)
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Schoenbrunner, Nancy
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61.2	61.2	61.2	61.2	61.2	61.2	61.2	61.2	63.3	63.3	63.3	63.3	63.3	63.3	63.3	65.3	69.4	69.4	73.5		83.7	83.7	83.7	83.7	83.7	83.7
471	471	408	403	390	301	102	95	259	259	250	189	159	114	96	319	676	666	30	610	<u> </u> 1	11	<u></u> 1	11	11	<u>بــر</u>
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Sequence 4, Appli	21,	Sequence 6, Appli	Sequence 6217, Ap	Sequence 11146, A		Sequence 189, App	Sequence 266, App	e 11	Sequence 3, Appli	Sequence 6, Appli	Sequence 130, App	Sequence 954, App	Sequence 74, Appl	Sequence 952, App	\circ				10,	17,	16,	<u>, , , , , , , , , , , , , , , , , , , </u>		ÇT,	Sequence 4, Appli

ALIGNMENTS

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; OTHER INFORMATION: X is V US-09-823-649A-5
                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn version 3.0 SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: HIGH TEMPERATURE REVERSE TRANSCRIPTION USING MUTANT DNA POLYME FILE REFERENCE: RPA1006 CURRENT APPLICATION NUMBER: US/09/823,649A CURRENT FILING DATE: 2001-03-30
                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 60/198,336 PRIOR FILING DATE: 2000-04-18
                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ 1D NOS: 21
                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: sequence motif
1 LSVRLGXPVKE 11
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1 LSVRLGXPVKE 11
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                                                                            Conservative
                                                                                         95.9%; Score 47;
100.0%; Pred. No.
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RESULT 4
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Sequence 4, Application US/09891332A Patent No. US20020168646A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/823,649A
CURRENT FILING DATE: 2001-03-50
PRIOR APPLICATION NUMBER: US 60/198,336
PRIOR FILING DATE: 2000-04-18
NUMBER OF SEQ LD NOS: 21
SOFTMARE: Patentin version 3.0
SEQ LD NO 16
SECTION 15
                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 95.9%;
Best Local Similarity 90.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 21
SOFTWARE: PatentIn version 3.0
SEQ ID NO 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 15, Application US/09823649A Patent No. US20020012970A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Patent No. US20020012970A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 16, Application US/09823649A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/823,649A CURRENT FILING DATE: 2001-03-30 PRIOR APPLICATION NUMBER: US 60/198,336 PRIOR FILING DATE: 2000-04-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: HIGH TEMPERATURE REVERSE TRANSCRIPTION USING MUTANT DNA POLYMERAS FILE REF GRENCE: RPA1006
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: HIGH TEMPERATURE REVERSE TRANSCRIPTION USING MUTANT DNA POLYMERAS FILE REFERENCE: RPA1006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Myers, Thomas
APPLICANT: Schoenbrunner, Nancy
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                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Thermotoga neapolitana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT ORGANISM: Thermotoga maritima
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                                                                                                                                                                                                   Local Similarity nes 10; Conserva
                                                                                                                                                  1 LSVRLGXPVKE 11
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Gelfand, David
Higuchi, Russell
Myers, Thomas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wang, Alice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Schoenbrunner, Nancy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gelfand, David
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                                                                                                                                                                                                                    95.9%; Score 47; DB 10; Length 11; 90.9%; Pred. No. 0.00037;
                                                                                                                                                                                                     0;
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Pred. No. 0.00037;
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RESULT 5
US-09-891-332A-3
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ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                      Solus, Joseph
Yang, Shuwei
TITLE OF INVENTION: Polymerases for Analyzing or Typing Polymorphic
Nucleic Acid Fragments and Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32.893
REFERENCE/DOCKET NUMBER: 0942.4250002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2540
TELEPAA: 202-371-2540
                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 New York Ave., N.W., Suite 600
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                      Application US/09891332A
                                                                           COUNTRY: USA
                                                                                               STATE: DC
                                                                                                               CITY: Washington
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APPLICATION NUMBER: US 60/037,393 FILING DATE: 07-FEB-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/09/891,332A
FILING DATE: 27-Jun-2001
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STREET: 1100 New York Ave., N.W., Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: not relevant
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                                                                                                                                                                                                                                                                                                                    Chatterjee, Deb K.
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90.9%;
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Pred. No. 0.034;
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1; Indels Length 708;

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US-09-891-332A-5
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                                             APPLICATION NUMBER: US 60/037,393
FILING DATE: 07-FEB-1997
AUTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                         ZIP: 20005-3934

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                       PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Polymerases for Analyzing or Typing Polymorphic Nucleic Acid Fragments and Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 0942.4250002 TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Chatterjee, Deb K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 677 amino acids
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                                                                                                            APPLICATION NUMBER: 09/019,160 FILING DATE: <Unknown>
                                                                                                                                                                              CLASSIFICATION: <Unknown>
                                                                                                                                                                                                  APPLICATION NUMBER: US/09/891,332A FILING DATE: 27-Jun-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C STREET: 1100 New York Ave., N.W., Suite 600
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APPLICATION NUMBER: US 60/037,393
FILING DATE: 07-FEB-1997
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SOFTWARE: Patentin Release #1.0, Version #1.30
      REGISTRATION NUMBER: 32,893
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TELEFAX: 202-371-2540
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                                                                                                                                                                                                                                                                                                                                                                                                  USA
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Pred. No. 0.038;
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                                          US-09-891-332A-2
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    Query Match
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                                                                                                                                                                                                             TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS:
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                                                          MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 07-FEB-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Polymerases for Analyzing or Typing Polymorphic Nucleic Acid Fragments and Uses Thereof
                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Chatterjee, Deb K.
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                                                                                                                                                                                                                                                                                                   NAME: Esmond, Robert W. REGISTRATION NUMBER: 32,893 REFERENCE/DOCKET NUMBER: 094
                                                                                                                                                TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: < 05known >
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/09/891,332A FILING DATE: 27-Jun-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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STREET: 1100 New York Ave., N.W., Suite 600
                                                                                                        TOPOLOGY: not relevant
                                                                                                                            STRANDEDNESS: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 60/037,393
                                                                                                                                                                                                                                                                                                                                                                                                                                    FILLING DAFFE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPELICATION NUMBER: 09/019,160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.30
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TELEFAX: 202-371-2540
                                                                                                                                                                     LENGTH: 893 amino acids
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90.9%;
  95.9%;
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  Score 47;
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DB 9;
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Length 893;

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Matches

RESULT 8

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US-09-891-332A-7
; Sequence 7, Application US/09891332A
; Patent No. US20020168646A1
; GENERAL INFORMATION:
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SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION TOTAL
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MEDIUM TYPE: Floppy disk
            APPLICANT: Chatterjee, Deb K. Solus, Joseph
                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: not relevant
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
STREET: 1100 New York Ave., N.W., Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Polymerases for Analyzing or Typing Polymorphic Nucleic Acid Fragments and Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION: TELEPHONE: 202-371-2600
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FILING DATE: <UDKNOWN>
APPLICATION NUMBER: US 60/037,393
FILING DATE: 07-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/09/891,332A FILING DATE: 27-Jun-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: <Unknown>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 893 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 20005-3934
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90.9%;
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0; Mismatches
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US-09-891-332A-8
                                                                                                                                                                                                                                                                                                                                            Sequence 8, Application US/09891332A Patent No. US20020168646A1 GENERAL INFORMATION:
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 LSVRLGXPVKE 11
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-INOS/MS-DOS
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ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 New York Ave., N.W., Suite 600
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TITLE OF INVENTION: Polymerases for Analyzing or Typing Polymorphic
Nucleic Acid Fragments and Uses Thereof
                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                     TITLE OF INVENTION: Polymerases for Analyzing or Typing Polymorphic Nucleic Acid Fragments and Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
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TELEPHONE: 202-371-2600
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                                                                                                                                                                                                                                                                                                                         APPLICANT: Chatterjee, Deb K.
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                                                                                COUNTRY: USA
ZIP: 20005-3934
                                                                                                                                                           ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C STREET: 1100 New York Ave., N.W., Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS: not relevant TOPOLOGY: not relevant
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FILING DATE: <UDKNOWN>
APPLICATION NUMBER: US 60/037,393
FILING DATE: 07-FEB-1997
                                                                                                                            STATE: DC
                                                                                                                                             CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Esmond, Robert W. REGISTRATION NUMBER: 32,893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
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FILING DATE: 27-Jun-2001
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                                                                                                                                                                                                                                                                                                         Joseph
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US-09-891-332A-8
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Best Local Similarity
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FELEPHONE: 202-371-2500
FELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 8:
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                                                        ATTORNEY/AGENT INFORMATION: NAME: Esmond, Robert W
                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/019,160
FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                  ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yang, Shuwei
TITLE OF INVENTION: Polymerases for Analyzing or Typing Polymorphic
Nucleic Acid Fragments and Uses Thereof
     TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: protein
SIQUENCE DESCRIPTION: SEQ ID NO: 8:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Chatterjee, Deb K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10;
                   NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 0942.4250002
                                                                                                                                                                                                        APPLICATION NUMBER: US/09/891,332A FILING DATE: 27-Jun-2001
                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/09/891,332A FILING DATE: 27-Jun-2001 CLASSIFICATION: <Unknown>
                                                                                             APPLICATION NUMBER: US 60/037,393 FILING DATE: 07-FEB-1997
                                                                                                                                                                                         CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                              STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C STREET: 1100 New York Ave., N.W., Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Esmond, Robert W. REGISTRATION NUMBER: 32,893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 60/037,393 FILING DATE: 07-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 0942.4250002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 09/019,160
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90.9%;
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Pred. No. 0.052;
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US-09-741-664-1
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Patent No. US20010041334A1
PRINTERAL INFORMATION:
                                                                                           Best
                                                                          Matches
                                                                                                             Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: kashtchian, Ayoub
APPLICANT: Solus, Joseph
TITLE OF INVENTION: Scable Compositions for Nucleic Acid
TITLE OF INVENTION: Sequencing and Amplification
NUMBER OF SEQUENCES: 2
                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION
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741 LSVRLGIPVKE 751
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                                                                                                                                                                                   STRANDEDNESS:
                                                                                         Local Similarity
                                                                                                                                                                                                                        LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE:
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
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                                   1 LSVRLGXPVKE 11
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                                                                                                                                                                                                                      893 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
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                                                                        Conservative
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                                                                                                                                                                   linear
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                                                                                       95.98;
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                                                                                                                                                                                                                                                                                                                                                   32,893
                                                                      0; Mismatches
                                                                                       Score 47; DB 10; Length 893; Pred. No. 0.052;
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                                                                      Indels
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Matches

RESULT 13 US-09-741-664-2

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US-10-053-632-4
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Patent No. US20010041334A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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Patent No. US20020095560A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                       APPLICANT: Sigua, Chris
APPLICANT: Myers, Thomas
TITLE OF INVENTION: THEMOSTABLE DNA PLOYMERASES INCORPORATING NUCLEOTIDE TRIPHOSPHAN
TITLE OF INVENTION: LABELED WITH FLUORESCEIN FAMILY DYES
TILE REFERENCE: 1803-339-999
CURRENT APPLICATION NUMBER: US/10/053,632
CURRENT FILING DATE: 2002-01-17
                                                                                                                                                                       APPLICANT: Gelfand, David
APPLICANT: Kalman, Lisa
APPLICANT: Reichert, Fred
APPLICANT: Sigua, Chris
  NUMBER OF SEQ ID NOS: 18 SOFTWARE: PatentIn versi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 202-371-2540 INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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APPLICANT: Solus, Joseph
TITLE OF INVENTION: Stable Compositions for Nucleic Acid
TITLE OF INVENTION: Sequencing and Amplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
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NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 09
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CORRESPONDENCE ADDRESS:
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APPLICATION NUMBER:
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STRANDEDNESS: single
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Local Similarity 90.9%;
les 10; Conservative
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                                                                                                                                                                                              Reichert, Fred
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version 3.0
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Pred. No. 0.052; 
0; Mismatches 1; Indels
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Query Match
Best Local Similarity
Thanks 9; Conserve
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Search completed: January 15, 2003, 12:39:51 Job time: 10.8571 secs
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                                                                                                                                                                                                                  ; INCAPTON: (4)...(4) ; OTHER INFORMATION: Xud at position 4 is any amino acid US-10-053-632-5
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Patent No. US20020095560A1
GENERAL INFORMATION:
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Best Local Similarity
Matches 10; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT FILING DATE: 2002-01-17
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE: 1803-329-999 CURRENT APPLICATION NUMBER: US/10/053,632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: THERMOSTABLE DNA PLOYMERASES INCORPORATING NUCLECTIDE TRIPHOSP
TITLE OF INVENTION: LABELED WITH FLUORESCEIN FAMILY DYES
                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Description of Artificial Se
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OTHER INFORMATION: Xaa at position 4 is any amino acid except glutamic acid resid NAME/KEY: VARIANT
                                                                                                                                                                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                        NAME/KEY: VARIANT
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                                                                      1 LSVXLGVPVKE 11
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Myers, Thomas
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                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                        Description of Artificial Sequence:
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Pred. No.
                                                                                                                                                           Score 41; DB 12; Pred. No. 0.0068;
                                                                                                                                              Mismatches
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Sequence:

on:

35, Appl

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                 Score
   BLOSUM62
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   Issued_Patents_AA:*
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/ACTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/backfiles1.pep:*
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   US-08-537-400-16
US-08-706-702-18
US-08-706-702-18
US-08-706-706-13
US-08-444-661A-39
US-08-484-661A-37
US-08-656-664-37
US-08-656-664-11
US-08-484-661A-11
US-08-484-661A-11
US-08-484-661A-11
US-08-484-661A-16
US-08-484-661A-26
US-08-484-661A-33
US-08-484-661A-33
US-08-484-661A-33
US-08-484-661A-33
US-08-656-664-8
US-08-656-664-23
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(without alignments)
34.855 Million cell updates/sec
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 8, Appli
16, Appli
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37, Appl
37, Appl
11, Appl
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  Query Match
Best Local Similarity
Watches 10; Conserve
                                                   ; MOLECULE TYPE: protein US-08-537-400-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 16, Application US/08537400
; Patent No. 5939301
                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/316,423
FILING DATE: 30-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/370,190
FILING DATE: 09-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: ESMOOT, ROBERT W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                   INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 230 amino acids
                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/537,400 FILING DATE: 02-OCT-1995 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                           TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
                                                                                                                                                           REGISTRATION NUMBER: 32,893 REFERENCE/DOCKET NUMBER: 09
                                                                                                                                                                                                                                                                                                                                                                                            CITY: Washington
                                                                         TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                   STATE:
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PCT-US96-09641-16
PCT-US96-09641-29
PCT-US96-09641-29
PCT-US96-09641-29
PCT-US96-09641-39
PCT-US96-09641-39
PCT-US96-09641-39
PCT-US96-09641-39
PCT-US96-09641-34
US-09-019-160-5
US-09-019-160-5
US-08-458-819-4
US-08-458-819-4
US-08-706-702-3
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US-08-656-664-54
US-09-019-160-4
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        Score 47; DB 2; Pred. No. 0.012; 0; Mismatches
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                              Length 230;
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Sequence 16, Appli
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Sequence 23, Appl
Sequence 24, Appl
Sequence 29, Appl
Sequence 33, Appl
Sequence 35, Appl
Sequence 34, Appli
Sequence 54, Appli
Sequence 4, Appli
Sequence 4, Appli
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WS-08-706-706-18

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Sequence 18, Application US/08706706

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US-08-706-702-18
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                 MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk
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APPLICATION NUMBER:
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APPLICATION NUMBER:
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APPLICATION NUMBER:
                                                                                             78
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                                                                                                                                                                                                                                                                     TYPE:
                                                                                                                                                                                                                                                                                                                                                 TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                              NAME: Esmond, Robert W
REGISTRATION NUMBER: 32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version #1.30
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                                                                                                            1 LSVRLGXPVKE 11
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                                                                                            LSVRLGIPVKE 88
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                                                                                                                                                                                                                                                                                   230 amino acids
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                                                                                                                                                                        95.9%;
90.9%;
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                                                                                                                                                                        Score 47; DB 2;
Pred. No. 0.012;
                                                                                                                                                         Mismatches
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US-08-484-661A-39
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                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 08-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Hughes, A. John
APPLICANT: Chatterjee, Deb K.
TITLE OF INVENTION: Cloned DNA Polymerases from Thermotoga and
NUMBER OF SEQUENCES: 26
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                                                                78 LSVRLGIPVKE 88
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & STREET: 1100 New York Ave., N.W., Suite
                                                                                              1 LSVRLGXPVKE 11
                                                                                                                                               Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                              l Similarity
10; Conserv
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                                                                                                                                                                                                                                            amino acid
                                                                                                                                                                                                                                                                                                                                                                                        Esmond, Robert W.
                                                                                                                                                                                                                                                        230 amino acros
                                                                                                                                                                                                                                                                                                            202-371-2540
                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
                                                                                                                                                                                                                              linear
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                                                                                                                                                                                                             protein
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                                                                                                                                            95.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US 08/537,397
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                                                                                                                              0;
                                                                                                                                          Score 47; DB 3;
Pred. No. 0.012;
                                                                                                                              Mismatches
                                                                                                                                                           Length 230;
                                                                                                                            Indels
                                                                                                                            0;
                                                                                                                           Gaps
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Sequence 39, Application US/08484661A Patent No. 6001645
GENERAL INFORMATION:

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APPLICANT:

SLATER, MICHAEL R. HARTNETT, JAMES R.

0;

Gaps

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US-08-656-664-39
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                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 39, Application US/08656664 Patent No. 6077664
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                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: HUANG, FEN
APPLICANT: BOLCHAKOYA
TITLE OF INVENTION: W
TITLE OF INVENTION: F
NUMBER OF SEQUENCES:
                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: PRITELECOMMUNICATION INFORMATION: TELEPHONE: (415) 705-8410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
ATTOLNEY/AGENT INFORMATION:
NAME: INGOLIA, DIANE E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                          TITLE OF INVENTION: THERMOPHILIC DNA POLYMERASES FROM TITLE OF INVENTION: THERMOTOGA NEAPOLITANA
                                                                                                                                                                                                                                                                                                               APPLICANT:
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                APPLICATION NUMBER:
                                                                                                                                        ZIP: 94104
                                                                                                                                                    COUNTRY:
                                                                                                                                                                      STATE:
                                                                                                                                                                                       CITY: San Francisco
                                                                                                                                                                                                     ADDRESSEE: Medlen & Carroll STREET: 220 Montgomery Street,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity nes 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 40,027
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
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amino acid
GY: linear . . .
                                                                                                                                                                      California
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                                                                                                                                                                                                                                                                                                             Otto, Paul
                                                                                                                                                                                                                                                                                                                             Storts,
                                                                                                                                                                                                                                                                                                                                          Bolchakova, Elena
                                                                                                                                                                                                                                                                                                                                                              Hartnett, James R.
                                                                                                                                                                                                                                                                                                                                                                                Huang,
                                                                                                                                                                                                                                                                                                                                                                                              Slater, Michael R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BOLCHAKOVA, ELENA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              UNITED STATES OF AMERICA
                                                                                                                                                    United States Of America
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                                                                                                                                                                                                                                                                                                                           Douglas R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MODIFIED THERMOPHILIC DNA POLYMERASES FROM THERMOTOGA NEAPOLITANA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95.9%; Score 47; DB 3; 90.9%; Pred. No. 0.029;
              US/08/656,664
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                                                                                                                                                                                                         Suite 2200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 3; Length 494;
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95.9%;
Bost Local Similarity 90.9%;
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                   TELEFAX: (415) 397-83: INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (415) 397-83 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
                                                                                       TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                           NAME: Inquila, Diane E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Slater, Michael R. APPLICANT: Huang, Pen APPLICANT: Hartnett, James R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     THILE OF INVENTION: THERMOPHILIC DNA POLYMI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                 NAME: Inquila, Diane E.
REGISTRATION NUMBER: 40,027
                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 31 CLASSIFICATION:
                                                                                                                                               LENGTH:
                                                                                                                                                                                                                      TELEPHONE:
                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE:
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                                                                                                                             amino acid
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                                                                                                                                               494 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                220 Montgomery Street, Suite 2200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                United States Of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Otto,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Storts, Douglas R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hartnett, James R. Bolchakova, Elena
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                                                                                                                                                                                                                                                                                                                                                                                                        SYSTEM: PC-BOS/MS DOS
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                                                                                                                                                                                                                    (415) 705-8410
                                                                                                                                                                                                                                                                                                                                                                                                                                          Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Paul
                                                                                                                                                                                                    397-8338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95.9%; Score 47; DB 3;
90.9%; Pred. No. 0.029;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       THERMOPHILIC DNA POLYMERASES FROM
                                                                                                                                                                                                                                                                                                                                                            PCT/US96/09641
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•
       0; Mismatches
                         Score 47; DB 5;
Pred. No. 0.029;
                                                                                                                                                                                                                                                        PRMG-02185
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       1; Indels
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Matches

RESULT 5

1 LSVRLGXPVKE 11

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US-08-656-664-37
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                                                                                                                                                                                                                                       RESULT 8
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US-08-484-661A-37
                                                                                                                                                                                                    Sequence 37,
                                                                                                                                                                                    Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Despuence 37, Application US/08484661A Patent No. 6001645
                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (415) 397-8338 INFORMATION FOR SEQ ID NO: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                          APPLICANT: Otto, Paul
TITLE OF INVENTION: THERMOPHILIC DNA POLYMERASES FROM
TITLE OF INVENTION: THERMOTOGA NEAPOLITIANA
                                                                                                  APPLICANT:
                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 571 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: PR
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
                                                                                                                                   APPLICANT:
                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: INGOLIA, DIANE E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: MEDLEN & CARROLL
CORRESPONDENCE ADDRESS:
                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: MODIFIED THERMOPHILIC DNA PTITLE OF INVENTION: FROM THERMOTOGA NEAPOLITIANA
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                                                                                                                                                                                                                                                                                       419 LSVRLGIPVKE 429
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                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                       1 LSVRLGXPVKE 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: FILING DATE: 07-JUN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1: 220 MONTGOMERY STREET, SUITE 2200 SAN FRANCISCO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CALIFORNIA
                                                                                                                                                                                                   Application US/08656664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      571 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HARTNETT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SLATER, MICHAEL R. HARTNETT, JAMES R.
                                                                               Storts, Douglas R.
                                                                                                Bolchakova,
                                                                                                                  Hartnett, James R.
                                                                                                                                  Huang, Fen
                                                                                                                                                 Slater, Michael R.
                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 UNITED STATES OF AMERICA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BOLCHAKOVA, ELENA
                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
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                                                                                                                                                                                                                                                                                                                                                                        95.9%;
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                                                                                                  Elena
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                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                      Score 47; DB 3; Pred. No. 0.034;
                                                                                                                                                                                                                                                                                                                                                      1; Indels
                                                                                                                                                                                                                                                                                                                                                                                        Length 571;
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                                                                                                                                                                                                                                                                    STATE:
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PCT-US96-09641-37
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; MOLECULE TYPE: protein
US-08-656-664-37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (415) 397-833
            ATTORNEY/AGENT INFORMATION:
NAME: Ingolia, Diame E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: PRI
                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDITIM TYPE: Floppy disk
TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: THERMOPOLIC DNA POLYMERASES FROM TUTLE OF INVENTION: THERMOPOLO NEAPOLITANA NUMBER OF SEQUENCES: 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 571 amino acids
                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: ofto, Paul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    419 LSVRLGIPVKE 429
                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                     APPLICATION NUMBER: FILING DATE: 31-MA
                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                 COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: FILING DATE: 31-MAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 LSVRIGXPVKE 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10; Conservative
                                                                                                                                                                                                                                                  94104
                                                                                                                                                                                                                                                                                                  San Francisco
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                                                                                                                                                                                                                                                        California
: United States Of America
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                                                                                                                                                                                                                                                                                                           E: Medlen & Carroll
220 Montgomery Street, Suite 2200
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Bolchakova, Bjena
Storts, Douglas R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Buang, Fen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hartnett, James R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         United States Of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              slater,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PatentIn Release #1.0, Version #1.30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31-MAY-1996
                                                                                                     31-MAY-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Michael R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US/08/656,664
                                                                                                                     PCT/US96/09641
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                PRMG-02185

 Mismatches

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Pred. No. 0.034;
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RESULT 11
US-08-656-664-11
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                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                        Query Match
Best Local :
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Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (415) 397-8338 INFORMATION FOR SEQ ID NO: 1
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                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: 1i
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LENGTH: 571 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 578 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 705-8410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: MODIFIED THERMOPHILL DNA M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: SLATER, MICHAEL R. APPLICANT: HARTNETT, JAMES R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
                                                                                                                  426 LSVRLGIPVKE 436
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        419 LSVRLGIPVKE 429
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OPERALING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Pcincip
                                                                                                                                                                     1 LSVRLGXPVKE 11
                                                                                                                                                                                                                         Local Similarity
les 10; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: INGOLIA, DIANE E. REGISTRATION NUMBER: 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/0 FILING DATE: 07-JUN-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: SAN FRANCISCO
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                                                                                                                                                                                                                                                                                                                                                                                                                     amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                         578 amino acids
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                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BOLCHAKOVA, ELENA
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                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PatentIn Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                                                                                                                         protein
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90.98;
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                                                                                                                                                                                                                                                  Score 47; DB 3; Pred. No. 0.035;
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Pred. No. 0.034;
                                                                                                                                                                                                                           Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 5;
                                                                                                                                                                                                                         1; Indels
                                                                                                                                                                                                                                                                            Length 578;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                PCT-US96-09641-11 : Sequence 11, Application PC/TUS96(9641; GENERAL INFORMATION:
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Best Local Similarity
Matches 10; Conserve
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GENERAL INFORMATION:
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APPLICANT:
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COMPUTER READABLE FORM
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APPLICANT:
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                                                                                                                                                                                                                                          TITLE OF INVENTION: THERMOPHILIC DNA POLYM
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                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   426 LSVRLGIPVKE 436
                                                                                                   ADDRESSEE: Medlen & Callul STREET: 220 Montgomery Street, Suite 2200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 31 CLASSIFICATION:
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                                                United States Of America
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; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-656-664-11
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                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                   REPERENCE/DOCKET NUMBER: 40,027
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX. (415)
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TITLE OF INVENTION: THERMOTOGA NEAPOLITANA
                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 578 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release.
                                                                                                                                                                                                                                                                                        NAME: Ingolia, Diane E. REGISTRATION NUMBER: 4(
                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/656,664
FILING DATE: 31-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              San Francisco
: California
                                                                                                                                                     578 amino acids
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     Conservative
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                     95.98;
90.98;
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                                                                                                                                                                                               11:
Score 47; DB 3; Length 578; Pred. No. 0.035; 0; Mismatches 1; Indels
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Gaps
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US-08-484-661A-8
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REGISTRATION NUMBER: 40.027
REFERENCE/POCKET NUMBER: PRWG
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEPHONE: (415) 397-8338
INFORMATION FOR SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patent No.
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Best Local Similarity
                                                                                  TELEFAX: (415) 397-83: INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                SEQUENCE CHARACTERISTICS:
LENGTH: 610 amino acid
                                                                                                                 REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: PRI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
                                                                                                                                                                                                  APPLICATION NUMBER: US/08
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
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ATTORNEY/AGENT INFORMATION:
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ADDRESSEE: MEDIEN & CARROLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: MODIFIED THERMOPHILIC DNA POLYMERASES TITLE OF INVENTION: FROM THERMOTOGA NEAPOLITANA
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MOLECULE TYPE:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                                                                                                                                                                                 STATE:
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CALIFORNIA
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                                                                                                                                                                                                                                                                                                                                                                                               UNITED STATES OF AMERICA
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protein
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Pred. No. 0.035;
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RESULT 15
US-08-484-661A-19
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US-08-484-661A-16
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                                                                                                                                                                                       Sequence 19, Application US/08484661A Patent No. 6001645 GENERAL INFORMATION:
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GENERAL INFORMATION:
GENERAL INFORMATION:
SLATER, MICHAEL R.
""""ILICANT: """"""""", JAMES R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPBRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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APPLICANT:
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ATTORNEY/AGENT INFORMATION:
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CORRESPONDENCE ADDRESS:
       APPLICANT: BOLCHAKOVA, ELENA TITLE OF INVENTION: MODIFIED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
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                                                                                                          HARTNETT,
                                                                                                              SLATER, MICHAEL R. HARTNETT, JAMES R.
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                                                                                   HUANG, FEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (415)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    705-8410
MODIFIED THERMOPHILIC DNA POLYMERASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MODIFIED THERMOPHILIC DNA POLYMERASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95.98;
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Pred. No. 0.037;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 610;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 610
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NUMBER OF SEQUENCES: 51

ADDRESSEE: ADDRESSE:
ADDRESSEE: ADDRESSEE
STREET: 220 MONTGOMERY STREET, SUITE 2200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
COMPUTER: HOME Compatible
OPERATING SYSTEM: PC-ODS/MS-DOS
SOFWARE: ADDRESSEE: OF AMERICA
COMPUTER: HOME Compatible
OPERATING SYSTEM: PC-ODS/MS-DOS
SOFWARE: ADDRESSEE: OF AMERICA
COMPUTER: HOME COMPATION
COMPUTER: HOME
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SUMMARIES

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-MODEL-frame+_D2n.model -DEV=xlh
-Q-/cgn2_1/USPTQ_spool/US09823649/runat_14012003_151001_29119/app_query.fasta_1.1393
-DB=\_Geneseq_101002 -OFMT=fastap -SUFF1X=rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -SYART=1 -END=-1 -MARIRIX=bitssum62 -TRAMS=bitman40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE-pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN-0 -MAXLEN-200000000
-USEE-US09823649 -GCGN_1_1_0_Grunat_14012003_151001_29119 -NCPU=6 -TCPU=3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARR_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Command line parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Title:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OM protein -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Xgapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
                                                                                                                                          9: /SIDS2/gcgdata/geneseq/geneseqn embl/NA1988.DAT:*
10: /SIDS2/gcgdata/geneseq/geneseqn embl/NA1989.DAT:*
11: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1990.DAT:*
12: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1991.DAT:*
12: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1991.DAT:*
13: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1992.DAT:*
14: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1993.DAT:*
15: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1994.DAT:*
16: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1995.DAT:*
17: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1996.DAT:*
18: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1997.DAT:*
18: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:*
19: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:*
20: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2000.DAT:*
21: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA20001B.DAT:*
22: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*
23: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*
23: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*
23: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N_Geneseq_101002:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-823-649A-4
50
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Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1985.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1985.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1985.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1988.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1988.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*/SIDS2/gcgdata/gcneseq/geneseqn-cmbl/NA1982.DAT:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1980.
                                                                                                                          /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*
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RESULT 1
AAQ24010
ID AAQ2
XX
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No.
                                                                                                                                                                                      5'-3'; exonuclease; PCR; amplification; SSR; sequencing; PLCR;
                                                                                                                                          Thermus species sps17.
                                                                                                                                                                                                                                                        Mutant thermostable DNA polymerase pSPSA288.
                                                                                                                                                                                                                                                                                                                    22-OCT-1992 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                             AAQ24010;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAQ24010 standard; DNA; 1635 BP
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Key old_sequence

Location/Qualifiers
1..2

SS

ALJGNMENTS

/*tag=

/note= "nucleotides 4-861 deleted from the native

Result No.	Score	Query Match	Length	DB	ID	Description
<u>, , , , , , , , , , , , , , , , , , , </u>	48	96.0	63	13	AAQ24010	Mutant thermostabl
ν	48	6.	68	13	2400	t thermosta
- ω		, 60	04		2400	t thermos
лф		۰.	υN		AAQ24007	_
יטר ער ביי	4- 4- 00 00	96.0	236/	<u>ــا د</u>	AAQ24006	thermostab
7		<u> </u>	10		AA080750	tant
œ		96.0	0	19	AAV65780	enaria - ANCI Su
9		5	4.9	20	340	DNA sequence encod
10		5	51	16	AAQ92369	Tfil DNA-polymeras
11	48		94	16	AAQ86927	17 polymerase
12	45		1600	16	AAQ80745	
سز د س	. A. IU I	90.0	1600	17	AAT27686	tant Thermus ac
ı ⊩	• # U		1600	~	AAT70347	
1 1	e al≏		1600	8	AAT76647	D.
17	Σ L	> 0	1600	2 L	AAV65786	Thermus aquaticus
18	4 5	9	1600	20	AAV63407	ന
19	45	C	1635	13	AAQ23998	Mutant thermostabl
20	. #A I UI	C	1635	34 33	AAQ24322	thermostab
2	. <u>,</u> 4	0	1635	13	AAQ24328	thermostab
2 2	4 4 U U	90.0	1682	2 K	AAZ29450	stabl
2	4.5	= :	783	2 6	AA9/47061	Taq
25	45	0	1686	20	AAX27130	FY2 polymerase and
26	45	0	1686	20	AAX27132	polymerase
27	· .4	0	1689	1.8	AAT47960	ant
200	A 4 7 U	o	1689	2 6	AAX27131	ymerase co
30	4.5	0 9	1794	7	AAP32327	Thermostable DNA Q
3	45	0	1794	17	AAT 27255	DNA DOLVERAGE DNA
32		С.	1812	22	AAS00717	eric CauTao
ى ر <u>ر</u> - ر		0	1812	22	071	CauTaq
א את	лu	٥.c	1000 968T	بار د نب د	399	hermosta
36	₽	90.0	1899	<u></u> ر	AA024321	
37	45	0	1899	24	81	Sulfolobus solfata
, ω ο α	, A	0	1904	24	8	acidoc
يا د ک د	n U	0	1965	24	482	(PL) -
C	n U	> <	2043	سر د	2399	he
S AP	э¢	2 0	2043	نب د	432	thermostab
- 12 - 12 - 13	4	20.0	2043	 	AAQ24326	Mutant thermostabl
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4	A 4 J (J	3 :	1.7(.(AAQ23994	
4 4 2 2	4 4 4 3 5 5	# 6 E	2277		A6023994 AA024013 Aa174325	Mutane Chemioscapi